

	107653	AA010210	Hs.47041	ESTs	0.073
	104798	AA029462	Hs.17235	ESTs	0.073
	134082	L16991	Hs.79006	deoxythymidylate kinase	0.073
5	119180	R80413	Hs.92520	ESTs	0.073
	107741	AA016982	Hs.64341	ESTs	0.073
	133683	AA335223	Hs.75558	pepsinogen 5; group I (pepsinogen A)	0.073
	111694	R22035	Hs.23331	ESTs	0.073
	120764	AA338729	Hs.133096	ESTs	0.073
10	119389	T88826	Hs.90973	ESTs	0.074
	100929	HG688-HT688		Major Histocompatibility Complex, Class II, Dr Beta 2 (Gb:X65561)	0.074
	119388	T88798		plasminogen activator inhibitor; type I	0.074
	133019	AF009674	Hs.184434	axin	0.074
	105185	AA191495	Hs.189937	ESTs	0.074
15	133413	S72043	Hs.73133	metallothionein 3 (growth inhibitory factor (neurotrophic))	0.074
	101017	J04599	Hs.821	biglycan	0.074
	132865	K02765	Hs.251972	complement component 3	0.074
	110882	N36001	Hs.17348	ESTs; Wkly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	0.074
	129197	T90303	Hs.109308	ESTs; Wkly smlr to leucine-rich glioma-inactivated prot precursor [H.sapiens]	0.074
20	101184	L19871	Hs.460	activating transcription factor 3	0.075
	134910	AA431320	Hs.9100	ESTs	0.075
	119411	T96621	Hs.203656	EST	0.075
	102000	U01824	Hs.380	solute carrier family 1 (glial high affinity glutamate transporter); member 2	0.075
	114691	AA121893	Hs.103779	ESTs; Weakly similar to envelope protein [H.sapiens]	0.075
25	134179	U53204	Hs.79706	plectin 1; intermediate filament binding protein; 500kD	0.075
	134503	U34880	Hs.84183	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1	0.075
	129719	N66396	Hs.167766	ESTs; Moderately similar to Pro-a2(XI) [H.sapiens]	0.075
	113916	W80464	Hs.31928	ESTs; Wkly smlr to alternatively spliced product using exon 13A [H.sapiens]	0.075
30	113897	W73926	Hs.4947	ESTs	0.075
	129697	R00841	Hs.172069	DKFZP434C212 protein	0.075
	112078	R44155	Hs.112218	ESTs	0.075
	121980	AA429886	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk173c12.5 [C.elegans]	0.075
	100898	HG4638-HT5050		Spliceosomal Protein Sap 49	0.075
35	121626	AA416974	Hs.98174	ESTs	0.075
	133670	AA243416	Hs.75470	hypothetical protein; expressed in osteoblast	0.075
	131879	AA017161	Hs.33792	ESTs	0.075
	100254	D38037	Hs.77643	FK506-binding protein 1B (12.6 kD)	0.075
	133194	AA291726	Hs.67201	ESTs	0.075
40	106081	AA418394	Hs.25354	ESTs	0.075
	115544	AA351433	Hs.66187	Homo sapiens clone 23700 mRNA sequence	0.076
	119955	W87460	Hs.58989	ESTs	0.076
	104407	H61361	Hs.102171	immunoglobulin superfamily containing leucine-rich repeat	0.076
	135019	X58431	Hs.98428	Human Hox2.2 gene for a homeobox protein	0.076
45	114815	AA161488	Hs.103931	DKFZP434B0335 protein	0.076
	119471	W31352	Hs.55445	ESTs	0.076
	117788	N48292	Hs.46849	ESTs	0.076
	119406	T95064	Hs.193771	EST	0.076
	130777	R61742	Hs.256554	ESTs	0.076
50	130494	L13197	Hs.75874	pregnancy-associated plasma protein A	0.076
	104107	AA424111	Hs.12598	T-cell lymphoma invasion and metastasis 2	0.076
	121483	AA411981	Hs.25274	ESTs; Modly smlr to putative seven pass transmembrane prot [H.sapiens]	0.076
	104451	M13299	Hs.102119	blue cone pigment	0.076
	118027	N52770	Hs.75968	thymosin; beta 4; X chromosome	0.076
55	109419	AA227560	Hs.86987	receptor-interacting serine-threonine kinase 3	0.076
	115783	AA424487	Hs.72289	ESTs; Weakly similar to LIV-1 protein [H.sapiens]	0.076
	110585	H62223	Hs.133526	ESTs; Wkly smlr to !!ALU SUBFAMILY SB1 WARNING ENTRY !![H.sapiens]	0.076
	123165	AA488863	Hs.105216	ESTs; Weakly smlr to !!ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.077
	103966	AA303166	Hs.127270	ESTs	0.077
60	109549	F01528	Hs.21192	Homo sapiens clone 25155 mRNA sequence	0.077
	106730	AA465520	Hs.22313	ESTs	0.077
	120310	AA193676	Hs.118926	DKFZP586K0919 protein	0.077
	104078	AA402801	Hs.222010	ESTs	0.077
	117624	N35978	Hs.82364	ESTs	0.077
65	112421	R62441	Hs.23127	ESTs	0.077
	106958	AA497026	Hs.22059	ESTs	0.077
	129984	W92811	Hs.183927	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.077
	122044	AA431456	Hs.98736	EST	0.077
	123280	AA491285	Hs.175144	ESTs	0.077
	115710	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2; neutra	0.077

			I membrane (neutral sphingomyelinase)	0.077
			KIAA0255 gene product	0.077
			Homo sapiens clone 643 unknown mRNA; complete sequence	0.078
			ESTs	0.078
5	134129	D87444	interferon; gamma-inducible protein 30	0.078
	129321	AA224502	ESTs	0.078
	130513	AA460257	KIAA0296 gene product	0.078
	100996	J03909	ESTs	0.078
	128358	A1095718	ESTs; Moderately similar to KIAA0544 protein [H.sapiens]	0.078
	128544	R59352	glycine receptor; beta	0.078
10	106040	AA412681	ESTs	0.078
	106495	AA452113	even-skipped homeo box 1 (homolog of Drosophila)	0.078
	131833	R40899	ESTs; Weakly similar to sphingosine kinase [M.musculus]	0.078
	119219	R97176	ESTs	0.078
	135415	X60655	ESTs	0.078
	109457	AA232646	EST	0.078
15	117137	H96670	EST; Weakly similar to hypothetical protein [H.sapiens]	0.078
	107094	AA609614	ESTs	0.078
	130165	T90529	EST	0.078
	124072	H05252	EST; Weakly similar to hypothetical protein [H.sapiens]	0.078
	126151	AA324743	ESTs	0.078
20	119035	R01779	ESTs	0.078
	110157	H18987	ESTs	0.078
	128515	AA149044	ESTs; Highly similar to HYPOTHETICAL PROTEIN KIAA0195 [H.sapiens]	0.078
	133069	U94836	protein with polyglutamine repeat	0.078
	112209	R49644	ESTs	0.078
25	133361	R28279	Human clone 23548 mRNA sequence	0.078
	134714	U89922	lymphotoxin beta (TNF superfamily; member 3)	0.078
	129905	T86796	ESTs; Weakly similar to predicted using Genefinder [C.elegans]	0.079
	120421	AA236166	ESTs; Weakly similar to chondromodulin-I precursor [H.sapiens]	0.079
	100985	HG4490-HT4876	Proline-Rich Protein Prb4, Allele	0.079
30	102789	U86759	netrin 2 (chicken)-like	0.079
	120139	Z39273	Human DNA from chromosome 19-specific cosmid R30923; genomic sequence	0.079
	135238	U76343	Human liver GABA transport protein mRNA; 3' end	0.079
	129518	N54845	ESTs	0.079
	132960	AA609742	KIAA0521 protein	0.079
35	108751	AA127063	ESTs	0.079
	134060	D42039	KIAA0081 protein	0.079
	111338	N79778	extracellular matrix protein 2; female organ and adipocyte specific	0.079
	112345	R56880	ESTs	0.079
	126456	W00881	za56d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	0.079
40	128937	Z39939	IMAGE:296547 5', mRNA sequence.	0.079
	103485	Y08409	ESTs	0.079
	111202	N68280	thyroid hormone responsive SPOT14 (rat) homolog	0.079
	132625	AA429890	ESTs	0.079
45	103434	X98085	cisplatin resistance associated	0.079
	102616	U65581	tenascin R (restritin; janusin)	0.079
	102667	U70867	ribosomal protein L3-like	0.079
	111422	R01127	solute carrier family 21 (prostaglandin transporter); member 2	0.079
	101411	M16938	ESTs	0.079
50	113267	T65058	homeo box C6	0.08
	103559	Z19585	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.08
	131588	AA258613	thrombospondin 4	0.08
	107821	AA020991	KIAA1021 protein	0.08
	134278	H82839	ESTs	0.08
55	120893	AA369800	ESTs; Weakly similar to DY3.6 [C.elegans]	0.08
	108786	AA128999	EST; Highly similar to CMP-N-acetylneuraminic acid hydroxylase [H.sapiens]	0.08
	106890	AA489245	zo8f12.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens	0.08
	119760	W72267	cDNA clone IMAGE:567119 3', mRNA sequence	0.08
	132999	Y00787	KIAA1066 protein; JSAP1 homolog (mouse); JIP3 homolog (mouse)	0.08
60	129156	AA028195	ESTs	0.08
	121171	AA400008	interleukin 8	0.08
	103864	AA207284	dolichyl-phosphate mannosyltransferase polypeptide 2; regulatory subunit	0.08
	128591	AA255537	ESTs	0.08
	122172	AA435753	ESTs; Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]	0.08
65	112802	R97647	ESTs; Weakly similar to O-linked GlcNAc transferase [H.sapiens]	0.08
	107723	AA015967	EST	0.08
	113011	T23737	EST	0.08
	131279	AA089853	chaperonin containing TCP1; subunit 5 (epsilon)	0.081
	103190	X70083	STIP1 homology and U-Box containing protein 1	0.081
			filamin C; gamma (actin-binding protein-280)	0.081

	103956	AA292411	Hs.233348	ESTs	0.081
	112706	R89828	Hs.138493	ESTs	0.081
	126126	M85370		EST01884 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCH10, mRNA sequence.	0.081
5	130094	H43286	Hs.167017	gamma-aminobutyric acid (GABA) B receptor; 1	0.081
	100800	HG3945-HT4215		Phospholipid Transfer Protein	0.081
	108675	AA115240	Hs.61816	ESTs	0.081
	129420	AA234259	Hs.99816	ESTs	0.081
	129666	M77349	Hs.118787	transforming growth factor; beta-induced; 68kD	0.081
10	101645	M59807	Hs.943	natural killer cell transcript 4	0.081
	130536	T17045	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin)	0.081
	107732	AA016181	Hs.59752	ESTs	0.081
	123071	AA482593	Hs.104285	ESTs	0.081
	113537	T90457	Hs.191293	ESTs	0.081
15	101250	L34060	Hs.79133	cadherin 8	0.081
	122521	AA449433	Hs.149227	ESTs; Weakly similar to PROLINE-RICH PROTEIN MP-3 [M.musculus]	0.081
	133914	N32811	Hs.77542	ESTs	0.081
	102038	U05659	Hs.477	hydroxysteroid (17-beta) dehydrogenase 3	0.081
	110336	H40338	Hs.174094	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.081
20	118637	N70274	Hs.49822	ESTs	0.081
	117966	N51589	Hs.94012	ESTs	0.082
	104424	H87671	Hs.182320	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	0.082
	100361	D78361	Hs.125078	Human mRNA for ornithine decarboxylase antizyme; ORF 1 and ORF 2	0.082
	112974	T17291	Hs.101174	microtubule-associated protein tau	0.082
25	132832	D63482	Hs.57734	KIAA0148 gene product	0.082
	132039	Z39489	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31	0.082
	113272	T65383	Hs.12807	ESTs	0.082
	104924	AA058532	Hs.28774	ESTs	0.082
	111061	N58054	Hs.36859	ESTs	0.082
30	129269	R45977	Hs.163593	ribosomal protein L18a	0.082
	102453	U48437	Hs.74565	amyloid beta (A4) precursor-like protein 1	0.082
	126204	AI080388	Hs.134296	ESTs	0.082
	116615	D80666	Hs.45203	ESTs	0.082
	128856	AA219552	Hs.204144	ESTs; Modly smlr to tumor necrosis factor-alpha-induced prot B12 [H.sapiens]	0.082
35	112776	R95850	Hs.34494	ESTs	0.082
	105494	AA256273	Hs.29288	Homo sapiens mRNA; cDNA DKFZp434P174 (from clone DKFZp434P174)	0.082
	117000	H84718	Hs.112236	ESTs; Weakly similar to repressor protein [H.sapiens]	0.082
	112656	R85260	Hs.133151	transient receptor potential channel 7	0.082
	128963	J03890	Hs.1074	surfactant; pulmonary-associated protein C	0.083
40	116957	H79292	Hs.39960	ESTs	0.083
	101057	K03430		Human complement C1q B-chain gene, exon A+1	0.083
	121948	AA429452	Hs.98582	ESTs	0.083
	130822	M80647	Hs.2001	thromboxane A synthase 1 (platelet; cytochrome P450; subfamily V)	0.083
	122743	AA458674	Hs.99478	EST	0.083
45	114569	AA053316		zm2d1.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:512947 3' similar to TR:E198281 E198281 THIOREDOXIN REDUCTASE ;contains Alu repetitive element; mRNA sequence	0.083
	132270	U70671	Hs.43509	ataxin 2 related protein	0.083
	108126	AA052951	Hs.47413	ESTs	0.083
50	102880	X04325	Hs.2679	gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.083
	115365	AA282089	Hs.88599	ESTs	0.083
	114529	AA052980	Hs.206704	ESTs	0.083
	135017	AA249586	Hs.9315	ESTs; Weakly similar to NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN [H.sapiens]	0.083
55	123776	AA610071	Hs.112813	ESTs	0.083
	114454	AA021091	Hs.226208	ESTs	0.083
	101246	L33799	Hs.202097	procollagen C-endopeptidase enhancer	0.083
	107366	U78310	Hs.13501	pescadillo (zebrafish) homolog 1; containing BRCT domain	0.083
60	132779	T89601	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPORTER TYPE 5; SMALL INTESTINE [H.sapiens]	0.083
	129709	AA112209	Hs.1209	acyl-Coenzyme A dehydrogenase; long chain	0.083
	115244	AA278767	Hs.914	Human mRNA for SB classII histocompatibility antigen alpha-chain	0.083
	123253	AA490878	Hs.111334	ferritin; light polypeptide	0.083
65	128469	T23724	Hs.258677	EST	0.083
	132220	AA431847	Hs.42409	ESTs; Highly similar to CGI-146 protein [H.sapiens]	0.083
	111664	R17939	Hs.22344	ESTs	0.083
	102354	U38268		Human cytochrome b pseudogene, partial cds	0.084
	112828	R98774	Hs.194338	ESTs	0.084

5	110410	H47868	Hs.34024	ESTs	0.084
	102620	U66052		Human clone W2-6 mRNA from chromosome X	0.084
	102550	U58087	Hs.14541	culin 1	0.084
	108417	AA075716		zm89e5.s1 Stratagene ovarian cancer (#537219) H sapiens cDNA clone IMAGE:54512 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence	0.084
10	113299	T67285	Hs.13089	ESTs	0.084
	117869	N49947	Hs.46990	ESTs	0.084
	113734	T98484	Hs.18377	EST	0.084
	133325	C00424	Hs.7101	periodontal ligament fibroblast protein	0.084
	123368	AA505022	Hs.124838	ESTs	0.084
	101615	M55153	Hs.8265	transglutaminase 2 (C polypeptide; protein-glutamine -gamma-glutamyltransferase)	0.084
15	119352	T65972	Hs.193365	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.084
	123828	AA620686	Hs.112884	EST	0.084
	103611	Z38133	Hs.113973	myosin; heavy polypeptide 8; skeletal muscle; perinatal	0.084
	131289	AA485697	Hs.25334	ESTs; Weakly similar to ION CHANNEL HOMOLOG RIC PRECURSOR [M.musculus]	0.084
20	128678	T15896	Hs.103535	ESTs	0.084
	130814	AA256695	Hs.19813	ESTs	0.084
	133391	X57579	Hs.727	inhibin; beta A (activin A; activin AB alpha polypeptide)	0.084
	129322	AA437153	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk173c12.5 [C.elegans]	0.084
25	109284	AA196995	Hs.86092	ESTs	0.084
	116689	F09222	Hs.66099	ESTs	0.085
	100545	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	0.085
	102634	U66711	Hs.77667	lymphocyte antigen 6 complex; locus E	0.085
30	111735	R25389	Hs.23856	ESTs; Weakly similar to FAST kinase [H.sapiens]	0.085
	105181	AA190676	Hs.10974	ESTs; Moderately similar to unknown [R.norvegicus]	0.085
	122681	AA455350	Hs.99401	EST	0.085
	114543	AA056121	Hs.158419	ESTs	0.085
	133597	AA425908	Hs.75139	partner of RAC1 (arfatpin 2)	0.085
	121064	AA398647	Hs.97406	ESTs	0.085
35	122231	AA438369	Hs.197728	ESTs; Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]	0.085
	100309	D50550	Hs.95659	lethal giant larvae (Drosophila) homolog 1	0.085
	101727	M73481	Hs.73883	gastrin-releasing peptide receptor	0.085
	131226	AA165400	Hs.24476	ESTs	0.085
40	133580	AA095041	Hs.181073	ESTs	0.085
	102792	U87964	Hs.227576	GTP binding protein 1	0.085
	104976	AA086480	Hs.183669	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.085
	120865	AA350631	Hs.96963	EST	0.085
	106080	AA418046	Hs.35124	ESTs	0.085
	128571	AA416619	Hs.101661	ESTs	0.085
45	101838	M92934	Hs.75511	connective tissue growth factor	0.085
	128514	H84261	Hs.100843	ESTs; Weakly similar to similar to GTP-binding protein [C.elegans]	0.085
	123099	AA485931	Hs.79	aminoacylase 1	0.085
	134067	Y08200	Hs.78920	Rab geranylgeranyltransferase; alpha subunit	0.085
	116967	H80336	Hs.40124	EST	0.085
	110053	H12586	Hs.89563	nuclear cap binding protein 1; 80kD	0.085
50	114395	AA007313	Hs.110155	ESTs	0.085
	107465	W44681	Hs.251385	murine retrovirus integration site 1 homolog	0.085
	101983	S85655	Hs.75323	prohibitin	0.085
	112544	R70948	Hs.29153	ESTs	0.086
	111423	R01165	Hs.188507	ESTs	0.086
	127918	AA806043	Hs.115396	Human germline IgD chain gene; C-region; C-delta-1 domain	0.086
55	107300	T40348	Hs.90488	ESTs	0.086
	134947	R51194		yj71a08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154166 5' similar to gb:L11284 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (HUMAN);, mRNA sequence.	0.086
				ESTs; Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]	0.086
				adducin 1 (alpha)	0.086
60	130471	Z68280	Hs.183706	ESTs	0.086
	116596	D60755	Hs.92955	ESTs	0.086
	105069	AA136345	Hs.23617	ESTs; Weakly similar to ZFOC1 gene product [H.sapiens]	0.086
	102491	U51010		Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region	0.086
65	130069	AA055896	Hs.146428	collagen; type V; alpha 1	0.086
	130234	AA280413	Hs.157441	spleen focus forming virus (SFFV) proviral integration oncogene spi1	0.086
	120540	AA262992	Hs.96417	ESTs	0.086
	122508	AA449221	Hs.20432	ESTs	0.086

5	128054	AI205718	Hs.125416	ESTs	0.086
	133020	AA053248	Hs.185182	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S10 [H.sapiens]	0.086
	130056	AA017356	Hs.171900	armadillo repeat gene deletes in velocardiofacial syndrome	0.086
	130504	U48865	Hs.158323	CCAAT/enhancer binding protein (C/EBP); epsilon	0.086
	133978	W73859	Hs.78061	transcription factor 21	0.086
10	105265	AA227941	Hs.26088	ESTs	0.086
	133035	T15965	Hs.6333	ESTs	0.086
	100768	HG3636-HT3846		Myosin, Heavy Polypeptide 9, Non-Muscle	0.086
	129338	T56800	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (from clone DKFZp564B176)	0.086
	132789	W23761	Hs.56876	ESTs	0.086
15	116099	AA458309	Hs.58831	regulator of Fas-induced apoptosis	0.086
	100721	HG3355-HT3532		Peroxisome Proliferator Activated Receptor (Gb:Z30972)	0.087
	112569	R73150	Hs.75270	GTP-binding protein homologous to Saccharomyces cerevisiae SEC4	0.087
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITAM domains 2	0.087
	100751	HG3527-HT3721		Luteinizing Hormone, Beta Subunit	0.087
20	134550	M27161	Hs.85258	CD8 antigen; alpha polypeptide (p32)	0.087
	130885	AA338646	Hs.20912	adenomatous polyposis coli like	0.087
	101446	M21302	Hs.58306	small proline-rich protein 2A	0.087
	116287	AA487856	Hs.155829	KIAA0676 protein	0.087
	134034	X89267	Hs.78601	uroporphyrinogen decarboxylase	0.087
25	130660	U66061	Hs.241395	protease; serine; 1 (trypsin 1)	0.087
	109901	H04992	Hs.30499	ESTs	0.087
	107537	Z20777	Hs.9857	ESTs; Weakly similar to peroxisomal short-chain alcohol dehydrogenase [H.sapiens]	0.087
	133232	AA496030	Hs.6845	ESTs	0.087
	108559	AA085161		zn12c5.s1 Stratagene hNT neuron (#937233) H sapiens cDNA clone IMAGE:54728 3' similar to TR:G1151228 G1151228 LPG1P. ; mRNA seq	0.087
30	121288	AA401735	Hs.97340	EST	0.087
	108844	AA132916	Hs.177961	Human Chromosome 16 BAC clone CIT987SK-A-388D4	0.087
	129874	AA406488	Hs.181551	ESTs	0.087
	105139	AA164543	Hs.110082	ESTs	0.088
	124789	R43803	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elegans]	0.088
35	115923	AA441929	Hs.38205	ESTs	0.088
	123640	AA609292	Hs.112681	ESTs	0.088
	131607	AA351409	Hs.172740	microtubule-associated protein; RP/EB family; member 3	0.088
	130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.088
	108752	AA127070	Hs.71055	ESTs	0.088
40	124249	H68077	Hs.108211	ESTs	0.088
	100109	AJ000480	Hs.143513	phosphoprotein regulated by mitogenic pathways	0.088
	104642	AA004662	Hs.184245	KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog	0.088
	131752	AA453311	Hs.31588	ESTs	0.088
	114727	AA132545	Hs.190202	ESTs	0.088
45	120965	AA398089	Hs.179715	ESTs	0.088
	100396	D84361	Hs.151123	Human mRNA for p52 and p64 isoforms of N-Shc; complete cds	0.088
	106218	AA428451	Hs.91146	DKFZP586E0820 protein	0.088
	111562	R08567	Hs.187569	ESTs	0.088
	121219	AA400606	Hs.144344	EST	0.088
50	101187	L20316	Hs.208	glucagon receptor	0.088
	101513	M28210	Hs.27744	RAB3A; member RAS oncogene family	0.088
	116454	AA621071	Hs.42034	ESTs; Moderately similar to T-complex protein 10A [H.sapiens]	0.088
	116171	AA463434	Hs.42658	ESTs	0.089
	117500	N31909	Hs.44278	ESTs	0.089
55	119978	W88623	Hs.59190	EST	0.089
	132005	D58231	Hs.173091	DKFZP434K151 protein	0.089
	109914	H05529	Hs.194704	leucine-rich; glioma inactivated 1	0.089
	130370	M55265	Hs.155140	casein kinase 2; alpha 1 polypeptide	0.089
	104262	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	0.089
60	129703	AA417181	Hs.120858	ESTs	0.089
	106398	AA447545	Hs.18268	adenylate kinase 5	0.089
	120884	AA365356	Hs.97041	ESTs	0.089
	130404	X72012	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	0.089
	114072	Z38184	Hs.123633	ESTs	0.089
65	131470	X54938	Hs.2722	inositol 1,4;5-trisphosphate 3-kinase A	0.089
	124573	N67935	Hs.194703	adaptor-related protein complex 4; mu 1 subunit	0.089
	114717	AA131240	Hs.252014	EST	0.089
	133806	M12759	Hs.76325	Human Ig J chain gene	0.09
	130470	AA398552	Hs.15711	KIAA0639 protein	0.09
	133182	Z80787	Hs.240135	H4 histone family; member J	0.09
	116036	AA452572	Hs.43866	ESTs	0.09

5	132404	AA393903	Hs.4768	ESTs	0.09
	122695	AA456048	Hs.99403	ESTs; Moderately similar to undulin 2 [H.sapiens]	0.09
	125975	AA495691	Hs.152290	ESTs; Highly similar to PACAP type-3/VIP type-2 receptor [H.sapiens]	0.09
	110783	N23669	Hs.26407	ESTs	0.09
	129860	AA410343	Hs.129826	tetraspan transmembrane 4 super family	0.09
10	120740	AA302650	Hs.96654	EST	0.09
	119564	W38206		Accession not listed in Genbank	0.09
	134474	AA054746	Hs.8379	ESTs	0.09
	119014	N95435	Hs.55144	ESTs	0.09
	109791	F10669	Hs.13228	DRE-antagonist modulator; calsenilin	0.09
15	117605	N35073	Hs.44433	ESTs	0.09
	121569	AA416627	Hs.191598	ESTs	0.09
	104326	D81655	Hs.143067	ESTs	0.09
	129861	N69507	Hs.129849	DKFZP564M182 protein	0.09
	102795	U88667	Hs.198396	ATP-binding cassette; sub-family A (ABC1); member 4	0.09
20	119626	W49499	Hs.184456	ESTs; Wkly smlr to !! ALU SUBFAMILY SX WARNING ENTRY !! [H.sapiens]	0.09
	110516	H56894	Hs.37368	EST	0.09
	105382	AA236853	Hs.111801	Homo sapiens mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023)	0.09
	123754	AA609964	Hs.102021	ESTs	0.09
	106008	AA039430	Hs.61820	ESTs	0.09
25	121057	AA398619	Hs.142375	ESTs; Moderately similar to putative envelope protein [H.sapiens]	0.091
	123675	AA609474	Hs.112713	EST	0.091
	135194	C20975	Hs.9613	ESTs; Highly similar to angiopoietin-related protein [H.sapiens]	0.091
	127070	AA641812	Hs.190037	ESTs	0.091
	134051	S67070	Hs.78846	heat shock 27kD protein 2	0.091
30	133382	AA112532	Hs.7247	ESTs	0.091
	103615	Z46967	Hs.115460	calicin	0.091
	118457	N66593	Hs.49230	EST	0.091
	118504	N67334	Hs.50158	ESTs	0.091
	112915	T10176	Hs.4254	ESTs	0.091
35	132088	AA470121	Hs.243960	HLA-B associated transcript-3	0.091
	101504	M27288	Hs.248156	oncostatin M	0.091
	112550	R71391	Hs.29074	ESTs	0.091
	128551	H09058	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	0.091
	112879	T03541	Hs.115960	ESTs	0.091
40	127079	AI364691	Hs.128628	ESTs; Moderately similar to CL3BC [R.norvegicus]	0.091
	101993	U01062	Hs.77515	inositol 1;4;5-triphosphate receptor; type 3	0.091
	113020	T23830	Hs.7303	ESTs; Weakly similar to PROHIBITIN [H.sapiens]	0.091
	120465	AA251505	Hs.130861	ESTs	0.091
	130152	U32645	Hs.151139	E74-like factor 4 (ets domain transcription factor)	0.091
45	104941	AA065169	Hs.17805	ESTs	0.091
	110090	H16076	Hs.6915	ESTs	0.091
	135375	AA480888	Hs.99741	ESTs; Weakly similar to BRAIN PROTEIN H5 [H.sapiens]	0.091
	123799	AA620418	Hs.112861	ESTs	0.092
	118966	N93438	Hs.76907	ESTs; Highly similar to HSPC002 [H.sapiens]	0.092
50	116969	H80633	Hs.143038	ESTs	0.092
	125147	W38150		Accession not listed in Genbank	0.092
	100836	HG4113-HT4383		Olfactory Receptor Or17-201	0.092
	114726	AA132509	Hs.103827	EST	0.092
	107311	T57738	Hs.174112	ESTs	0.092
55	112863	T03148	Hs.4610	EST	0.092
	129290	AA521407	Hs.110095	ESTs	0.092
	103384	X92762	Hs.79021	tafazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.092
	112508	R68213	Hs.28847	ESTs	0.092
	111863	R37495	Hs.23578	ESTs	0.092
60	131184	AA452705	Hs.23954	ESTs; Weakly similar to KIAA0584 protein [H.sapiens]	0.092
	107420	W26567	Hs.4775	ESTs	0.092
	111768	R27606	Hs.24185	ESTs	0.092
	112290	R53940	Hs.26016	ESTs	0.092
	130581	AA481982	Hs.16258	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-5A [H.sapiens]	0.092
65	120744	AA302772	Hs.228649	EST	0.093
	112226	R50761	Hs.25738	ESTs	0.093
	116154	AA460951	Hs.57100	ESTs	0.093
	102640	U67674	Hs.194783	solute carrier family 10 (sodium/bile acid cotransporter family); member 2	0.093
	129797	X53595	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	0.093
	102705	U77180	Hs.50002	small inducible cytokine subfamily A (Cys-Cys); member 19	0.093
	132408	AA035547	Hs.47822	KIAA0380 gene product; RhoA-specific guanine nucleotide exchange factor	0.093
	108441	AA079079		zm97c9.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone	0.093

			IMAGE:545872 3' similar to contains element MER22 MER22 repetitive element ;, mRNA sequence	0.093	
	108145	AA054133	Hs.63085	ESTs	0.093
	108486	AA449990	Hs.76057	lysophospholipase II	0.093
5	101697	M64358		Human rhom-3 gene, exon	0.093
	121294	AA401958	Hs.240170	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.093
	117824	N49065	Hs.125201	ESTs; Weakly similar to B7 [M.musculus]	0.093
	115771	AA422049	Hs.40780	ESTs	0.093
10	102303	U33053	Hs.2499	protein kinase C-like 1	0.093
	131405	U79255	Hs.26468	amyloid beta (A4) precursor protein-binding; family A; member 2 (X11-like)	0.093
	112909	T10069	Hs.101094	ESTs	0.093
	124173	H41281	Hs.107619	ESTs	0.093
	112488	R66896	Hs.28788	ESTs	0.093
15	130554	X59303	Hs.159637	valyl-tRNA synthetase 2	0.093
	106413	AA447964	Hs.6311	ESTs	0.093
	111711	R22891	Hs.7093	ESTs	0.094
	117595	N34933	Hs.44664	EST	0.094
	113813	W45174	Hs.31382	ESTs	0.094
20	107769	AA018449	Hs.125220	Homo sapiens DNA from chromosome 19-cosmids R30102:R29350:R27740 containing MEF2B; genomic sequence	0.094
	114966	AA250743	Hs.92198	ESTs; Highly similar to calcium-regulated heat stable protein CRHSP-24 [H.sapiens]	0.094
	130297	H94949	Hs.171955	trophinin-assisting protein (lastin)	0.094
25	109589	F02429	Hs.6581	ESTs	0.094
	112592	R77631	Hs.29126	ESTs	0.094
	102314	U34038	Hs.154299	coagulation factor II (thrombin) receptor-like 1	0.094
	116128	AA459915	Hs.112193	mutS (E. coli) homolog 5	0.094
30	108809	AA479704	Hs.220324	Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1; -2; MMP21/22A; -B and -C; a novel gene; the alternatively spliced CDC2L2 gene for	0.094
	130607	AA043894	Hs.16603	ESTs	0.094
	120592	AA281929	Hs.143974	ESTs	0.094
35	117230	N20535	Hs.43265	melastatin 1	0.094
	105948	AA404597	Hs.7133	ESTs	0.094
	101333	L47738	Hs.80313	p53 inducible protein	0.094
	101909	S69265		Homo sapiens mRNA for PLE21 protein; complete cds	0.094
	106959	AA497031	Hs.8657	ESTs; Highly similar to CTG7a [H.sapiens]	0.094
40	127034	AA352389		ESTs; Wkly smlr to glucose-6-phosphatase catalytic subunit [R.norvegicus]	0.095
	134430	H52105	Hs.8309	KIAA0747 protein	0.095
	120342	AA207105	Hs.45068	Homo sapiens mRNA; cDNA DKFZp4341143 (from clone DKFZp4341143)	0.095
	104450	L77564	Hs.103978	serine/threonine kinase 22B (spermiogenesis associated)	0.095
	130902	AA424530	Hs.21061	ESTs	0.095
45	102708	U77594	Hs.37682	retinoic acid receptor responder (tazarotene induced) 2	0.095
	107373	U85773	Hs.154695	phosphomannomutase 2	0.095
	123569	AA608952	Hs.195292	ESTs; Weakly similar to RNA helicase HDB/DICE1 [H.sapiens]	0.095
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.095
	128888	AA034951	Hs.106893	ESTs	0.095
50	100283	D43642	Hs.2430	transcription factor-like 1	0.095
	102747	U79303	Hs.82482	protein predicted by clone 23882	0.095
	107798	AA019346	Hs.60918	EST	0.095
	123565	AA608907	Hs.112614	EST	0.095
	116010	AA449450	Hs.56421	ESTs; Weakly similar to Similarity to H.influenza ribonuclease PH [C.elegans]	0.095
55	117155	H97536	Hs.42391	EST	0.095
	133094	AA115572	Hs.64746	chloride intracellular channel 3	0.095
	113174	T54659	Hs.9779	ESTs	0.095
	102016	U03270	Hs.122511	centrin; EF-hand protein; 1	0.095
	130126	AB002318	Hs.150443	KIAA0320 protein	0.095
60	134813	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A receptor; beta 1	0.095
	132055	N69440	Hs.38132	ESTs	0.095
	122229	AA436198	Hs.103902	ESTs	0.096
	127574	AA907314	Hs.188905	ESTs	0.096
	134432	AA053022	Hs.8312	ESTs	0.096
65	128052	AA878398	Hs.190491	ESTs	0.096
	101637	M59285	Hs.132834	hematopoietic protein 1	0.096
	103366	X92972	Hs.80324	protein phosphatase 6; catalytic subunit	0.096
	133079	AA477561	Hs.6449	ESTs	0.096
	120328	AA196979	Hs.104129	ESTs; Weakly similar to protease [H.sapiens]	0.096

	107640	AA009615	Hs.257808	ESTs	0.096
	123389	AA521176	Hs.221231	ESTs	0.096
	103222	X74795	Hs.77171	minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 45)	0.096
5	111704	R22450	Hs.23396	ESTs; Highly similar to ZINC FINGER PROTEIN 140 [H.sapiens]	0.096
	126856	AA306523		EST177475 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence.	0.733
	127071	AA250806		ESTs	0.096
	114550	AA056755	Hs.151714	ESTs	0.096
	125955	AI356943	Hs.143761	ESTs	0.096
10	134363	M37033	Hs.82212	CD53 antigen	0.096
	128550	W76492	Hs.170142	ESTs	0.096
	122598	AA453465	Hs.99329	ESTs	0.096
	118898	N90703	Hs.4236	KIAA0478 gene product	0.096
	117661	N39092	Hs.44940	ESTs	0.096
	120996	AA398281	Hs.143684	ESTs	0.096
15	123388	AA521172	Hs.134417	ESTs	0.096
	106700	AA463929	Hs.28701	ESTs	0.096
	112962	T16814	Hs.6828	ESTs	0.096
	121262	AA401372	Hs.97723	ESTs	0.096
	134551	R44839	Hs.8526	i-beta-1;3-N-acetylglucosaminyltransferase	0.096
20	112060	R43754	Hs.21164	ESTs	0.096
	134678	AA039935	Hs.182595	dynein; axonemal; light polypeptide 4	0.096
	100855	HG4234-HT4504		Methylenetetrahydrofolate Reductase	0.097
	132414	N91193	Hs.48145	ESTs	0.097
	112900	T08758	Hs.3813	ESTs	0.097
25	115989	AA447777	Hs.93135	ESTs	0.097
	103561	Z21488	Hs.143434	contactin 1	0.097
	131087	AA009733	Hs.22824	ESTs; Weakly similar to p160 myb-binding protein [M.musculus]	0.097
	120293	AA190859	Hs.191428	ESTs	0.097
	111830	R36081	Hs.25085	EST	0.097
30	113654	T95770	Hs.17686	ESTs	0.097
	132675	AA179338	Hs.5476	serine proteinase inhibitor	0.097
	120182	Z40125	Hs.91968	ESTs	0.097
	132879	U16282	Hs.5881	ELL gene (11-19 lysine-rich leukemia gene)	0.097
35	134211	AA056681	Hs.80021	ESTs; Weakly similar to 62D9.p [D.melanogaster]	0.097
	115448	AA284845	Hs.165051	ESTs	0.097
	118118	N56901	Hs.47995	ESTs	0.097
	107598	AA004528	Hs.169444	ESTs	0.097
	128933	H01824	Hs.760	GATA-binding protein 2	0.097
	114892	AA235988	Hs.86024	ESTs	0.097
40	101822	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.097
	105444	AA252374	Hs.19333	ESTs; Weakly similar to ATP(GTP)-binding protein [H.sapiens]	0.097
	128155	AA926843	Hs.143302	ESTs	0.097
	116276	AA485870	Hs.44914	ESTs	0.097
	111964	R41227	Hs.21860	ESTs	0.097
45	135100	AA398926	Hs.251108	Homo sapiens mRNA; chromosome 1 specific transcript KIAA0493	0.097
	124872	R69251	Hs.101506	EST	0.097
	103084	X59932	Hs.77793	c-src tyrosine kinase	0.097
	124138	H23199	Hs.107010	ESTs	0.098
	130048	R31745	Hs.211612	SEC24 (S. cerevisiae) related gene family; member A	0.098
50	100208	D26129	Hs.78224	ribonuclease; RNase A family; 1 (pancreatic)	0.098
	123537	AA608775	Hs.112589	ESTs	0.098
	118999	N95019	Hs.55092	ESTs	0.098
	119847	W60364	Hs.9853	ESTs	0.098
	112819	R98618	Hs.35984	ESTs	0.098
55	131080	J05008	Hs.2271	endothelin 1	0.098
	127353	AA190853	Hs.155360	ESTs	0.098
	132068	X66365	Hs.38481	cyclin-dependent kinase 6	0.098
	105744	AA293436	Hs.12909	ESTs	0.098
	133680	M92357	Hs.101382	tumor necrosis factor; alpha-induced protein 2	0.098
60	122899	AA469960	Hs.178420	ESTs; Highly similar to WASP interacting protein [H.sapiens]	0.098
	128700	U59286	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys); member 11	0.098
	104393	H46486	Hs.226499	nesca protein	0.098
	123320	AA496792	Hs.139572	EST	0.098
	129169	N31641	Hs.109058	ribosomal protein S6 kinase; 90kD; polypeptide 5	0.098
65	135093	U51333	Hs.159237	hexokinase 3 (white cell)	0.098
	113269	T65159	Hs.85044	ESTs	0.098
	124283	H86783	Hs.194136	ESTs; Moderately similar to zinc finger protein RIN ZF [R.norvegicus]	0.098
	114376	GMCSF		Accession not listed in Genbank	0.099
	100881	HG4458-HT4727		Immunoglobulin Heavy Chain, Vdjc Regions (Gb:123563)	0.099

5	116572	D45654	Hs.65582	DKFZP586C1324 protein	0.099
	123956	AA621747	Hs.112847	EST	0.099
	100818	HG4018-HT4288		Opioid-Binding Cell Adhesion Molecule	0.099
	132754	W47419	Hs.56007	Human DNA from chromosome 19-specific cosmid F25965; genomic sequence	0.099
	112741	R93080	Hs.35035	ESTs	0.099
10	112748	R93299	Hs.166492	ESTs	0.099
	130858	S57235	Hs.246381	CD68 antigen	0.099
	124870	R69233	Hs.101504	ESTs	0.099
	125304	Z39833	Hs.124940	GTP-binding protein	0.099
	121297	AA401995	Hs.97860	ESTs	0.099
15	128602	AA046103	Hs.102367	ESTs	0.099
	124062	H00440	Hs.144524	ESTs; Weakly similar to signal transducer and activator of transcription 2 [M.musculus]	0.099
	100547	HG2149-HT2219		Mucin (Gb:M57417)	0.099
	105652	AA282505	Hs.19015	ESTs	0.099
	133390	AA459945	Hs.72660	KIAA0585 protein	0.099
20	133503	M33195	Hs.743	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	0.099
	109461	AA232667	Hs.58210	ESTs	0.099
	102068	U09117	Hs.80776	phospholipase C; delta 1	0.099
	113464	T86931	Hs.16295	ESTs	0.099
	104240	AB002368	Hs.70500	KIAA0370 protein	0.099
25	121113	AA399109	Hs.161813	ESTs	0.1
	122896	AA469952	Hs.97899	ESTs; Weakly similar to dal2; len:343; CAI: 0.17; ALC_YEAST P25335	0.1
	102405	U43148	Hs.159526	ALLANTOICASE [S.cerevisiae]	0.1
	103599	Z33905	Hs.81218	patched (Drosophila) homolog	0.1
	121079	AA398719	Hs.14169	receptor-associated protein of the synapse; 43kD	0.1
30	115820	AA427487	Hs.39619	ESTs; Weakly similar to CREB-binding protein [H.sapiens]	0.1
	125106	T95766	Hs.189760	ESTs; Weakly similar to RETICULOCALBIN 1 PRECURSOR [H.sapiens]	0.781
	131373	N68116	Hs.26146	ESTs	0.1
	120224	Z41239	Hs.106960	Down syndrome critical region gene 3	0.1
	133090	AA448228	Hs.6468	ESTs	0.1
35	132300	AA133244	Hs.44234	ESTs	0.1
	113129	T49384	Hs.8988	EST	0.1
	110638	H73197	Hs.17241	ESTs	0.1
	131364	R53255	Hs.26010	ESTs	0.1
	105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane protein with EGF-like and two follistatin-like domains 1 [H.sapiens]	0.238
40					

TABLE 11A shows the accession numbers for those primekeys lacking unigeneID's for Table 11. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Key:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
10	100610	19864_1	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F06553 AI936671 AA476718 AW772454 AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85809 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221 D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T06745 AI699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13912 R19056 AI681231 AI590200 R37671 AA861828 AI990023 AI935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W26930 R44098 R51045
20	100674	21517_2	AW403342 AW248986 BE561709 AA357312 BE311834 BE389496 BE294887 AW732696 BE047868 AI702383 BE019155 AI702367 BE408966 BE280458 BE313759 BE513492 BE535404 BE280258 AC005263 NM_007165 L21990 AW732711 AI564920 AW249094 BE265365 AW607186 AW607346 BE005217 H27211 U46230 BE260066 BE207043 BE546782 AW248659
25	108559	41469_9	AA085228 AA085161
30	100721	19818_1	L40904 NM_005037 X90563 AB005526 H21598 AA088517
35	100748	41861_1	X06096 X05826
40	100750	15759_1	BE157260 BE157265 R48118 H43827 Z17877 AW379070 AW291778 M20605 J03253 M14206 V00568 AI860465 AW296022 M13930 AL047400 J00120 BE018476 AW675223 T26980 F06694 R22709 R24720 H22753 AI903100 AI903094 AW937823 X00364 D10493 K01904 K01906 K00535 L00058 AA410662 AW384760 AA304930 AI680985 X00198 H53025 AW998901 AV653447 N31654 AW610357 AW610369 AW862480 BE223010 AW384172 AW384219 AW384171 AW384218 AA298522 BE140421 AW945162 AW751711 AA514409 AW747912 AI214214 W87741 AA972406 AA554513 BE302087 AI249030 AA477850 AV653129 AI281360 AI274110 W87861 AA641366 X66258 AI051600 AA877139 AA527483 AA857219 AI250782 AA625531 AA807892 AI278811 AI224033 H24033 AA593396 AW129709 R45453 N22772 AA235530 T29737 AI016409 AI688907 AA568370 AA722760 AI539329 AA550843 AW674698 AI538452 AI538453 AI337957 AA477744 AA464600 AI140319 AW949294 AI339781 AI828736 AA923634 AA344094 AI278350 AA975567 AA908416 AA857170 AW023520 R43413 R48004 F02958 AI989439 R11207 AA737307 D10493 AW950652 AI093842 AI474024 AA703369 R11264 M13930 M13930 M13930 M13930 J00120 M13930 M13930 X00364 J00120 R19507 AA639812
45	100751	24700_1	N32759 N29730 N30831 N32604 N31955 AI206390 H87574 R23494 AI186215 N30036 AI741512 J00117 NM_000737 AI453626 AA330974 AI188729 AI188604 AI188964 N30276 AI188947 AI188830 AI188303 AI200457 AI219166 AI192459 AI183280 AI189275 AI188639 AI186353 AI189616 AI184224 AI130720 AI188454 AI188391 AI148857 AI192447 AI209155 AI190013 AI206355 AI188721 AI189429 AI189364 AI186330 AI431595 AI189595 AI188781 AI148647 AI200022 AI221552 AI220923 AI188728 AA233034 AI189807 AI189641 AI219044 AI148774 AI200658 W71989 AI207360 AI188824 AI200559 AI200270 AA644163 AI199943 AI151301 AI189555 AI262724 AI148590 AI148695 AI126906 AI149163 K03183 K03189 AI189842 AI221014 N30608 AI186465 AI220865 AI188498 AI138226 AI189968 AI221019 AI138197 AI149426 AI148904 AI186218 AI188348 AI160579 AI198480 AI149039 AI160936 AI219055 AI184784 AI221590 AI161082 AI160814 AI123898 AI417614 AI126101 AI188872 AI149571 AI168533 AI149072 AI149467 AI131286 N30684 AI160705 AI160692 AI149559 AI273580 AI189442 AI138448 AI149591 N27302 AA400910 AI138431 AI138435 AI128407 N30216 AI128296 AI219589 AI188492 AI149447 AI168482 H95374 AI219009 N31616 AI276216 N32233 AI291937 N30741 AI188689 N27111 R23214 AI221605 AI184348 AI200375 H94451 N26397 AI871881 AA232905 N30833 AI220760 H94446 N30822 H87464 R68815 N30290 AI128424 H12587 T47334 H87631 H87156 AI219133 AI868741 AA330859 H86993 AA330413 H93656 N30817 T90191 H93668 AI200054 H95207 T47316 H95381 T49170 R00880 T49171 N27381 H94107 R63352 T85053 AW451899 H95142 N30313 H94015 H66987 T28278 N29701 C18834 AA331267 AA330939 AI654493 N27073 N29831 R68113 N30758 R26086 N32108 H95135 AA330414 AA330978 AI219422 AI189453 AI199951 X00264 NM_000894 AA371909 AA063496 T29543 AA371971 AA372026 AA371978 AA371346 AI051683 AI186418 AI220659 AI189068 AI219266 AI188552 AI188715 AI149156
50	100760	1334_7	AW794626 M27126 M27014
55	100775	18179_3	J05581 M61170 T27692 M34088 M34089 AW860335 AW579047 AW610437 AW610386 AW610422 AW610473 AW579078 AW604897 AW860163 AW579067 AW682410 AI16584 AW177757 AW602769 AI909790 AW860331 AI909787 AI909811
60			
65			

		AI909813 AW845083 AI905920 AW387919 BE140766 AI909279 AW369405 AA429321 AA429320 AA367451 AA847972 AW001137 AI567905 T84561 AI631295 AA151351 H02932 AI884519 AA367457 AW369421 AI678846 AW391803 AI610869 AW192838 AI922289 AI952140 AI910233 AI479474 AW001395 AA488073 AI985760 AW130017 AI859369 AA627845 AW081805 AA158865 AI624443 AA344985 AA589793 R72486 AI589329 AI903204 AI269893 AA641284 AI279932 AA149270 AI697120 AA729146 AI589353 AA480067 AI923310 AA530908 AI275395 AA425062 AA580280 AA889527 AA158866 AW131341 AA573028 AA877326 T29335 AW951288 H04235 AA099243 AA994659 AI659618 AA887919 AI299297 AW001116 AW283844 AI270578 AA970828 AW572126 AA775299 AW369449 AW369398 AW369452 AI933677 AI870710 AI092911 AI582464 AI497674 AA937026 AA885865 L38597 AA908325 AW369432 AW026623 AA627778 AI264942 AA932409 AI187328 AI672970 AI886098 AW440471 AW138860 AI866858 AI802528 AI926172 AW243914 AI933690 AA996114 AA536189 AW009937 AI918060 AI270379 AI973169 AW175638 AW369413 NM_006227 L26232 R50649 AU077024 AL008726 AA411079 R35151 BE278153 BE278139 AI459777 R88036 Z43210 F07326 AF052157 R17844 BE615476 T82160 R71985 H21963 AA299158 AW368246 R48123 R50628 R70441 H27245 H72015 R72345 R39392 AI909738 BE612778 BE613234 D52116 D52136 D52132 D52067 D51922 D51995 D51905 N34249 N25459 AA464436 AA297350 AA297466 R81736 H02737 AW582505 R27523 AI834241 AW130867 W72668 W76426 AA358363 R50262 AW473860 H52335 H43953 H21964 T39505 AI887517 AW156925 AW839850 H02628 AW007705 AI561008 F22392 R71279 AA995433 R50725 W24462 R71931 AA464437 AW591731 R25667 R52695 R50810 AI560805 AI089266 H68386 H41353 H28590 AW001860 AI141623 AA250773 AI284778 AW511412 AW083975 AA130377 AW026047 R50551 R81494 AI357668 AI078272 F32666 F36981 AW304865 H43906 AA931068 R48010 AI540217 AI017339 AI291812 AI741954 AA458490 AI088378 AA298764 H61168 AA358362 AA298725 AA298515 AA464148 AA443538 R43046 AA084314 T40641 T47608 T48940 AI082477 AW470145 N92284 AI758958 AA298512 AA284588 AI597777 AA480277 AI932559 AI869081 AA476615 AA503651 AI656024 AW168522 AI682051 AI689106 AI274592 AI520917 BE258916 BE615861 BE280282 R53386 BE278255 BE278398 T47607 AA477662 H68385 100817 19648_1 L34355 L46810 NM_000023 U08895 AA424260 AI097272 AA424162 N79764 F19290 F25278 AI479385 AA460662 AA432059 AW016935 F25770 F32549 F36677 F33016 F35992 F36010 AW172497 AA835076 F28727 AA211643 AA453282 100818 19604_3 U79251 AA843851 R38201 R66461 R44908 AA683289 H17477 R37364 R52832 AW298336 AA351391 NM_002545 L34774 AA296886 AW967001 T28889 R13451 T77331 AL119196 AL118830 H08459 AW892812 AW905838 H17585 R52878 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865 BE396881 BE560031 BE514199 BE560037 BE560454 100885 12707_3 X07881 NM_006249 X07637 AA376715 AA376677 X07715 X07704 S80916 100898 8542_1 BE387614 R51501 AA199714 AW674779 F08178 BE269071 AA376313 H08264 AA380420 H18785 AL042151 BE277758 BE267438 NM_005850 L35013 BE540833 BE390902 BE391494 BE277459 BE385592 BE390612 BE384263 BE387779 BE388647 BE537373 BE547158 AW409585 AW374033 AW602185 AA355725 AW577548 AW935015 AW935160 W40232 AW938647 AW374332 AA434040 BE293488 AL138361 BE560260 AI745075 AA317980 AW949382 AI834311 AI653582 AI831042 AI361878 AA618606 AA729052 AI424969 AA199715 AW769374 AI828422 AW044307 AI862816 AI203583 AW084461 AW514655 AA831883 AA290672 AA831288 AA578510 AW089965 AW150748 AA292743 H22232 AI469275 AA439312 AA292744 AW471443 AI473989 AA593336 AA464070 AI678937 AW069451 AA970763 AA610480 AA593328 AA464009 AA768985 AI298928 AA436600 AA464718 AA699361 D61482 D55935 AI369591 AA470695 AI809135 AA640627 AI568446 R51502 W45467 AI655316 AA463934 AW168609 AW518663 BE045525 Z41251 AI868091 AA908160 AI026697 AI868259 AI612932 AA215437 AI956014 BE541087 BE255652 BE265878 BE394102 W27502 AI48936 L36592 X87160 NM_001039 AL036606 AL036420 U35630 AW298574 WB0551 M85370 126126 1630017_1 AA976427 U66052 102620 16821_37 AI457548 U72509 102673 24986_6 U72512 T98357 R31335 F18090 102675 5145_4 L32961 NM_000663 U80226 S75576 AA425061 AA429317 AI815143 AA910669 AI286022 AI286019 102753 2226_1 U88896 U88898 AA916056 T03265 AI341594 AI359534 AI634031 U88897 102799 34624_4 BE397750 AA232171 BE562900 BE384894 BE242228 BE206819 BE261742 AA296468 AW959763 BE276164 BE264109 127034 51148_2 BE392626 BE256735 AA301453 N55872 H01676 AA292746 AA427485 AA496400 AA352389 50 103522 21640_1 Y10518 Y10514 Z83935 Y10508 AK000055 Y10519 AI142012 AI681175 BE222219 AA890586 BE504347 BE328064 N63044 N51226 AI151248 AI521996 AI924777 AW375954 AI860275 W00549 AI742673 AW612288 AI763062 AA632510 AI087347 AI088070 AI214349 AA890297 AI494156 AI698598 AA631658 AA504593 AA860733 AI266761 AW663214 AW771231 AA639610 AI769806 AI769746 AW014326 AI288611 127071 188097_1 AA250806 AA459220 126456 291965_1 AA429212 W00381 119388 1762256_1 T88798 R92430 126856 20669_1 AI084125 AI083773 AI479687 AI939609 AI968662 AF129507 NM_013282 AW971840 AW298508 AA744240 AA811217 AA827671 AA811055 AA806567 AA488977 AA908902 AI637637 AA927056 AI870139 AW340492 AA488755 AA129794 AA306523 AA354253 BE256277 AC053467 AW962084 60 103996 224545_1 AA321355 AW964592 R23284 H73883 R23382 N47914 C01377 H04668 AW606248 R34447 AA847136 AI684489 AI523112 AW044269 AI379138 N29366 AA761543 N79248 AA960845 AA768316 AI147926 AI718599 AI880620 R67467 AI216016 AI738663 H04648 113213 23798_1 NM_001395 Y08302 AI434619 AI470328 AI261807 AW024965 AI806537 AI830549 AI640337 AI219065 AW271700 AW028488 AI133339 AI859205 R51175 U87167 BE379324 BE392008 AA340819 AA343110 T57275 D59164 AW299312 AI434422 AI936390 AW024975 R40262 65 134947 844579_1 AW269126 R09430 T56590 AI367247 AI253132 BE464248 T58658 AW207785 T58607 129311 18078_1 R51194 AI732276 R53587 AI820697 AK000528 BE550084 W30689 AW271859 AA411456 AI341551 AA242990 AA243027 H87046 D20360 AI184053 AA146956 AI721023 AI718944 AA146955 F18215 AA903890 AI700355 AI075430 AA411584 AA878210 AI476760 AW945637 AA630596
--	--	--

		AA431522 AA301989 AI909058 D12149 N41960 BE222214 AA609922 AA828176 AA393359 AA398693 AWC24956 BE467805 AW298623 AW264085 AI024454 AI024719 AI431927 T55087 AI611014 T54920 AA131253 AI436344 AA017176 AI359979 AA047836 AA017063 AA016303 AA001545 AA063315 AA063316 AF015910 AA305746 D90187 T63943 AW951154 T29182 AI734941 D13264 AI299239 Z18812 AW299659 W24476 AA933064 AA489759 AW688554 AW607282 AA319986 M26590 M55405 AW752552 AA326895 M10036 NM_000365 N84665 H69414 N84657 AA380453 AA329743 AA357367 AA188770 AA376532 AA353653 AA158953 AA083176 BE537313 AA181433 D53373 R57376 AA206698 R14807 H18899 H11191 H93892 R25593 T61134 N93285 AA083081 AA831789 H13137 AA497014 AA079330 AA182861 H13138 W47161 R62913 AA687089 AA211112 AA429237 AL035923 AA100070 AW392898 AI568433 AA866006 AA214002 AW392865 N79454 AA197181 AI680371 AA176501 AA737967 AI089225 F34874 AW571437 AI620620 AA573489 AA423816 AA164917 AA458455 T47072 AI569087 AI261656 AA730919 AI633441 AW195182 AI351622 AW243465 AI872649 AI359227 AA987941 AI693770 T47073 AW779948 AW510580 AI635626 AW627601 AA864326 AA953578 AI341418 BE222853 AI241963 AI094663 AA928380 AA493373 AW043762 AI377783 AW958987 BE619760 AA385240 BE277975 BE280095 AW631443 AA581048 BE618715 BE299610 C14874 BE559858 BE378455 BE618290 BE544585 AI525575 BE548897 BE267110 AA804738 BE269821 AA918133 BE277647 AA599947 BE280735 BE390239 N74150 T12504 AI208197 AW955527 AA113897 N40081 H73835 H70393 AI434041 W22950 AI192661 BE264461 W26486 AA626424 AA196694 T69209 AA857976 AI540287 AA410599 AA864287 AW950564 AA013320 T49283 AI541438 AW804703 AA335534 AA335659 BE562269 BE618802 BE277850 BE546413 BE280994 AA204813 BE561694 BE543524 BE253647 AW001452 W19116 BE542508 AA205894 BE254875 BE270033 AI525906 BE251782 AA975700 BE272138 AW607671 N87686 M10036 BE515060 BE298607 AI745178 U47924 H03193 Z25424 M88357 L29141 M69180 M81105 L33999 U04688 U09806 U12139 T91518 X65561 W38150 U38268 U51010 U51010 U67092 N74496 K01160 K03430 AA070473 AA070853 AA075749 AA075716 AA079079 AA128999 M60299 M64358 N27645 M85220 S69265 Y10141 Z26256 T54095 R48295 W38206 GMCSF M22406 M57417 Z11585
5	114427 9724_2	
	114569 110077_1	
	100106 15621_-5	
	100515 342_1	
10	100531 48038_1	
	100545 22955_11	
	100574 17320_2	
15		
20		
25	100627 tigr_HT2798	
	100756 tigr_HT3768	
	100768 tigr_HT3846	
	100813 tigr_HT4265	
	100836 tigr_HT4383	
	100855 tigr_HT4504	
30	102104 entrez_U12139	
	125091 genbank_T91518	
	100929 tigr_HT688	
	125147 entrez_W38150	
35	102354 entrez_U38268	
	102491 entrez_U51010	
	102636 entrez_U67092	
	118769 genbank_N74496	
	101046 entrez_K01160	
	101057 entrez_K03430	
40	108334 genbank_AA070473	
	108417 483241_1	
	108441 genbank_AA079079	
	108786 genbank_AA128999	
45	101655 entrez_M60299	
	101697 entrez_M64358	
	117437 genbank_N27645	
	101798 entrez_M85220	
	101909 entrez_S69265	
50	103508 entrez_Y10141	
	103575 entrez_Z26256	
	119332 genbank_T54095	
	112161 genbank_R48295	
	119564 NOT_FOUND_entrez_W38206	W38206
	114376 NOT_FOUND_entrez_GMCSF	GMCSF
55	100478 tigr_HT1067	
	100547 tigr_HT2219	
	100564 tigr_HT2324	

TABLE 12: shows genes, including expression sequence tags, that are down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu01 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Background subtracted normal prostate : prostate tumor tissue			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	100522	HG1763-HT1780		Prolactin-Induced Protein	17.4
	130803	M81650	Hs.1968	semenogelin I	16.785
	118068	N53943	Hs.13743	ESTs	13.225
20	114251	Z39898	Hs.21948	ESTs	12.7
	112134	R46025	Hs.7413	ESTs	8.735
	101436	M20642	Hs.158295	Human alkali myosin light chain 3 mRNA; complete cds	8.175
	104028	AA361094	Hs.221128	ESTs	8.15
	109944	AA149204	Hs.175783	ESTs; Highly similar to growth arrest inducible gene product [H.sapiens]	7.535
25	103838	AA174173	Hs.12622	ESTs	7.212
	120469	AA251741	Hs.25882	DKFZP586M1824 protein	7.175
	110279	H29231	Hs.27384	ESTs	6.701
	127472	AA761378	Hs.192013	ESTs	6.642
	133301	N35229	Hs.7037	pallid (mouse) homolog; pallidin	6.411
30	102457	U48807	Hs.2359	dual specificity phosphatase 4	6.395
	114011	W90385	Hs.15082	ESTs	6.15
	101249	L33881	Hs.1904	protein kinase C; iota	6
	123265	AA491209	Hs.105265	ESTs; Weakly similar to reverse transcriptase [M.musculus]	6
	119322	T49655	Hs.241569	ESTs; Modly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	5.95
35	101673	M61906	Hs.6241	phosphoinositide-3-kinase; regulatory subunit; polypeptide 1 (p85 alpha)	5.925
	115586	AA399218	Hs.92423	ESTs	5.7
	120590	AA281780	Hs.111441	ESTs; Weakly similar to similar to Kruppel-like zinc finger protein [C.elegans]	5.7
	109748	F10192	Hs.248323	Tubulin; alpha; brain-specific	5.625
	134727	X80507	Hs.8939	yes-associated protein 65 kDa	5.5
40	129171	AA234048	Hs.7753	calumenin	5.486
	120390	AA233122	Hs.111460	ESTs; Highly similar to multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform [H.sapiens]	5.4
	131699	R68657	Hs.90421	ESTs; Modly smlr to !! ALU SUBFAMILY SX WARNING ENTRY !! [H.sapiens]	5.279
	104490	N71503	Hs.43087	ESTs; Weakly similar to dysferlin [H.sapiens]	5.266
45	102124	U14528	Hs.29981	solute carrier family 26 (sulfate transporter); member 2	5.151
	109280	AA196635	Hs.86081	ESTs	5.134
	109707	F09739	Hs.185701	Homo sapiens mRNA full length insert cDNA clone EUROMAGE 21920	5.075
	108087	AA045709	Hs.40545	ESTs	5.075
50	135006	M21665	Hs.929	myosin; heavy polypeptide 7; cardiac muscle; beta	5.055
	119182	R80664	Hs.77067	ESTs	5.033
	129806	R62444	Hs.173373	KIAA0931 protein	4.675
	101435	M20543	Hs.1288	actin; alpha 1; skeletal muscle	4.626
	125954	R93943		yf72c12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:275735 5'	4.6
55	113989	W87544	Hs.221184	ESTs	4.559
	104432	J03460	Hs.99949	prolactin-induced protein	4.451
	112326	R56068	Hs.4268	ESTs	4.45
	119063	R16933	Hs.53106	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	4.45
	130376	R40873	Hs.155174	KIAA0432 gene product	4.301
	122484	AA448286	Hs.98074	ESTs; Highly similar to atrophin-1 interacting protein 4 [H.sapiens]	4.2
60	104142	AA447006		ESTs; Moderately similar to !! ALU SUBFAMILY SQ WARNING	4.175
	129413	N32787	Hs.11123	ESTs; Moderately similar to hypothetical protein 2 [H.sapiens]	4.1
	103678	Z84483		Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-134.05	
	114266	Z40186	Hs.26409	ESTs	4.05
	115206	AA262491	Hs.186572	ESTs	4.048
65	123723	AA609749	Hs.112759	ESTs; Highly similar to unknown protein [R.norvegicus]	4.041
	129130	H97993	Hs.172788	ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	4.028

	120217	Z41078	Hs.66035	ESTs	4.028
	108536	AA084524		zn19d8.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA	4.023
	134460	AA400030	Hs.8360	ESTs; Weakly similar to !! ALU CLASS B WARNING ENTRY !! [H.sapiens]	3.925
	120418	AA236010	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	3.91
5	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	3.889
	125052	T80174	Hs.222779	ESTs; Moderately similar to similar to NEDD-4 [H.sapiens]	3.85
	108600	AA099585	Hs.41175	ESTs	3.833
	103099	X61100	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme	3.818
	134948	H06773	Hs.93850	protein kinase; AMP-activated; gamma 2 non-catalytic subunit	3.792
10	120511	AA258144	Hs.221576	ESTs	3.779
	111861	R37460	Hs.25231	ESTs	3.768
	113966	W86600	Hs.9842	ESTs	3.75
	131649	AA481254	Hs.30120	ESTs	3.708
	129775	R94659	Hs.12420	ESTs	3.707
15	110191	H20568	Hs.27182	phospholipase A2-activating protein	3.7
	112678	R87160	Hs.33665	ESTs	3.7
	127115	AA375791	Hs.131894	ESTs	3.674
	132892	W92797	Hs.59378	DKFZP434G162 protein	3.653
20	115023	AA252079	Hs.63931	dachshund (Drosophila) homolog	3.625
	114932	AA242751	Hs.16218	KIAA0903 protein	3.62
	106865	AA487228	Hs.19479	ESTs	3.614
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 5 (13kD; B13)	3.613
	124780	R42493	Hs.220839	ESTs	3.6
25	130631	AA025399	Hs.169737	ESTs	3.592
	134154	AA211320	Hs.79404	neuron-specific protein	3.568
	104160	AA455706	Hs.99722	ESTs; Weakly similar to 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR	3.559
	105524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	3.542
30	110168	H19673	Hs.176586	ESTs	3.525
	109480	AA233299	Hs.72158	ESTs	3.522
	109585	F02367	Hs.27252	ESTs	3.5
	115134	AA257107	Hs.194331	ESTs	3.5
	116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROTEIN 6 [H.sapiens]	3.459
35	120524	AA261852	Hs.192905	ESTs	3.45
	116932	H74330	Hs.150000	ESTs	3.425
	130746	AA256976	Hs.18800	ESTs; Weakly similar to KIAA0579 protein [H.sapiens]	3.42
	107513	X05451	Hs.158295	Human alkali myosin light chain 3 mRNA; complete cds	3.417
	118641	N70298	Hs.49829	ESTs	3.407
40	126584	AI028384	Hs.127331	ESTs	3.399
	105134	AA159953	Hs.22895	ESTs; Weakly similar to arylsulfatase B precursor [H.sapiens]	3.325
	123502	AA600116	Hs.112526	ESTs	3.318
	132389	N50866	Hs.47135	ESTs	3.317
	105691	AA287097	Hs.75356	transcription factor 4	3.315
45	131505	H85897	Hs.27755	ESTs	3.309
	120775	AA342104	Hs.96777	EST	3.3
	105579	AA278824	Hs.19218	ESTs	3.295
	128190	AA946876	Hs.148376	ESTs	3.292
	100819	HG4020-HT4290		Transglutaminase	3.288
50	130217	D29956	Hs.152818	ubiquitin specific protease 8	3.273
	130068	AA608903	Hs.106220	KIAA0336 gene product	3.269
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.266
	110277	H29209	Hs.151231	ESTs; Highly similar to FYVE finger-containing phosphoinositide kinase [M.musculus]	3.26
	127354	AA418880	Hs.185797	ESTs	3.212
55	129173	R60523	Hs.109087	ESTs	3.197
	127464	AA970504	Hs.146103	ESTs	3.179
	124923	R94500	Hs.108046	ESTs	3.175
	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sapiens]	3.151
	122027	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapiens]	3.151
60	103329	X85134	Hs.72984	retinoblastoma-binding protein 5	3.15
	129937	M95767	Hs.135578	chitinase; di-N-acetyl-	3.15
	134197	AA057341	Hs.87889	helicase-moi	3.15
	107764	AA018219	Hs.226923	ESTs	3.125
	121775	AA421773	Hs.161008	ESTs	3.125
65	114768	AA149007	Hs.182339	Ets homologous factor	3.12
	132381	N48818	Hs.46884	ESTs	3.11
	123105	AA485973	Hs.143947	ESTs	3.104
	121176	AA400080	Hs.97774	ESTs	3.1
	125053	T80620	Hs.186473	ESTs	3.075
	105909	AA401739	Hs.5111	ESTs	3.066

	119767	W72562	Hs.58119	ESTs	3.057
	115776	AA424038	Hs.58197	ESTs	3.056
	111713	R22988	Hs.220950	ESTs	3.05
5	115301	AA280047	Hs.43948	ESTs	3.05
	118448	N65412	Hs.49189	ESTs	3
	106586	AA456598	Hs.256269	ESTs	2.995
	110415	H48239	Hs.29739	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-3A [H.sapiens]	2.979
	105173	AA182030	Hs.8364	ESTs	2.978
	101102	L07594	Hs.79059	transforming growth factor; beta receptor III (betaglycan; 300kD)	2.976
10	110543	H58383	Hs.258544	ESTs	2.976
	125593	R24464	Hs.202949	KIAA1102 protein	2.964
	100824	HG4058-HT4328		Oncogene Aml1-Evi-1, Fusion Activated	2.957
	106822	AA481068	Hs.31835	ESTs	2.95
	131963	D11930	Hs.3592	ESTs	2.95
15	111221	N68868	Hs.15119	ESTs	2.936
	113620	T93795	Hs.17252	EST	2.917
	105220	AA210695	Hs.17212	ESTs	2.917
	123234	AA490227	Hs.105252	ESTs	2.904
	125250	W67465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	2.9
20	116196	AA465160	Hs.63386	ESTs	2.9
	122100	AA432243	Hs.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PROTEIN [H.sapiens]	2.896
	111712	R22905	Hs.113716	ESTs	2.895
	126589	W78107	Hs.187698	ESTs; Weakly similar to Yer140wp [S.cerevisiae]	2.895
	111132	N64378	Hs.13149	ESTs; Highly similar to unknown function [H.sapiens]	2.894
25	115307	AA280300	Hs.191346	ESTs	2.886
	108989	AA152263	Hs.18827	KIAA0849 protein	2.883
	129486	H03686	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein	2.879
	119805	W73768	Hs.43213	ESTs	2.875
	125721	R59881	Hs.7503	ESTs	2.871
30	103704	AA028171	Hs.153688	ESTs	2.868
	128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	2.866
	120571	AA280738	Hs.128679	ESTs	2.863
	123059	AA482019	Hs.238202	EST	2.86
	129462	D84239	Hs.111732	IgG Fc binding protein	2.856
35	125166	W45491	Hs.172609	nucleobindin 1	2.854
	125992	W01626		za36e07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone	2.852
	109431	AA227972	Hs.43635	ESTs	2.85
	105077	AA142919	Hs.5558	ESTs	2.847
	131388	R34531	Hs.92200	KIAA0480 gene product	2.846
40	121080	AA398720	Hs.177953	ESTs	2.838
	112575	R73816	Hs.17385	ESTs	2.836
	130244	R26206	Hs.153293	KIAA0701 protein	2.825
	134698	AA427783	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	2.816
	116355	AA504356	Hs.88650	ESTs	2.813
45	115316	AA280627	Hs.57846	ESTs	2.806
	129677	U48736	Hs.198891	serine/threonine-protein kinase PRP4 homolog	2.8
	130971	H20332	Hs.28707	signal sequence receptor; gamma (translocon-associated protein gamma)	2.799
	115054	AA252863	Hs.87729	ESTs	2.795
	130285	AA063546	Hs.202968	ESTs	2.792
50	124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142)	2.783
	125502	AA732329	Hs.191959	ESTs	2.778
	114800	AA159825	Hs.131887	ESTs; Weakly similar to ORF YNL227c [S.cerevisiae]	2.768
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	2.766
	130159	H51098	Hs.151310	PDZ domain protein (Drosophila inaD-like)	2.75
55	107127	AA620504	Hs.22119	ESTs	2.742
	113547	T90746	Hs.15233	ESTs	2.734
	104639	AA004622	Hs.18214	ESTs	2.727
	127609	AA622559	Hs.150318	ESTs	2.726
	106922	AA490964	Hs.10056	ESTs	2.725
60	124825	R52088		yg85c3.s1 Soares infant brain 1NIB Homo sapiens cDNA clone	2.725
	124333	H96683	Hs.154054	ESTs	2.708
	117634	N36421	Hs.107854	ESTs; Weakly similar to SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSP	2.706
65	101609	M54927	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbacher disease; spastic paraplegia 2; uncomplicated)	2.704
	117142	H96908	Hs.42251	ESTs	2.7
	112602	R79147	Hs.203365	ESTs	2.695
	106828	AA481505	Hs.13797	ESTs	2.68
	124377	N25996	Hs.179833	ESTs	2.675

	101026	J04970	carboxypeptidase M	2.675
	124560	N66393	Hs.102754 ESTs	2.675
	124066	H02494	Hs.101615 ESTs	2.671
5	130281	R12777	Hs.15395 ESTs; Weakly similar to ARGINYL-TRNA SYNTHETASE [H.sapiens]	2.66
	110949	N49602	Hs.13308 ESTs	2.65
	111031	N54839	Hs.221085 ESTs; Highly similar to mediator [H.sapiens]	2.633
	121770	AA421714	Hs.11469 KIAA0896 protein	2.63
	134132	U32519	Hs.220689 Ras-GTPase-activating protein SH3-domain-binding protein	2.626
10	112424	R62452	Hs.191265 ESTs	2.625
	122544	AA451679	Hs.194410 ESTs	2.625
	134425	X90568	Hs.172004 titin	2.624
	111114	N63391	Hs.9238 ESTs	2.619
	116119	AA459242	Hs.44445 ESTs; Weakly similar to Kelch motif containing protein [H.sapiens]	2.615
	112079	R44164	Hs.23014 ESTs	2.6
15	123033	AA481271	Hs.193945 ESTs	2.591
	124196	H52617	Hs.144167 ESTs	2.586
	125873	H14437	y125a04.r1 Soares breast 3NbHBst Homo sapiens cDNA clone	2.58
	117684	N40184	Hs.45050 ESTs	2.575
20	134938	D30037	Hs.168326 phosphatidylinositol transfer protein; beta	2.575
	131822	AA215647	Hs.200332 ESTs	2.568
	135185	U71203	Hs.96038 Ric (Drosophila)-like; expressed in many tissues	2.564
	117690	N40467	Hs.93834 ESTs	2.557
	118807	N78582	Hs.50732 protein Kinase; AMP-activated; beta 2 non-catalytic subunit	2.552
25	121369	AA405657	Hs.128791 Human DNA sequence from clone 967N21 on chromosome 20p12.3-13. Contains	2.55
	114860	AA235112	Hs.106227 ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	2.549
	121857	AA426017	Hs.62694 ESTs; Highly similar to DNA-REPAIR PROTEIN COMPLEMENTING	2.548
	110190	H20560	Hs.244624 ESTs	2.548
	132573	AA045333	Hs.51743 ESTs; Weakly similar to !! ALU SUBFAMILY SB2 WARNING ENTRY !! [H.sapiens]	2.542
30	109706	F09729	Hs.12780 ESTs	2.537
	135109	AA410391	Hs.94592 klotho	2.525
	132810	R37027	Hs.5737 KIAA0475 gene product	2.525
	124879	R73588	Hs.101533 ESTs	2.525
	103840	AA174190	Hs.50932 ESTs	2.525
35	119066	R22196	Hs.34492 ESTs	2.519
	114833	AA234362	Hs.87310 ESTs; Moderately similar to CGI-66 protein [H.sapiens]	2.507
	112998	T23555	Hs.103288 ESTs	2.5
	123312	AA496258	Hs.99601 ESTs	2.499
	121873	AA426270	Hs.145696 splicing factor (CC1.3)	2.491
40	123321	AA496884	Hs.23972 ESTs	2.491
	107760	AA018042	Hs.95078 EST	2.483
	102590	U60608	Hs.152981 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	2.481
	103053	X56741	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	2.475
	124756	R38100	Hs.106294 ESTs	2.475
45	112936	T15665	Hs.6185 ESTs; Weakly similar to BcDNA.GH12174 [D.melanogaster]	2.475
	125178	W58202	Hs.125731 ESTs	2.475
	112423	R62447	Hs.22123 ESTs	2.471
	123515	AA600323	Hs.112535 EST	2.462
	102842	U95020	Hs.21903 calcium channel; voltage-dependent; beta 4 subunit	2.457
50	102400	U42390	Hs.171957 triple functional domain (PTPRF interacting)	2.455
	113187	T56056	Hs.9992 ESTs	2.452
	131687	L11066	Hs.3069 heat shock 70kD protein 9B (mortalin-2)	2.448
	115314	AA280583	Hs.256501 ESTs	2.437
	128211	AI206427	Hs.166707 ESTs; Highly similar to Ran-binding protein 2 [H.sapiens]	2.43
55	134281	L11005	Hs.81047 aldehyde oxidase 1	2.425
	115985	AA447709	Hs.132094 ESTs; Moderately similar to putative transcription factor CA150 [H.sapiens]	2.425
	111348	N90041	Hs.9585 ESTs	2.418
	129430	AA258842	Hs.197877 Homo sapiens clone 23777 putative transmembrane GTPase mRNA; partial cds	2.418
	133863	C13990	Hs.76930 synuclein; alpha (non A4 component of amyloid precursor)	2.417
60	111164	N66857	Hs.14808 ESTs; Weakly similar to !! ALU CLASS C WARNING ENTRY !! [H.sapiens]	2.416
	132143	AA257056	Hs.7972 KIAA0871 protein	2.412
	130330	M55047	Hs.154679 synaptotagmin 1	2.408
	114219	Z39451	Hs.27369 ESTs	2.406
	117101	H94043	Hs.24341 DKFZP586I1419 protein	2.403
65	125433	AA034325	Hs.54320 ESTs	2.4
	111069	N62506	Hs.21958 ESTs	2.4
	120323	AA195405	Hs.110347 Homo sapiens mRNA for alpha integrin binding protein 80; partial	2.397
	118624	N69998	Hs.21801 ESTs	2.394
	123570	AA608955	Hs.109653 ESTs	2.389
	123562	AA608893	Hs.190065 ESTs	2.388

	131546	AA262821	Hs.28578	muscleblind (Drosophila)-like	2.385
	103143	X66141	Hs.75535	myosin; light polypeptide 2; regulatory; cardiac; slow	2.384
	123645	AA609310	Hs.188681	ESTs	2.383
5	130123	AA001835	Hs.150390	zinc finger protein 262	2.379
	131682	AA428368	Hs.30654	ESTs	2.378
	115909	AA436666	Hs.59761	ESTs	2.375
	125168	W45574	Hs.252497	ESTs	2.372
	123973	C14805	Hs.182151	ESTs	2.361
	135197	U76456		Homo sapiens tissue inhibitor of metalloproteinase 4 mRNA, complete cds	2.357
10	118689	N71545	Hs.184544	ESTs	2.357
	107734	AA016225	Hs.93386	ESTs	2.354
	124590	N69220	Hs.41381	ESTs; Weakly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	2.35
	111163	N68850	Hs.17606	ESTs	2.348
	112349	R58877	Hs.22665	ESTs; Moderately similar to dJ83L6.1 [H.sapiens]	2.345
15	129076	AA262179	Hs.169343	ESTs	2.345
	134238	R81509	Hs.184571	splicing factor; arginina/serine-rich 11	2.341
	116766	H13260	Hs.95097	ESTs	2.336
	106331	AA436853	Hs.34795	ESTs	2.333
20	129003	AA443752	Hs.10784	ESTs	2.332
	132368	AA599814	Hs.46637	ESTs; Weakly similar to cDNA EST yk289g5.5 comes from this gene [C.elegans]	2.332
	124697	R06273	Hs.186467	ESTs; Modly smlr to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	2.322
	120273	AA176688	Hs.221139	ESTs	2.313
	127110	AA304993	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapiens]	2.307
25	105450	AA252621	Hs.93842	ESTs	2.301
	119819	W74371	Hs.58383	ESTs	2.297
	102302	U33052	Hs.69171	protein kinase C-like 2	2.288
	130596	N74353	Hs.16475	ESTs	2.282
	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	2.278
30	130542	U64675		Human sperm membrane protein BS-63 mRNA, complete cds	2.277
	104491	N71513	Hs.39328	ESTs	2.275
	116988	H62527		ys69e12.s1 Soares retina N2b4HR Homo sapiens cDNA clone	2.275
	126823	AA370120	Hs.7870	ESTs; Weakly similar to Ylr350wp [S.cerevisiae]	2.273
	108800	AA129731	Hs.90424	ESTs	2.273
35	101310	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2; l-branching enzyme	2.269
	126842	W19498	Hs.21085	ESTs	2.255
	127251	AA936428	Hs.128638	ESTs	2.251
	124647	N91947	Hs.125033	ESTs	2.249
	127112	AI143906	Hs.125103	ESTs	2.247
40	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	2.246
	120899	AA398302	Hs.127437	ESTs	2.245
	130225	AA599583	Hs.15299	HMBa-inducible	2.243
	119980	W88678	Hs.249247	heterogeneous nuclear protein similar to rat helix destabilizing protein	2.243
	124222	H61053	Hs.222844	ESTs	2.24
45	129199	H90914	Hs.128629	ESTs	2.236
	106802	AA479101	Hs.16570	ESTs; Weakly similar to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	2.231
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-related protein [H.sapiens]	2.229
	104627	AA001976	Hs.19603	ESTs	2.228
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	2.226
50	113096	T40927	Hs.8345	ESTs	2.225
	135336	AA452822	Hs.99027	ESTs	2.225
	135344	R62976	Hs.168491	ESTs; Moderately similar to TRF1-interacting ankyrin-related	2.225
	126156	AA508354	Hs.118448	ESTs; Moderately similar to AKT3 protein kinase [H.sapiens]	2.222
	128885	AA397841	Hs.180141	cofilin 2 (muscle)	2.218
55	107900	AA026385	Hs.176600	ESTs; Moderately similar to !! ALU SUBFAMILY SB2 WARNING	2.217
	114481	AA033562	Hs.151572	ESTs	2.212
	109292	AA199828	Hs.188662	ESTs	2.212
	104257	AF008265	Hs.9222	estrogen receptor-binding fragment-associated gene 9	2.209
	132932	T15482	Hs.6093	ESTs	2.204
60	127392	AA262728	Hs.14896	Homo sapiens clone 24590 mRNA sequence	2.204
	104641	AA004652	Hs.18564	ESTs	2.2
	122529	AA449828	Hs.99229	ESTs	2.195
	124307	H93562	Hs.162395	proline synthetase co-transcribed (bacterial homolog)	2.193
	133601	S95936	Hs.75155	transferrin	2.193
65	119904	W85709	Hs.128927	ESTs; Weakly similar to !! ALU SUBFAMILY SP WARNING ENTRY !! [H.sapiens]	2.192
	100348	D64109	Hs.4994	transducer of ERBB2; 2 (TOB2)	2.185
	126871	AA351779	Hs.200334	ESTs	2.18
	127793	AI298835	Hs.30445	ESTs; Weakly similar to transcription regulator Stat-50 [H.sapiens]	2.178
	105149	AA169253	Hs.8958	ESTs	2.177
	121367	AA405648		zw39g8.s1 Soares_total_fetus_Nb2HF8_9w H sapiens cDNA clone IMAGE:772478	2.177

	111836	R36228	Hs.25119	ESTs	2.175
	133394	R16759	Hs.237225	ribosomal protein S5 pseudogene 1	2.175
	123207	AA489697	Hs.145053	ESTs	2.175
	129801	F11087	Hs.239666	ESTs	2.175
5	103393	X94612	Hs.41749	protein kinase; cGMP-dependent; type II	2.161
	132415	AA043223	Hs.4815	nudix (nucleoside diphosphate linked moiety X)-type motif 3	2.157
	106369	AA443628	Hs.25324	ESTs	2.157
	122963	AA478446	Hs.69559	KIAA1096 protein	2.156
	133473	M19309	Hs.73980	troponin T1; skeletal; slow	2.155
10	134257	C06270	Hs.8078	Homo sapiens mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081)	2.155
	135156	AA056012	Hs.8552	binder of Arl Two	2.151
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [H.sapiens]	2.15
	102313	U33921		HSU33921 Clontech adult lung cDNA library (HL1158a) Homo sapiens cDNA	2.15
	109788	F10638	Hs.12432	Homo sapiens clone 24407 mRNA sequence	2.15
15	103507	Y10032	Hs.159640	serum/glucocorticoid regulated kinase	2.15
	116000	AA448710	Hs.41327	ESTs	2.15
	105858	AA399164	Hs.227676	ESTs; Moderately similar to !! ALU SUBFAMILY SQ	2.137
	103153	X66534	Hs.75295	guanylate cyclase 1; soluble; alpha 3	2.137
	126202	AA652238	Hs.199726	ESTs	2.135
20	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	2.134
	104164	AA458770	Hs.27023	KIAA0917 protein	2.132
	108892	AA121270	Hs.82960	ESTs	2.128
	122878	AA465341	Hs.99640	ESTs	2.126
	134771	L13939	Hs.89576	adaptor-related protein complex 1; beta 1 subunit	2.125
25	104298	D31120	Hs.40368	adaptor-related protein complex 1; sigma 2 subunit	2.125
	104840	AA039595	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817)	2.125
	122180	AA435798	Hs.98835	ESTs; Moderately similar to putative ring zinc finger protein	2.125
	131012	H01992	Hs.202949	KIAA1102 protein	2.125
	134092	H17490	Hs.7905	ESTs; Highly similar to sorting nexin 9 [H.sapiens]	2.123
30	118617	N69666	Hs.183413	ESTs; Modtly smlr to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	2.123
	107155	AA621202	Hs.7946	DKFZP586D1519 protein	2.12
	130925	N71935	Hs.169378	multiple PDZ domain protein	2.12
	135167	U63717	Hs.95821	osteoclast stimulating factor 1	2.118
	105952	AA405263	Hs.181400	ESTs	2.109
35	110308	H38148	Hs.32775	ESTs	2.108
	116368	AA521186	Hs.94217	ESTs	2.107
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	2.102
	117881	N50073	Hs.84926	ESTs; Highly similar to B-IND1 protein [M.musculus]	2.1
	121723	AA419622	Hs.104800	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	2.096
40	103500	Y09443	Hs.22580	alkylglycerone phosphate synthase	2.094
	121429	AA406293	Hs.193498	ESTs	2.093
	134632	AA398710	Hs.174139	chloride channel 3	2.091
	129785	F10980	Hs.184780	ESTs	2.09
	111065	N58193	Hs.18740	ESTs; Weakly similar to 1-evidence	2.089
45	114710	AA129931	Hs.79081	protein phosphatase 1; catalytic subunit; gamma isoform	2.083
	132711	N73702	Hs.238927	ESTs	2.083
	133377	R05490	Hs.7239	SEC24 (S. cerevisiae) related gene family; member B	2.079
	124773	R40923	Hs.106604	ESTs	2.078
	117759	N47587	Hs.97345	ESTs; Weakly similar to TROPOMODULIN [H.sapiens]	2.076
50	127386	A1457411	Hs.106728	ESTs	2.076
	101167	L15309	Hs.193677	zinc finger protein 141 (clone pHZ-44)	2.075
	109597	F02582	Hs.14474	ESTs	2.074
	124390	N29325	Hs.7535	ESTs; Highly similar to COBW-like placental protein [H.sapiens]	2.07
	116225	AA478609	Hs.47278	Human Chromosome 16 BAC clone CIT987SK-A-735G6	2.07
55	131243	R16667	Hs.24752	spectrin SH3 domain binding protein 1	2.069
	130557	T90830	Hs.15981	ESTs; Weakly similar to line-1 protein ORF2 [H.sapiens]	2.067
	134103	D14826	Hs.155924	cAMP responsive element modulator	2.064
	108833	AA131866	Hs.61661	ESTs; Weakly similar to DY3.6 [C.elegans]	2.063
	112286	R53765	Hs.158135	KIAA0981 protein	2.063
60	125624	AA165411		zq49a01.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone	2.061
	124612	N72200	Hs.13913	ESTs	2.058
	116335	AA495830	Hs.87013	ESTs	2.057
	112248	R51361	Hs.23423	ESTs	2.056
	115789	AA424754	Hs.43149	ESTs	2.056
65	107029	AA599219	Hs.187492	ESTs; Weakly similar to ALR [H.sapiens]	2.056
	110294	H30270	Hs.165062	ESTs	2.054
	120532	AA262354	Hs.186648	ESTs	2.054
	118180	N59249	Hs.48349	ESTs	2.052
	132018	AA293194	Hs.3737	ESTs	2.052

	132617	AA171913	Hs.5338	carbonic anhydrase XII	2.05
	131526	N36167	Hs.28274	ESTs	2.05
	113254	T64438	Hs.11449	DKFZP564O123 protein	2.05
	122785	AA459978	Hs.99508	ESTs	2.05
5	107203	D20426	Hs.5656	EST	2.05
	105713	AA291321	Hs.184319	ESTs; Moderately similar to KIAA1006 protein [H.sapiens]	2.046
	129385	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.042
	119116	R43845	Hs.64595	DKFZP566E2346 protein	2.04
	116405	AA600253	Hs.55601	ESTs; Highly similar to host cell factor 2 [H.sapiens]	2.04
10	125924	AA526849	Hs.82109	syndecan 1	2.039
	105599	AA279442	Hs.143460	protein kinase C; nu	2.037
	119741	W70205	Hs.43670	kinesin family member 3A	2.037
	101449	M21494	Hs.118843	creatine kinase; muscle	2.036
	107109	AA609943	Hs.32793	ESTs	2.034
15	117040	H89112		yw25a5.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:25328	2.034
	132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	2.031
	105479	AA255546	Hs.23467	ESTs	2.027
	102031	U04898	Hs.2156	RAR-related orphan receptor A	2.027
	119846	W80363	Hs.58446	ESTs	2.024
20	124809	R46482	Hs.106875	ESTs	2.024
	130286	AA041548	Hs.154023	KIAA0573 protein	2.023
	124457	N50114	Hs.128704	ESTs	2.017
	125144	W37999	Hs.24336	ESTs	2.017
	120581	AA281257	Hs.125868	ESTs	2.014
25	104931	AA062731	Hs.108319	thyroid hormone receptor-associated protein; 150 kDa subunit	2.012
	120548	AA278846	Hs.187634	ESTs	2.011
	113933	W81362	Hs.30567	ESTs	2.011
	123072	AA485041	Hs.104308	ESTs	2.009
	123648	AA609323	Hs.112689	ESTs	2.008
30	116875	H67749	Hs.161022	EST	2.003
	103179	X69398	Hs.82685	CD47 antigen (Rh-related antigen; integrin-associated signal transducer)	1.995
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.995
	111007	N53378	Hs.22543	ESTs	1.995
	120470	AA251797		zs11f3.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone	1.989
35	112280	R53457	Hs.26040	ESTs; Weakly similar to fatty acid omega-hydroxylase [H.sapiens]	1.989
	114127	Z38652	Hs.106961	ESTs; Weakly similar to TYL [H.sapiens]	1.988
	129863	AA151005	Hs.129872	sperm surface protein	1.988
	106320	AA436608		ESTs	1.988
	108933	AA147224	Hs.71814	ESTs	1.986
40	105906	AA401633	Hs.22380	ESTs	1.982
	109029	AA157911	Hs.72200	ESTs	1.982
	118470	N66769	Hs.82781	ESTs	1.975
	115358	AA281886	Hs.88923	ESTs	1.975
	115257	AA279060	Hs.193516	B-cell CLL/lymphoma 10	1.974
45	126879	AA719776		zh38g04.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414390	1.974
	109547	F01479	Hs.26966	ESTs	1.973
	127111	AA805726	Hs.220509	ESTs	1.969
	101266	L36645	Hs.73964	EphA4	1.966
	129319	AA037467	Hs.30340	ESTs	1.965
50	106211	AA428240	Hs.126083	ESTs	1.962
	112753	R93696	Hs.169882	ESTs	1.961
	120489	AA255538	Hs.190504	ESTs	1.959
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiquitin-protein ligase Rsp5	1.956
	105425	AA251129	Hs.24416	ESTs	1.953
55	134740	L37362	Hs.89455	opioid receptor; kappa 1	1.95
	109324	AA210700	Hs.86405	Homo sapiens mRNA; cDNA DKFZp564P056 (from clone DKFZp564P056)	1.95
	124303	H83043	Hs.107070	ESTs	1.95
	102337	U36922		Human fork head domain protein (FKHR) mRNA, 3' end	1.948
	109441	AA228100	Hs.86998	nuclear factor of activated T-cells 5	1.946
60	127364	AA179573	Hs.90061	progesterone binding protein	1.942
	105255	AA227498	Hs.3623	ESTs	1.942
	130672	L19783	Hs.177	phosphatidylinositol glycan; class H	1.942
	104301	D45332	Hs.6783	ESTs	1.94
	132442	R62589	Hs.167419	ESTs	1.939
65	105519	AA258063	Hs.23438	ESTs	1.937
	132902	AA490969	Hs.168147	ESTs	1.936
	118873	N89881	Hs.44577	ESTs	1.936
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein [H.sapiens]	1.934
	115075	AA255486	Hs.88045	ESTs	1.933

	110695	H93483	Hs.124777	ESTs	1.931
	105360	AA236209	Hs.187626	ESTs	1.931
	124998	T56013	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.929
5	121816	AA424814	Hs.187509	ESTs	1.927
	111717	R23241	Hs.110776	STAT induced STAT inhibitor-2	1.925
	128874	H06245	Hs.106801	ESTs	1.925
	109391	AA219699	Hs.184245	KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog	1.913
	126129	H82165	Hs.40334	ESTs	1.911
10	115553	AA369027	Hs.71414	ESTs	1.905
	113811	W44928	Hs.4878	ESTs	1.905
	108345	AA070906		zm66d1.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone	1.904
	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [M.musculus]	1.903
	116602	D80063	Hs.241673	EST	1.901
15	121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein SALL1 [H.sapiens]	1.9
	125330	AA401804	Hs.114574	ESTs	1.896
	130095	F01831	Hs.14838	ESTs	1.894
	119762	W72982	Hs.58262	ESTs	1.894
	104115	AA428090	Hs.26102	ESTs	1.893
20	131313	C17938	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)	1.891
	105583	AA278907	Hs.24549	ESTs	1.891
	122825	AA461195	Hs.99580	ESTs	1.887
	119495	W35390	Hs.55533	ESTs	1.886
	130309	AA134289	Hs.15423	Homo sapiens BAC clone RG114B19 from 7q31.1	1.886
	125628	AA418069	Hs.241493	natural killer-tumor recognition sequence	1.886
25	110611	H66947	Hs.14671	ESTs; Highly similar to gene ERCC5 protein [H.sapiens]	1.885
	117301	N22569	Hs.43215	ESTs	1.884
	131406	N92239	Hs.28471	Wnt inhibitory factor-1	1.881
	126428	AA013312	Hs.64988	ESTs	1.881
30	120285	AA182882	Hs.111110	titin-cap (telethonin)	1.878
	112724	R91753	Hs.17757	ESTs	1.878
	103121	X63679	Hs.4147	translocating chain-associating membrane protein	1.875
	124381	N26765	Hs.109008	ESTs	1.875
	117226	N20468	Hs.177322	ESTs; Weakly similar to putative p150 [H.sapiens]	1.875
35	105610	AA279991	Hs.124691	ESTs; Weakly similar to trithorax homologue 2 [H.sapiens]	1.875
	111229	N69113	Hs.110855	ESTs	1.875
	120627	AA285079	Hs.190474	ESTs	1.873
	107048	AA600012	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.sapiens]	1.872
	104041	AA381902	Hs.197114	RNA binding protein	1.872
40	115182	AA258366	Hs.227806	ras GTPase activating protein-like	1.872
	102239	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.87
	100043	M10098		AFFX control: 18S ribosomal RNA	1.868
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	1.867
	129011	S72869	Hs.107932	DNA segment; single copy; probe pH4 (transforming sequence; thyroid-1;	1.867
45	134851	R44479	Hs.90232	KIAA0552 gene product	1.866
	117392	N26175	Hs.93405	ESTs	1.864
	114530	AA053027	Hs.191797	ESTs	1.863
	123541	AA608794	Hs.112592	ESTs	1.863
	124890	R78618	Hs.34145	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-8 [H.sapiens]	1.862
50	105299	AA233511	Hs.194720	ATP-binding cassette; sub-family G (WHITE); member 2	1.861
	103560	Z20656	Hs.182787	myosin; heavy polypept 6; cardiac muscle; alpha (cardiomyopathy; hypertrophic 1)	1.861
	113073	T33637	Hs.6841	ESTs	1.86
	120407	AA235040	Hs.107283	ESTs	1.859
	103892	AA243523	Hs.17155	ESTs	1.858
55	123795	AA620381	Hs.70488	ESTs	1.857
	108524	AA084323	Hs.68138	ESTs	1.857
	113953	W85812	Hs.187554	ESTs	1.856
	110721	H97678	Hs.31319	ESTs	1.856
	129426	AA412087	Hs.168272	EST; Highly smir to prot inhibitor of activated STAT prot PIASx-alpha [H.sapiens]	1.853
60	112102	R44840	Hs.21303	ESTs	1.852
	118502	N67317	Hs.50150	ESTs	1.852
	107619	AA004955	Hs.60015	ESTs	1.851
	100436	D87446	Hs.75912	KIAA0257 protein	1.85
	120652	AA287312	Hs.191648	ESTs	1.85
65	121643	AA417078	Hs.193767	ESTs	1.843
	117387	N26011	Hs.53810	ESTs	1.843
	132034	Y12394	Hs.3886	karyopherin alpha 3 (importin alpha 4)	1.843
	124449	N48593	Hs.121820	ESTs	1.841
	120263	AA173440	Hs.193919	ESTs	1.838
	127226	AA731036	Hs.3463	ribosomal protein S23	1.838

	111837	R36447	Hs.24453	ESTs	1.835
	128727	M64174	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	1.834
	114439	AA018937	Hs.128629	ESTs	1.833
5	102332	U35637		Human nebulin mRNA, partial cds	1.83
	126579	W72979	Hs.146082	ESTs	1.83
	102341	U37122	Hs.8110	adducin 3 (gamma)	1.83
	114246	Z39848	Hs.12079	ESTs	1.828
	131757	D17532	Hs.316	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase; 54kD)	1.823
	108904	AA136521	Hs.71148	ESTs; Weakly similar to putative p150 [H.sapiens]	1.823
10	115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	1.823
	131957	AA609008	Hs.183232	ESTs	1.822
	100131	D12485	Hs.11951	phosphodiesterase 1/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen)	1.822
	124163	H30539	Hs.189838	ESTs	1.821
15	118204	N59859	Hs.48443	ESTs	1.821
	107727	AA016021	Hs.173091	DKFZP434K151 protein	1.82
	100357	D78156	Hs.241548	RAS p21 protein activator 2	1.82
	116295	AA489016	Hs.91216	ESTs; Highly similar to partial CDS; human putative tumor suppressor [H.sapiens]	1.82
20	124833	R54112	Hs.128697	ESTs	1.817
	122587	AA453255	Hs.6968	ESTs	1.817
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride channel [H.sapiens]	1.815
	111289	N72253	Hs.238246	ESTs	1.813
	110826	N30068	Hs.15347	ESTs	1.812
	104106	AA422123	Hs.42457	ESTs	1.811
25	130043	AA055404	Hs.193953	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.253
	115864	AA432060	Hs.81200	ESTs	1.81
	129737	AA056140	Hs.122684	ESTs	1.81
	124477	N53158	Hs.102682	ESTs	1.809
30	100782	HG3740-HT4010		Basic Transcription Factor 2, 34 Kda Subunit	1.806
	106101	AA421053	Hs.34395	ESTs	1.806
	115479	AA287596		zs52h09.s1 NCI_CGAP_GCB1 H sapiens cDNA clone IMAGE:701153	1.804
	116104	AA456635	Hs.78524	ESTs	1.804
	114173	Z39050	Hs.21963	ESTs	1.804
35	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1.803
	119135	R49548	Hs.169681	death effector domain-containing	1.802
	131559	N91087	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.elegans]	1.801
	126922	AA177138	Hs.161671	ESTs	1.8
	117375	N25427	Hs.108812	ESTs	1.8
40	103571	Z25535	Hs.211608	nucleoporin 153kD	1.8
	105978	AA406367	Hs.15973	ESTs	1.8
	125904	H22372	Hs.163586	ESTs	1.799
	133883	AA397915	Hs.77221	choline kinase	1.798
	105777	AA348412	Hs.23096	ESTs	1.797
	110166	H19480	Hs.174309	ESTs	1.796
45	105038	AA130273	Hs.7584	ESTs; Weakly similar to hypothetical protein; similar to [H.sapiens]	1.796
	105427	AA251330	Hs.28248	ESTs	1.795
	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.melanogaster]	1.794
	133104	L13698	Hs.65029	growth arrest-specific 1	1.794
	131170	N48674	Hs.23796	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the	1.792
50	100136	D13540	Hs.22868	protein tyrosine phosphatase; non-receptor type 11	1.791
	127263	AA331157		EST35035 Embryo, 6 week, subtracted (total cDNA) I Homo sapiens cDNA	1.79
	114157	Z38878	Hs.24979	ESTs	1.79
	125601	AI096717	Hs.247043	KIAA0525 protein	1.788
55	118472	N66818	Hs.42179	ESTs	1.787
	112456	R63925	Hs.28464	ESTs	1.787
	130236	N69682	Hs.51957	SC35-interacting protein 1	1.786
	133297	AA600057	Hs.70266	KIAA0905 protein	1.784
	125650	R40096	Hs.176578	ESTs	1.784
	132056	T89386	Hs.38176	KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP)	1.783
60	129093	AA262710	Hs.108614	KIAA0627 protein	1.783
	123176	AA489020	Hs.193424	ESTs	1.782
	106340	AA441792	Hs.22857	chord domain-containing protein 1	1.781
	100598	HG2463-HT2559		Guanine Nucleotide-Binding Protein G25k	1.779
	104038	AA374532		EST86676 HSC172 cells I Homo sapiens cDNA 5' end, mRNA sequence	1.778
65	122235	AA436475	Hs.190104	ESTs	1.777
	105104	AA151771	Hs.76941	ATPase; Na+/K+ transporting; beta 3 polypeptide	1.776
	107601	AA004636	Hs.50223	ESTs	1.776
	131467	W68255	Hs.27194	DKFZP434K171 protein	1.776
	118449	N66413	Hs.172466	ESTs; Weakly similar to KIAA0775 protein [H.sapiens]	1.776

	107969	AA034030	Hs.155212	methylmalonyl Coenzyme A mutase	1.775
	115527	AA342079	Hs.252055	ESTs	1.775
	132471	T16305	Hs.49349	beta-site APP-cleaving enzyme	1.775
5	105966	AA406105	Hs.5344	adaptor-related protein complex 1; gamma 1 subunit	1.774
	127548	AA373091	Hs.93832	Homo sapiens clone 24483 unknown mRNA; parital cds	1.774
	106217	AA428379	Hs.24870	ESTs	1.773
	131214	N26777	Hs.172635	ESTs	1.773
	106295	AA435664	Hs.8583	similar to APOBEC1	1.773
10	106328	AA436705	Hs.28020	KIAA0766 gene product	1.772
	124661	N93797	Hs.3090	EphB1	1.772
	122988	AA479166	Hs.105633	ESTs	1.772
	115504	AA291946	Hs.42736	ESTs	1.771
	105168	AA180208	Hs.16606	ESTs; Highly similar to CGI-32 protein [H.sapiens]	1.767
	129153	AA188618	Hs.181461	ariadne; Drosophila; homolog of	1.766
15	105829	AA398290	Hs.21965	ESTs	1.764
	101811	M86917	Hs.24734	oxysterol binding protein	1.764
	100138	D13628	Hs.2463	angiotensin 1	1.764
	124704	R07335	ye96c1.s1	Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	1.763
20	122314	AA442257	Hs.192076	ESTs	1.762
	109865	H02566	Hs.191268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.761
	106206	AA428069	Hs.89519	KIAA1046 protein	1.758
	107135	AA620782	Hs.23247	ESTs	1.757
	105760	AA336960	Hs.28170	ESTs	1.756
25	106288	AA435536	Hs.24336	ESTs	1.756
	103968	AA304566	Hs.3542	ESTs	1.756
	129559	AA234945	Hs.11360	ESTs	1.756
	117885	N50112	Hs.47023	ESTs	1.754
	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subunit	1.754
30	124807	R45963	Hs.233811	ESTs; Weakly similar to ORF2 [M.musculus]	1.753
	100276	D42047	Hs.82432	KIAA0089 protein	1.753
	110924	N47938	yy84a09.s1	Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone	1.751
	133002	AF006082	Hs.62461	ARP2 (actin-related protein 2; yeast) homolog	1.751
	132530	AA455917	Hs.50785	SEC22; vesicle trafficking protein (S. cerevisiae)-like 1	1.75
35	110759	N21671	Hs.19025	ESTs	1.75
	106138	AA424515	Hs.33264	ESTs	1.75
	107348	U43701	Hs.184776	ribosomal protein L23a	1.75
	115867	AA432162	Hs.165986	DKFZP586B2022 protein	1.749
	135398	AA194075	Hs.99908	nuclear receptor coactivator 4	1.747
40	113783	W19222	Hs.7041	ESTs; Weakly similar to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.747
	134898	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	1.745
	132215	T10132	Hs.4236	KIAA0478 gene product	1.744
	104229	AB002346	Hs.61289	synaptotagmin 2	1.743
	116166	AA461556	Hs.202949	KIAA1102 protein	1.743
45	115433	AA284252	Hs.58372	ESTs	1.743
	114908	AA236545	Hs.54973	ESTs	1.742
	127425	AA470941	Hs.143162	ESTs	1.741
	131089	Z38807	Hs.22870	ESTs	1.739
	113498	T88908	Hs.189746	ESTs	1.738
50	116710	F10577	Hs.70312	ESTs	1.735
	127210	R51476	yg76f04.r1	Soares infant brain 1NIB Homo sapiens cDNA clone	1.733
	120554	AA279654	Hs.194524	ESTs	1.733
	129940	U18242	Hs.13572	calcium modulating ligand	1.732
	117023	H88157	Hs.41105	ESTs	1.731
55	111700	R22212	Hs.23361	ESTs	1.731
	116911	H72240	Hs.39292	ESTs; Moderately similar to KIAA0745 protein [H.sapiens]	1.731
	106025	AA412063	Hs.6065	ESTs	1.728
	108626	AA101984	Hs.61697	G-protein coupled receptor	1.726
	111614	R12581	Hs.191146	ESTs	1.726
60	134134	L76703	Hs.173328	protein phosphatase 2; regulatory subunit B (B56); epsilon isoform	1.725
	106886	AA489086	Hs.36545	ESTs	1.725
	117998	N52136	Hs.93828	ESTs	1.725
	121204	AA400422	Hs.55896	ESTs	1.725
	121342	AA404995	Hs.192490	ESTs	1.725
65	131129	R27296	Hs.23240	ESTs	1.725
	116235	AA479181	Hs.186726	ESTs	1.725
	102423	U44754	Hs.179312	small nuclear RNA activating complex; polypeptide 1; 43kD	1.724
	110273	H29050	Hs.24096	ESTs	1.722
	108758	AA127395	Hs.222414	ESTs	1.722
	110672	H88477	Hs.191178	ESTs	1.721

	120271	AA176404	Hs.111092	ESTs; Weakly similar to ZINC FINGER PROTEIN 136 [H.sapiens]	1.72
	100227	D28915	Hs.82316	interferon-induced; hepatitis C-associated microtubular aggregate prot (44kD)	1.719
	129232	W69459	Hs.109655	sex comb on midleg (Drosophila)-like 1	1.719
5	134663	W73367	Hs.8750	ESTs	1.717
	104902	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.717
	120582	AA281290	Hs.125287	ESTs; Weakly similar to BC331191_1 [H.sapiens]	1.717
	134891	F03517	Hs.90787	ESTs	1.716
	106219	AA428567	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	1.715
	116372	AA521311	Hs.13854	ESTs	1.713
10	107570	AA001870	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	1.713
	106198	AA427816	Hs.11803	ESTs	1.712
	125136	W31479	Hs.129051	ESTs	1.712
	104973	AA085676	Hs.6763	KIAA0942 protein	1.712
	128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (niphedipine oxidase); polypeptide 5	1.711
15	123994	D20899	Hs.107127	Homo sapiens mRNA; cDNA DKFZp564G022 (from clone DKFZp564G022)	1.711
	127871	AA766511	Hs.128848	ESTs	1.71
	116089	AA455933	Hs.41324	ESTs	1.709
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevisiae]	1.708
	123619	AA609200	Hs.162696	ESTs	1.708
20	104781	AA026617	Hs.21610	ESTs; Highly similar to BAI1-associated protein 1 [H.sapiens]	1.707
	115114	AA256468	Hs.88148	ESTs	1.705
	117852	N49408	Hs.136102	KIAA0853 protein	1.705
	127644	T57570	Hs.77039	ribosomal protein S3A	1.704
	111359	N91273	Hs.27179	ESTs	1.702
25	131721	L36644	Hs.31092	EphA5	1.7
	132438	F08925	Hs.48610	ESTs	1.7
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat region mRNA	1.7
	130990	F02488	Hs.21917	KIAA0768 protein	1.7
	128499	AA467503	Hs.100636	ESTs	1.698
30	120780	AA342337	Hs.241569	ESTs; Modtly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.697
	132920	L06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide (Menkes syndrome)	1.696
	135037	U77948	Hs.184122	general transcription factor II; i	1.696
	110024	H11297	Hs.31050	ESTs	1.695
	134415	AA329274	Hs.82911	protein tyrosine phosphatase type IVA; member 2	1.694
35	102223	U24685	Hs.148226	Human anti-B cell autoantibody IgM heavy chain variable V-D-J region (VH4) gene; clone E11; VH4-63 non-productive rearrangement	1.694
	126712	AA205862	Hs.7942	ESTs	1.694
	101507	M27492	Hs.82112	interleukin 1 receptor; type I	1.692
	106291	AA435551	Hs.30824	ESTs	1.691
40	116826	H58691	Hs.8215	ESTs; Weakly similar to double-stranded RNA-binding nuclear protein DRBP76 [H.sapiens]	1.69
	135339	D59269	Hs.127842	Homo sapiens mRNA full length Insert cDNA clone EUROIMAGE 783648	1.69
	118250	N62602	yz75b6.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288851 3' similar to contains Alu repetitive element; mRNA sequence	1.689	
45	106470	AA450116	Hs.186180	ESTs	1.688
	108203	AA057678	Hs.63408	ESTs	1.687
	119748	W70313	Hs.126906	ESTs	1.686
	116576	D51228	Hs.79404	neuron-specific protein	1.683
	123035	AA481392	Hs.105166	ESTs	1.683
50	126668	AA011616	Hs.184086	ESTs	1.681
	101512	M28209	Hs.250716	RAB1; member RAS oncogene family	1.678
	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.677
	126218	AA256386	Hs.13649	Novel human gene mapping to chromosome 13; similar-to rat RhoGAP	1.676
	111180	N67277	Hs.9403	ESTs	1.676
55	105937	AA404342	Hs.173531	ESTs	1.675
	114118	Z38520	Hs.175930	ESTs	1.675
	109203	AA190634	Hs.108787	endoplasmic reticulum membrane protein	1.675
	125245	W86608	Hs.7243	ubiquitin specific protease 24	1.675
	102906	X06956	Hs.75318	tubulin; alpha 1 (testis specific)	1.675
60	125914	AA262925	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subunit 3; 77kD	1.674
	134294	U63289	Hs.81248	CUG triplet repeat; RNA-binding protein 1	1.674
	109742	F10108	Hs.183333	ESTs	1.673
	134674	D63876	Hs.87726	KIAA0154 protein	1.673
	104079	AA402937	Hs.103238	ESTs	1.671
65	107554	AA001386	Hs.59844	ESTs	1.671
	132439	AA243139	Hs.4863	Homo sapiens clone 25068 mRNA sequence	1.669
	124515	N58172	Hs.109370	ESTs	1.668
	124300	H92575	Hs.105959	ESTs; Weakly similar to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.668
	126809	AA743475	Hs.171693	ESTs	1.667

	106095	AA419547	Hs.11713	ESTs	1.664
	101754	M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	1.663
	105188	AA192306	Hs.23926	ESTs	1.663
	113582	T91371	Hs.16824	EST	1.661
5	119559	W38197		Accession not listed in Genbank	1.661
	119961	W87535	Hs.59015	ring finger protein 9	1.657
	123255	AA490890	Hs.105273	ESTs	1.657
	111078	N59230	Hs.186574	ESTs	1.655
	113082	T40528	Hs.8246	ESTs	1.654
10	119569	W44692	Hs.124177	ESTs	1.652
	104308	D53639	Hs.77904	ribosomal protein S26	1.65
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alpha type; 6	1.65
	124424	N35314	Hs.107265	ESTs	1.65
15	128890	AA096157	Hs.182364	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	1.65
	119400	T92767		ye27d06.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118955 3', mRNA sequence.	1.65
	131631	AA486868	Hs.29802	slit (Drosophila) homolog 2	1.65
	118229	N62339	Hs.180532	heat shock 90kD protein 1; alpha	1.649
	118533	N67954	Hs.49413	ESTs	1.648
20	130666	AA476307	Hs.194035	KIAA0737 gene product	1.647
	103093	X60708	Hs.44926	dipeptidylpeptidase IV (CD26; adenosine deaminase complexing protein 2)	1.647
	128667	U69140	Hs.103419	fasciculation and elongation protein zeta 2 (zyglin II)	1.646
	112933	T15530	Hs.221439	ESTs	1.646
	114546	AA056263	Hs.132747	ESTs	1.645
25	126705	AA579377	Hs.180532	heat shock 90kD protein 1; alpha	1.644
	114399	AA007595	Hs.220937	ESTs	1.642
	118836	N79820	Hs.50854	ESTs	1.64
	100401	D85423		Homo sapiens mRNA for Cdc5, partial cds	1.64
30	105681	AA284865	Hs.171228	KIAA1040 protein	1.639
	132526	AA460128	Hs.5074	similar to S. pombe dim1+	1.639
	133809	AA034002	Hs.76359	catalase	1.639
	115968	AA447083	Hs.134522	ESTs	1.637
	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]	1.631
35	109644	F04477	Hs.204802	ESTs; Moderately similar to GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE; LIVER [H.sapiens]	1.627
	103427	X97303		H.sapiens mRNA for Ptg-12 protein	1.627
	132186	T33888	Hs.221040	KIAA1038 protein	1.626
	131428	U17838	Hs.26719	PR domain containing 2; with ZNF domain	1.626
40	126638	AA649257	Hs.188602	ESTs	1.625
	114503	AA039568	Hs.188083	ESTs	1.625
	121242	AA400857	Hs.97509	EST	1.625
	122414	AA446885	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.625
	110632	H72344	Hs.171635	ESTs	1.624
45	111389	N95837	Hs.169111	ESTs; Weakly similar to L82A [D.melanogaster]	1.624
	112449	R63802	Hs.124186	ring finger protein 2	1.623
	113070	T33464	Hs.6298	ESTs	1.622
	107229	D59284	Hs.34644	ESTs	1.618
50	132710	W93726	Hs.55279	protease inhibitor 5 (maspin)	1.617
	124664	N94814	Hs.33540	ESTs; Weakly similar to KIAA0765 protein [H.sapiens]	1.617
	130166	AA350690	Hs.151411	KIAA0916 protein	1.616
	125040	T78451	Hs.199961	ESTs	1.615
	132972	H39627	Hs.164967	ESTs; Weakly similar to !! ALU SUBFAMILY SB WARNING ENTRY !! [H.sapiens]	1.615
	115873	AA433916	Hs.90093	heat shock 70kD protein 4	1.611
55	120408	AA235045	Hs.190151	ESTs	1.61
	120934	AA383773	Hs.191500	ESTs	1.61
	115259	AA279071	Hs.13453	splicing factor 3b; subunit 1; 155kD	1.609
	134330	D20113	Hs.8185	ESTs; Highly similar to CGI-44 protein [H.sapiens]	1.607
	115117	AA256492	Hs.49007	poly(A) polymerase	1.606
60	125162	W44692	Hs.109896	ESTs	1.605
	103946	AA285246	Hs.111650	ESTs; Weakly similar to Prt1 homolog [H.sapiens]	1.604
	133389	AA166917	Hs.72639	ESTs	1.603
	115528	AA342301	Hs.53929	ESTs; Weakly similar to !! ALU CLASS B WARNING ENTRY !! [H.sapiens]	1.602
	129704	W81301	Hs.12064	ubiquitin specific protease 22	1.602
65	109313	AA206800	Hs.86276	ESTs; Moderately similar to zinc finger protein dp [H.sapiens]	1.601
	130457	U58091	Hs.155976	cullin 4B	1.6
	123076	AA485211	Hs.190046	ESTs	1.6
	115113	AA256460	Hs.44610	ESTs	1.6
	117731	N46433	Hs.46609	ESTs	1.6

5	123344	AA504338	Hs.171857	ESTs	1.599
	131798	X86098	Hs.3238	adenovirus 5 E1A binding protein	1.597
	125370	AA256743	Hs.151791	KIAA0092 gene product	1.596
	114918	AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapiens]	1.596
	114807	AA160805	Hs.199832	ESTs	1.596
10	105103	AA151593	Hs.10130	ESTs	1.594
	125004	T60120		yb68f02.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:76347 3', mRNA sequence.	1.592
	105658	AA282914	Hs.10176	ESTs	1.589
	110455	H52172		yt85e8.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:23111 3' similar to contains Alu repetitive element, mRNA sequence	1.589
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.587
15	126983	AA211537		zn55d01.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562081 5', mRNA sequence.	1.586
	134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalytic; beta	1.584
	105431	AA252033	Hs.15036	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.584
	120187	Z40251	Hs.56974	ESTs	1.584
	115830	AA428137	Hs.86434	ESTs	1.581
20	135069	AA456311	Hs.93961	ESTs; Weakly similar to !! ALU CLASS A WARNING ENTRY !! [H.sapiens]	1.581
	122997	AA479295	Hs.106290	Kelch motif containing protein	1.581
	119707	W67569	Hs.44143	ESTs; Weakly similar to SNF2alpha protein [H.sapiens]	1.58
	131934	D80948	Hs.34922	ESTs	1.58
	106141	AA424558	Hs.9302	phosducin-like	1.58
25	115271	AA279422	Hs.5724	ESTs	1.579
	131468	R27598	Hs.27197	KIAA0797 protein	1.577
	131165	R98173	Hs.23763	Max-interacting protein	1.575
	117273	N21680	Hs.43047	ESTs	1.575
	101569	M33772	Hs.182421	troponin C2; fast	1.575
30	116127	AA459703	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	1.575
	120022	W90625	Hs.58432	ESTs	1.575
	117512	N32157	Hs.82207	ESTs	1.574
	106511	AA452865	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase; polypeptide 2	1.573
	116415	AA609204	Hs.27973	KIAA0874 protein	1.573
35	127879	AA810215	Hs.189079	ESTs	1.571
	125211	W72798	Hs.103177	ESTs; Wkly smlr to cDNA EST EMBL:D32579 comes from this gene [C.elegans]	1.571
	114746	AA135638	Hs.223756	ESTs	1.571
	122698	AA458112	Hs.99410	ESTs	1.57
	116765	H12636	Hs.121585	ESTs; Weakly similar to reverse transcriptase [H.sapiens]	1.568
40	130895	AA608828	Hs.21015	ESTs; Highly similar to tetracycline transporter-like protein [M.musculus]	1.568
	114338	Z41366	Hs.40109	KIAA0872 protein	1.567
	111005	N53076	Hs.5996	ESTs	1.567
	128135	AA913491	Hs.189143	ESTs; Modrtly smlr to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.567
	112046	R43365	Hs.22273	ESTs	1.566
45	132160	AA281770	Hs.184081	seven in absentia (Drosophila) homolog 1	1.566
	111568	R10153	Hs.20561	ESTs	1.566
	127775	H04106	Hs.179902	ESTs; Weakly similar to NG22 [H.sapiens]	1.566
	115359	AA281936	Hs.88914	ESTs	1.566
	121845	AA425734	Hs.165066	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.565
50	127854	AA769520		ESTs; Weakly similar to REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 [H.sapiens]	1.564
	120287	AA187679	Hs.111114	ESTs	1.563
	114940	AA243012	Hs.75928	ESTs	1.562
	126716	AA031700	Hs.251962	ESTs	1.562
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	1.561
55	125390	H95034	Hs.75187	translocase of outer mitochondrial membrane 20 (yeast) homolog	1.561
	115334	AA281244	Hs.65300	ESTs	1.559
	113721	T97931	Hs.18190	EST	1.558
	114895	AA236177	Hs.76591	KIAA0887 protein	1.558
	119341	T62571	Hs.146388	microtubule-associated protein 7	1.558
60	108012	AA039616	Hs.61933	ESTs	1.558
	130335	AA156499	Hs.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.557
	134351	R82074	Hs.82109	syndecan 1	1.557
	133300	D51401	Hs.70333	ESTs	1.553
	106920	AA490899	Hs.24462	ESTs	1.553
65	118744	N74075	Hs.94293	EST	1.552
	126489	W20016	Hs.144228	ESTs; Weakly similar to ZINC FINGER PROTEIN 83 [H.sapiens]	1.55
	115913	AA436720	Hs.65487	ESTs	1.55
	107868	AA025234	Hs.61260	ESTs	1.55
	134520	N21407	Hs.257325	ESTs	1.55

	109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w [S.cerevisiae]	1.55
	120288	AA187938	Hs.55189	ESTs; Weakly similar to F25B5.3 [C.elegans]	1.548
	106356	AA443277	Hs.31034	peroxisomal biogenesis factor 11A	1.548
5	129460	AA235627	Hs.11171	APG5 (autophagy 5; S. cerevisiae)-like	1.547
	133950	D11961	Hs.77823	ESTs	1.546
	128172	AI400862	Hs.142607	ESTs	1.546
	114162	Z38909	Hs.22265	ESTs	1.545
	101803	M86546	Hs.155691	pre-B-cell leukemia transcription factor 1	1.544
	113617	T93630	Hs.17207	ESTs	1.542
10	104896	AA054228	Hs.23165	ESTs	1.541
	114477	AA032013	Hs.144260	EST	1.54
	110731	H98653	Hs.188006	KIAA0878 protein	1.54
	130367	Z38501	Hs.8768	ESTs; Wkly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.538
	130539	L07044	Hs.250857	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA; partial cds	1.538
15	134921	W60186	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	1.537
	130593	W24957	Hs.16281	ESTs; Moderately similar to similar to C.elegans protein encoded in cosmid T20D3 [H.sapiens]	1.537
	133723	AA088851	Hs.75744	S-adenosylmethionine decarboxylase 1	1.537
20	106450	AA449469	Hs.11859	ESTs	1.536
	104120	AA429838	Hs.89519	KIAA1046 protein	1.536
	100533	HG1879-HT1919		Ras-Like Protein Tc10	1.535
	130664	R09049	Hs.17625	ESTs	1.535
	127122	AA279153	Hs.190049	ESTs	1.535
25	134264	T03391	Hs.8087	ESTs	1.535
	132319	AA418682	Hs.44625	ESTs	1.535
	115465	AA286941	Hs.43691	ESTs	1.533
	125003	T59442	Hs.100445	ESTs	1.532
	102273	U30888	Hs.75981	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	1.532
30	121875	AA426299	Hs.96510	ESTs	1.532
	114366	Z41747	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.531
	132944	AA054515	Hs.6127	ESTs; Weakly similar to prostate-specific transglutaminase [H.sapiens]	1.53
	111199	N68210	Hs.29822	ESTs	1.53
	113494	T88878	Hs.258738	ESTs	1.529
35	129515	AA490882	Hs.112227	ESTs	1.528
	133124	AA156049	Hs.65490	ESTs	1.528
	104785	AA027163	Hs.7942	ESTs	1.526
	105595	AA279408	Hs.25866	ESTs	1.526
40	130198	U67156	Hs.151988	mitogen-activated protein kinase kinase kinase 5	1.526
	114297	Z40758	Hs.173091	DKFZP434K151 protein	1.525
	112876	T03488	Hs.4842	ESTs	1.525
	127500	AA525014	Hs.162115	ESTs	1.525
	120519	AA258585	Hs.129887	cadherin 19 (NOTE: redefinition of symbol)	1.525
	119859	W80702	Hs.58461	ESTs	1.525
45	129944	L00389	Hs.1361	cytochrome P450; subfamily I (aromatic compound-inducible); polypeptide 2	1.524
	118854	N89670	Hs.42148	ESTs; Weakly similar to Su(P) [D.melanogaster]	1.523
	123964	C13961	Hs.210115	EST	1.523
	111676	R19414	Hs.166459	ESTs	1.522
	128332	AI079523	Hs.134173	ESTs	1.522
50	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)	1.521
	125181	W58461	Hs.12396	ESTs	1.521
	127093	AA768241		oa72d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1317795 3', mRNA sequence.	1.521
	132156	AA157401	Hs.4113	S-adenosylhomocysteine hydrolase-like 1	1.521
55	125303	Z39821	Hs.107295	ESTs	1.52
	132697	AA281951	Hs.5518	Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146)	1.52
	117086	H93135	Hs.41840	ESTs	1.519
	113355	T79203	Hs.14480	ESTs	1.518
	108621	AA101811	Hs.69506	ESTs	1.518
60	109384	AA219172	Hs.86849	EST	1.518
	128510	X94703	Hs.100816	RAB28; member RAS oncogene family	1.517
	132968	N77151	Hs.61638	myosin X	1.515
	117035	H88798	Hs.41182	ESTs	1.515
	116781	H22985	Hs.52132	ESTs	1.513
65	108677	AA115629	Hs.118531	ESTs	1.513
	130214	H78003	Hs.15266	ESTs	1.513
	134700	AA481414	Hs.8868	golgi SNAP receptor complex member 1	1.512
	116618	D80783	Hs.45224	ESTs	1.508
	126257	N99638		tumor necrosis factor receptor superfamily; member 10b	1.508
	125859	AA806808	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	1.508

	113837	W57698	Hs.8888	ESTs	1.507
	114317	Z41038	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.507
	100311	D50640	Hs.184653	phosphodiesterase 3B; cGMP-inhibited	1.507
	126802	AA947601	Hs.97056	ESTs	1.506
5	128661	R82837	Hs.103329	KIAA0970 protein	1.506
	134194	AA233231	Hs.79828	ESTs	1.506
	108953	AA149652	Hs.42128	ESTs	1.504
	133240	D31161	Hs.68613	ESTs	1.502
	132671	X76302	Hs.54649	putative nucleic acid binding protein RY-1	1.501
10	132609	Z48923	Hs.53250	bone morphogenetic protein receptor; type II (serine/threonine kinase)	1.501
	105574	AA278678	Hs.258567	ESTs	1.5
	113718	T97782	Hs.256268	ESTs	1.5
	127824	AI208365	Hs.127811	ESTs	1.5
	130132	U55936	Hs.184376	synaptosomal-associated protein; 23kD	1.5
15	127394	AA453224		ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.5
	100485	HG11111-HT1111		Ras-Like Protein Tc21	1.5
	101078	L04510	Hs.792	ADP-ribosylation factor domain protein 1; 64kD	1.5
	128611	AA456845	Hs.102471	KIAA0680 gene product	1.5

TABLE 12A shows the accession numbers for those primekeys lacking unigeneID's for Table 12. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
20	108536	119811_1	AA084524 AA339253 AW966289
	117040	46956_1	AW970600 AA503323 H89218 AF086031 H89112
	100782	18457_1	AA355435 NM_001516 Z30093 T26405 AW949486 AA461142 AA410532 AI652073 AA521208 AI970141 AI968234 AI026102 AA713583 AW135876 AA936614 AA770300 AI242635 AA377033 AW960263 AW607683 AI273603 AA410287 AI040513 AA460838 AI803916 AW294095 AW449680 AW798677 AW675048 BE542116 AL120521
	100819	3022_1	L34840 NM_003241 U31905 AI546931 AI791616 AI973065 AI792321 AI546937 AI685880 AI732835 AI682360 AA420653 AA564047 AI682323 AI824614 AI659889 AI680052 AI970887 AI623108 AA420692 AI418074 AA631018 AI810595 AW291463 AW449930 AI688908 AI970818
25	100824	5_36	AI393237 AI521317 AI761348 AF025841 D43968 AW994987 L34598 AF025841 D89789 D89788 D89790 AW998932 AI971742 AI310238 X90976 AW139668 AW674280 AI365552 AA877452 AV657554 C75229 AA376077 AI798056 AW609213 W25586 H30149 BE075089 BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158126 BE158145 N92860 AA847246 AI961688 AI361423 AA878154 AA043767 AI663712 AI559226 AW339007 AI371266 AI368901 AA046624 AA134739 AW449154 AA130232 AI458720 AA962511 AI700627 R70437 AW004008 AA045229 AI671572 H99599 AA043768 AI685454 AI871685 N29937 X90977 AA524240 AI142114 AI825750 AI567805 AI631365 AI347893 AA134740 F20669 AA046707 AW793216 AW963298 AW959380 AA363265 AI784593 AI268201 R69451 AV657618 AI695588
30	125004	264197_1	BE312163 AJ230798 AA374482 AI926059 AA622653 AI860704 BE139185 AW296684 T60238 T60120
	102313	27608_1	U33921 AI190489 AA573311
	102337	553_1	AI814663 AA806761 AA765241 AA019317 AA092255 AA035405 T85079 AA890151 AI373959 T85080 BE153728 AA740848 BE090682 AL048137 AW182316 AI699468 AW274481 AW407538 AA306562 AW950024 AW949943 AL045703 AW843196 W25132 BE612794 AA304266 AW958054 H25673 AV646563 AV646573 BE172990 AW593488 AA385181 AA164998 AI246476 AA345406 AI277554 AA134749 AA856624 BE613247 AA299003 AL048138 AA028121 T92510 AI923835 AW020440 AI401594 AI889401 N93290 AA044247 AA028100 AI582845 AA811151 AI925878 AA448277 AA172221 AI214763 BE220793 AA022746 AI082882 AA022849 AI928385 AA573472 AI420686 AW072902 AI799493 AI873506 AI468977 AI192079 AI468976 AA044272 AW015701 AW316979 AA933042 AA609017 AI318393 AI424571 AI934945 AA172023 AW050917 AA846180 AA134748 AI003947 AI766769 AW006697 AA653517 AW575680 AI474214 AA401478 U36922 AA927064 AA868000 D62654 T91745 AW500202 AA194764 AA746346 AA130464 AW117498 AA054526 N26432 H02534 H04964 AW303367 BE300931 AI218049 AI208073 AW182749 AA983630 AI147585 AA194765 AA054534 AA922720 AI436585 AI346535 AA134269 AA280923 AA897422 AA019559 AW274010 AA035406 AA917879 H99327 W32908 AI216046 AW496823 AA019414 H82288 W35284 AI936621 AI767113 AA866177 AW367874 H82398 AF032885 AW300151 AW467069 AA809346 AI188507 AI494178 AA872752 AI631631 U02310 NM_002015 AA815006 AI382453 AW197658 AI761654 AI804396 AI382221 AI813640 AI439635 AI523901 AW517242 AI221705 AW298104 AW204560 AW573095 AW028783 AW014650 AI766744 AI808294 AI698758 AI041809 AI766667 AI479103 AA872797 AA769305 AA765080 AA334166 AI472322
40	124704	292319_1	R07335 R07640
	116988	185904_1	AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
	124825	330773_1	AA501669 R52088
	110455	46874_1	H52576 AF085971 H52172
45	126257	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
	125624	154135_1	AW968363 AA465492 R34539 AA165411
	104038	264235_1	AA374532 AA421255
	103427	43892_1	BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355 BE071965 AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000192 BE562219 BE266655 BE264970
50	104142	113242_1	AA074713 AA447006
	127093	47721_1	AW977549 AA256038 AL365415 AW500455 AA768241 AW968097 Z17849 AA256104

5	125873	10492_1	AW271838 AL133805 C01646 H29959 AA999896 D60676 AW999454 AW961176 AA315244 H14437 AW386118 N46512 AW272021 AI768516 BE466421 AI082809 AI804454 AA905101 AW173368 N38942 AW614169 AI080483 N29489 AI500550 AA994475 AA614464 AA707368 AA593145 AA569473 AW627815 AI828244 N63226 N42300
	125954	4457_1	NM_016353 AB023584 W44753 R09585 AA382865 R23772 AI814257 AA974046 AK001608 AI935638 AW440609 AI420022 AA777386 AA806969 AI554876 AI584006 AI688556 AI688634 AI697997 AI014540 AI806683 AI741202 AW263154 AW297238 AI149951 AI589076 AW082158 AW614265 AA931887 AA781969 R09490 AA484643 AI207121 AI088390 AI538065 AI619547 AI741925 AI702846 H40846 R93943 AW747979 AA461348 U30163 AA326023 AI535992 AW242870 AI244025 AI222558 W38425 AW473630 AI624599 AI921226 AI683152 AI096458 AI123822 AW170802 C16447 AI337674 D25726 AW339366 AW771259 AA461174
	125992	1589048_1	H48372 W01626
	127210	15307_6	AA305278 AA223833
			110924 6443_1 AW058463 AF195766 AA680145 T86901 W60373 W60281 NM_007222 AF106862 AI000795 AA167188 AW884503 AW891313 AW891332 AW891312 AI984924 AI123518 N75170 AA131614 H25330 AI913358 AI742277 W25576 R58771 AW445159 AW886628 AW886627 AW274674 AI088482 N52314 N34282 AW001769 AI338943 T66784 AI288983 AW468676 AW237528 H25289 N71690 AA610128 AI143458 AI082599 N49144 AA854773 AW663411 AW610151 N47938 AW601626 AA167189 AA918304 AA805205 BE069496 AA652836 BE069499 AI699298 AW249926 AW888578 BE567635 T10726 AW604715 D54245 D53062 D55610 D55555 AA301376 AI133498 N77788 AI936320 AW090734 AI269977 N50828 AA550814 AI421993 AI005394 N50813 D60292 D59349 AA131710 D81698 D81699
20	127263	232161_1	AA331156 AA331157 AA331155
	135197	29440_1	U76456 NM_003256 AF057532 AA193414 AW233304 AW963378 AA313095 AI359841 AI969312 AI080163 AW448926 AI671136 BE466399 AI637967 AI671873 AW196583 AW071635 AI634427 AW296872 AW292470 AA193650
	127394	304844_1	BE161832 AA453224 AA485772
	126879	1860_2	D90391 M55575 AI652268 AA719776
	126983	171841_1	AA524886 AW971347 AA211537
25	120470	188975_1	AW971327 AA524988 AW628653 AA251797
	127854	443883_1	AW976796 AA769520
	121367	280429_1	AA432071 AA405648 AW000908 T16347
	106320	6435_1	AB028957 AL120001 AI267678 H10928 R19844 AW970334 AA393182 F05472 F11711 H09908 N50250 AI815411 BE463679 D61468 AW970253 D60889 C15548 D61011 D60867 AI815795 AA534831 D81386 AW235039 AI382158 D81174 AA416899 AA852310 H09789 H10929 H09813 F09369 R44721 D51515 Z38456 R14004 T66255 F12148 F12139 AW351702 M85350 AI018713 AW972450 AW972645 AA514964 T66172 F09785 F09776 AA436608 T05327 T07118 AA339352 AW301608 N46706 AA649093 AA287595 AW811753 AA287596 N39260
			NM_001874 J04970 T91426 AW205201 T84979 AA255727 AA847837 R02164 T91339 AV651884 AV651835 AV651350 AV650118 AV651338 AI272002 AI367796 AA830651 AA262112 AW151198 AU076696 AA219720 AL135197 AA305877 N56376 AA318069 AA130725 AW954903 BE541230 AW383312 U86753 D85423 AI679458 AI122932 AB007892 AI583919 BE160134 F08104 R34903 F13440 AA095444 AA262453 AA191036 R17895 T81266 BE149776 AI279537 AI143113 AA361072 AW959030 AW268817 AA811533 BE275179 AI221677 T65147 R49293 AA249176 BE000290 AA768053 F09494 BE092645 BE172099 Z41177 AA044750 AI909768 BE140795 BE140574 AW845210 AW752452 BE243244 AA843684 AI300080 BE169032 AW189979 BE004869 AA621872 AI951772 AI678897 AI926598 N62813 AI350912 AW608791 AI309602 AI983138 AW875592 AI655073 AW875626 AA130606 AI370827 C75528 C75554 AW263335 AI344426 BE004788 AA576220 AA604824 AI431405 AA749378 R38882 AW955075 AA173821 C75657 AA219672 AW768408 R43141 AI431414 AA483343 AI673792 T17294 AW770187 N74285 AI476404 AI088288 AA654152 AW974864 BE617311 BE243328 BE168049
30	115479	201515_1	U64675 AW167507 AW167508 BE218568 AA779360 W85722 AL044843 BE159404 AF012086 AW898611 AW898610 BE159405 BE092191 AW890826 AW369841 AW368064 AW606702 AL044731 R82691 AA419346 AA416558 H96045 AL040450 AI640531 AI808434 AL046613 AW855784 AW362469 AL048881 AL049015 AA094272 AA888908 AA417294 AW237786 R59793 AL044916 D82402 AI216854 AI079342 H96406 AL037845 AI915900 AA972133 AI478783 T31074 Z21135 Z21396 AA352182 R13918 AA430178 C17811 AI371824 AI742256 AA926801 N79156 AA350610 AA081971 N83639 R35544 AA312292 AW952080 N42322 AA171957 AA565297 R89207 AA504106 AI630782 AA826482 AI301579 T36241 AW966618 Z28426 AL043480 AI124636 AA393449 T19504 AW887623 AI289814 N53979 AL043571 AI632764 AI859613 AI986308 AI683212 AI984499 AI133258 C05898 AW512761 AI041260 BE466240 Z19161 AI351190 N67549 AI373374 AA400873 AW440914 AW514879 AA770146 AI358754 R51113 AI283773 AA649886 T30543 D54358 R37750 T03358 T15451 T15880 AA899689 N67396 AI056289 T85597 N62441 R89099 R00035 T85596 R61335 R00128 N63359 AI535964 AI207768 M31468 NM_012250 W01322 AA253280 AA253233 AA293148 AW582106 R79880 AA459547 AA363459 AA234396 N31669 H44468 AA434587 AW363088 AW993541 AA070906 AA070934
	100401	24827_1	X51501 NM_002652 Y10179 J03460 AI791618 AI821473 AA916588 AA564296 AA916110 AI972286 AI420470 AI568790 AI597724 AW205207 AI659305 AI791620 AA532383 AI821475 AA526498
			NM_012249 M31470 AL043108 AA262561 AA178883 T29433 AA313329 W48807 AW404323 AA453560 AW403227 H94816 W17101 AA165152 W23989 AA091310
			AL121734 D54896 AA424289 BE242906 AA362118 BE018454 AI280348 AL048769 M35543 AA757734 AI128865 H20289 H23728 AI203445 H41481 H18237 H44081 H92839 AI928621 H75675 D51148 AI796198 AW390453 D55579 D54145 D53996 D54015 R37664 H17541 AA688681 T65061 R15867 AW468123 R16049 H69030 AA054226 H16070 F09655 R92144 T03521 R05473 H92840 AA018186 R91707
			U35637 AA112989 Z19308
45	130542	28089_3	
50			
55	100485	30576_2	
	108345	112277_6	
	100522	19669_1	
60	100533	32905_1	
	100598	23902_2	
65	102332	14745_3	
	118250	genbank_N62602	N62602
	103678	entrez_Z84483	Z84483
	119400	genbank_T92767	T92767
	119559	entrez_W38197	W38197

MISSING AT THE TIME OF PUBLICATION

TABLE 13: shows genes, including expression sequence tags, up-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

5

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Background subtracted normal prostate : prostate tumor tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
15	333516		CH22_FGENES.173_1	0.028
	337954		CH22_EM:AC005500.GENSCAN.96-3	0.029
	332496	R73299	Hs.204354 ras homolog gene family; member B	0.03
	337944		CH22_EM:AC005500.GENSCAN.89-7	0.033
	334111		CH22_FGENES.330_10	0.033
20	333657		CH22_FGENES.241_2	0.034
	327718		CH.04_hs gi 6525284	0.034
	336355		CH22_FGENES.817_5	0.035
	322011	AL137354	EST cluster (not in UniGene)	0.035
	336377		CH22_FGENES.821_5	0.036
25	300254	AW079607	Hs.188417 ESTs; Weakly similar to ZnT-3 [H.sapiens]	0.037
	330096		CH.19_p2 gi 6015278	0.037
	335191		CH22_FGENES.507_6	0.038
	334040		CH22_FGENES.322_8	0.039
	333586		CH22_FGENES.204_2	0.04
30	333295		CH22_FGENES.132_2	0.042
	313326	AI088120	Hs.122329 ESTs	0.043
	329517		CH.10_p2 gi 3983513	0.043
	333403		CH22_FGENES.144_21	0.043
	335226		CH22_FGENES.513_11	0.044
35	335976		CH22_FGENES.652_11	0.045
	333637		CH22_FGENES.229_2	0.046
	334582		CH22_FGENES.407_5	0.046
	336437		CH22_FGENES.826_4	0.047
	337461		CH22_FGENES.782-1	0.047
40	302892	N58545	Hs.6975 histone deacetylase 3	0.049
	338689		CH22_EM:AC005500.GENSCAN.475-3	0.049
	334721		CH22_FGENES.421_32	0.049
	305867	AA864572	EST singleton (not in UniGene) with exon hit	0.049
	335498		CH22_FGENES.571_7	0.05
45	311596	AI682088	Hs.223368 ESTs	0.05
	326959		CH.21_hs gi 6469836	0.051
	311688	AW025661	Hs.240090 ESTs	0.052
	317288	AI022374	Hs.158549 ESTs	0.052
	332984		CH22_FGENES.54_6	0.052
50	321039	AW247083	EST cluster (not in UniGene)	0.053
	335844		CH22_FGENES.623_4	0.053
	325371		CH.12_hs gi 5866920	0.054
	335667		CH22_FGENES.590_18	0.054
	333635		CH22_FGENES.228_2	0.054
55	336736		CH22_FGENES.110-2	0.055
	335893		CH22_FGENES.635_1	0.055
	333170		CH22_FGENES.94_5	0.055
	329768		CH.14_p2 gi 6015501	0.055
	334030		CH22_FGENES.320_2	0.055
60	323359	AA234172	Hs.137418 ESTs	0.055
	300453	AW051431	Hs.113029 ribosomal protein S25	0.055
	334262		CH22_FGENES.367_12	0.055
	306590	AI000246	EST singleton (not in UniGene) with exon hit	0.055
	331087	R22520	Hs.23398 ESTs	0.055
65	338620		CH22_EM:AC005500.GENSCAN.450-18	0.056
	339045		CH22_DA59H18.GENSCAN.28-5	0.056
	308023	AI452732	EST singleton (not in UniGene) with exon hit	0.057

	339067		CH22_DA59H18.GENSCAN.33-3	0.057
	335689		CH22_FGENES.596_4	0.057
	339069		CH22_DA59H18.GENSCAN.33-5	0.057
	338176		CH22_EM:AC005500.GENSCAN.219-4	0.057
5	328159		CH.06_hs gjl5868065	0.058
	335655		CH22_FGENES.590_6	0.058
	336371		CH22_FGENES.820_1	0.058
	336558		CH22_FGENES.842_3	0.059
	337738		CH22_EM:AC000097.GENSCAN.100-4	0.059
10	334273		CH22_FGENES.369_2	0.059
	335889		CH22_FGENES.633_3	0.059
	327807		CH.05_hs gjl5867968	0.059
	333315		CH22_FGENES.138_7	0.059
	338825		CH22_DJ246D7.GENSCAN.4-6	0.06
15	337612		CH22_C20H12.GENSCAN.22-5	0.06
	333897		CH22_FGENES.293_4	0.06
	335990		CH22_FGENES.655_4	0.06
	334264		CH22_FGENES.367_15	0.06
	338653		CH22_EM:AC005500.GENSCAN.460-39	0.061
20	322303	W07459	EST cluster (not in UniGene)	0.061
	333498		CH22_FGENES.168_8	0.061
	336522		CH22_FGENES.839_3	0.061
	301357	AW295677	Hs.137840 ESTs; Moderately similar to HOMEBOX	
			PROTEIN SIX1 [H.sapiens]	0.062
25	305917	AA876469	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.062
	336143		CH22_FGENES.705_5	0.063
	333493		CH22_FGENES.168_2	0.063
	332533	M99487	Hs.1915 folate hydrolase (prostate-specific membrane antigen) 1	0.063
	325844		CH.16_hs gjl6552453	0.063
30	336402		CH22_FGENES.823_17	0.063
	335767		CH22_FGENES.607_1	0.064
	301893	T80334	EST cluster (not in UniGene) with exon hit	0.064
	324019	AW177009	EST cluster (not in UniGene)	0.064
	305801	AA845997	EST singleton (not in UniGene) with exon hit	0.064
35	335188		CH22_FGENES.507_3	0.065
	337533		CH22_FGENES.828-2	0.065
	333311		CH22_FGENES.138_3	0.065
	335668		CH22_FGENES.590_19	0.065
	306786	AI041589	EST singleton (not in UniGene) with exon hit	0.066
40	306365	AA962086	EST singleton (not in UniGene) with exon hit	0.066
	306249	AA933840	EST singleton (not in UniGene) with exon hit	0.066
	335018		CH22_FGENES.474_6	0.066
	333594		CH22_FGENES.210_3	0.066
	333900		CH22_FGENES.293_7	0.066
45	325207		CH.10_hs gjl6552430	0.067
	329888		CH.15_p2 gjl6067149	0.067
	326238		CH.17_hs gjl5867260	0.067
	333658		CH22_FGENES.241_4	0.067
	335809		CH22_FGENES.617_6	0.068
50	307427	AI243437	EST singleton (not in UniGene) with exon hit	0.068
	318428	AI949409	Hs.224583 ESTs	0.069
	327005		CH.21_hs gjl5867664	0.069
	330463	HG998-HT998	Sulfotransferase, Phenol-Preferring	0.069
55	333318		CH22_FGENES.138_10	0.07
	333313		CH22_FGENES.138_5	0.07
	325937		CH.16_hs gjl5867132	0.07
	335663		CH22_FGENES.590_14	0.07
	335349		CH22_FGENES.539_2	0.07
	303396	AA224470	Hs.25426 ESTs; Weakly similar to unknown [H.sapiens]	0.07
60	332603	N66681	Hs.33470 ESTs	0.07
	333310		CH22_FGENES.138_2	0.071
	309924	AW340812	EST singleton (not in UniGene) with exon hit	0.071
	336340		CH22_FGENES.814_15	0.071
	308025	AI453365	Hs.172928 collagen; type I; alpha 1	0.071
65	306805	AI055966	EST singleton (not in UniGene) with exon hit	0.071
	335499		CH22_FGENES.571_8	0.071
	329669		CH.14_p2 gjl6272129	0.071
	321666	D28390	EST cluster (not in UniGene)	0.071
	338174		CH22_EM:AC005500.GENSCAN.219-2	0.072

	336556		CH22_FGENES.842_1	0.072
	305451 AA738105	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.072
	336684		CH22_FGENES.46-1	0.072
5	326943		CH.21_hs gij6004446	0.073
	333947		CH22_FGENES.303_1	0.074
	333214		CH22_FGENES.104_5	0.074
	331917 AA446572	Hs.174007	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	0.074
	339102		CH22_DA59H18.GENSCAN.44-9	0.074
10	328122		CH.06_hs gij5868031	0.075
	332250 N62712	Hs.226223	KIAA0618 gene product	0.075
	328506		CH.07_hs gij5868471	0.075
	331756 AA291468	Hs.98504	ESTs	0.075
	335193		CH22_FGENES.507_8	0.076
	317729 AA971718	Hs.128141	ESTs	0.076
15	304515 AA458708	Hs.251577	hemoglobin; alpha 2	0.076
	313644 AI565768	Hs.124960	ESTs	0.076
	326145		CH.17_hs gij5867204	0.076
	336394		CH22_FGENES.823_6	0.077
	306516 AA989542		EST singleton (not in UniGene) with exon hit	0.077
20	300629 AA152119	Hs.155101	ATP synthase; H+ transporting; mitochondrial F1 complex; alpha subunit; isoform 1; cardiac muscle	0.077
	333160		CH22_FGENES.91_2	0.077
	337490		CH22_FGENES.799-5	0.077
	305403 AA723748		EST singleton (not in UniGene) with exon hit	0.077
25	331747 AA281765	Hs.193689	ESTs	0.077
	332792		CH22_FGENES.3_2	0.078
	330513 M81057	Hs.180884	carboxypeptidase B1 (tissue)	0.078
	308905 AI859636	Hs.8102	ribosomal protein S20	0.078
30	337419		CH22_FGENES.759-4	0.078
	333459		CH22_FGENES.167_8	0.078
	334851		CH22_FGENES.440_3	0.078
	329046		CH.X_hs gij5866569	0.078
	327879		CH.06_hs gij5868142	0.079
35	305830 AA857665		EST singleton (not in UniGene) with exon hit	0.079
	302928 AL137719		EST cluster (not in UniGene) with exon hit	0.079
	304321 AA136698	Hs.113029	ribosomal protein S25	0.079
	326390		CH.19_hs gij5867340	0.079
	335230		CH22_FGENES.514_2	0.08
40	334622		CH22_FGENES.412_6	0.08
	335331		CH22_FGENES.535_4	0.08
	304753 AA578840	Hs.77961	major histocompatibility complex; class I; B	0.08
	301863 AI418863		EST cluster (not in UniGene) with exon hit	0.081
	336561		CH22_FGENES.842_6	0.081
	335611		CH22_FGENES.583_5	0.081
45	305060 AA635771		EST singleton (not in UniGene) with exon hit	0.081
	306051 AA905130		EST singleton (not in UniGene) with exon hit	0.082
	308289 AI571211		EST singleton (not in UniGene) with exon hit	0.082
	334365		CH22_FGENES.378_13	0.082
	335496		CH22_FGENES.571_4	0.082
50	332634 S38953		Human unidentified gene complementary to P450c21 gene; partial cds	0.082
	337824		CH22_EM:AC005500.GENSCAN.13-18	0.082
	335822		CH22_FGENES.619_7	0.082
	334758		CH22_FGENES.428_7	0.082
55	309641 AW194230	Hs.253100	EST	0.082
	333064		CH22_FGENES.75_7	0.083
	338695		CH22_EM:AC005500.GENSCAN.477-25	0.083
	331809 AA402482	Hs.97312	ESTs	0.083
	326138		CH.17_hs gij5867203	0.083
60	328304		CH.07_hs gij6004478	0.083
	330570 U60276	Hs.165439	arsA (bacterial) arsenite transporter; ATP-binding; homolog 1	0.083
	334305		CH22_FGENES.373_8	0.083
	335885		CH22_FGENES.632_3	0.083
	325839		CH.16_hs gij6552452	0.083
65	333531		CH22_FGENES.175_18	0.084
	330385 AA449749	Hs.31386	ESTs; Highly similar to secreted apoptosis related protein 1 [H.sapiens]	0.084
	323305 AA811351	Hs.25307	Homo sapiens clone 24812 mRNA sequence	0.084
	331698 Z39929	Hs.65843	ESTs	0.084

	335888		CH22_FGENES.633_2	0.084
	306008	AA894390	EST singleton (not in UniGene) with exon hit	0.084
	334249		CH22_FGENES.365_15	0.084
5	318303	AW451197	Hs.113418 ESTs	0.084
	330171		CH.02_p2 gil6648220	0.084
	336682		CH22_FGENES.41-1	0.085
	320506	AI815668	Hs.157476 suc1-associated neurotrophic factor target 2 (FGFR signalling adaptor)	0.085
	316974	AI740721	Hs.128292 ESTs	0.085
10	336492		CH22_FGENES.832_9	0.085
	335750		CH22_FGENES.602_4	0.085
	335676		CH22_FGENES.594_1	0.086
	336093		CH22_FGENES.691_2	0.086
	310932	AI933861	Hs.222852 ESTs	0.086
15	335160		CH22_FGENES.502_4	0.086
	334306		CH22_FGENES.373_9	0.086
	334793		CH22_FGENES.433_5	0.086
	333936		CH22_FGENES.301_2	0.087
	336413		CH22_FGENES.823_35	0.087
20	333775		CH22_FGENES.272_6	0.087
	335971		CH22_FGENES.652_4	0.087
	301737	AI815981	EST cluster (not in UniGene) with exon hit	0.087
	339101		CH22_DA59H18.GENSCAN.44-6	0.087
25	327612		CH.04_hs gil6525283	0.087
	326241		CH.17_hs gil5867260	0.088
	338386		CH22_EM:AC005500.GENSCAN.331-4	0.088
	327762		CH.05_hs gil5867961	0.088
	305266	AA679772	EST singleton (not in UniGene) with exon hit	0.088
30	334359		CH22_FGENES.378_4	0.088
	335500		CH22_FGENES.571_10	0.088
	329687		CH.14_p2 gil6117856	0.088
	333654		CH22_FGENES.240_2	0.088
	324430	AA464018	EST cluster (not in UniGene)	0.088
35	325999		CH.16_hs gil5867073	0.089
	334832		CH22_FGENES.439_1	0.089
	339115		CH22_DA59H18.GENSCAN.49-3	0.089
	300896	AI916902	Hs.213882 ESTs	0.089
	328784		CH.07_hs gil5868309	0.089
40	335044		CH22_FGENES.480_1	0.089
	329791		CH.14_p2 gil6469354	0.089
	333656		CH22_FGENES.240_4	0.089
	326180		CH.17_hs gil5867211	0.089
	333391		CH22_FGENES.144_6	0.089
	338324		CH22_EM:AC005500.GENSCAN.306-3	0.089
45	305396	AA721052	EST singleton (not in UniGene) with exon hit	0.089
	337483		CH22_FGENES.795-7	0.09
	326424		CH.19_hs gil5867369	0.09
	306454	AA977992	EST singleton (not in UniGene) with exon hit	0.09
	338893		CH22_DJ32H10.GENSCAN.7-6	0.09
50	327470		CH.02_hs gil5867772	0.09
	333165		CH22_FGENES.91_7	0.09
	307155	AI186738	Hs.182426 ribosomal protein S2	0.09
	330717	AA233926	Hs.23635 ESTs	0.09
55	335334		CH22_FGENES.535_10	0.09
	335907		CH22_FGENES.636_2	0.09
	333885		CH22_FGENES.292_7	0.09
	331034	N51868	Hs.31965 ESTs; Moderately similar to 40S RIBOSOMAL PROTEIN S20 [H.sapiens]	0.09
	304660	AA534416	Hs.162185 ESTs	0.09
60	328217		CH.06_hs gil5868096	0.091
	336068		CH22_FGENES.684_13	0.091
	302833	AA295381	Hs.44423 ESTs	0.091
	328668		CH.07_hs gil5868254	0.091
	335309		CH22_FGENES.532_2	0.091
65	338481		CH22_EM:AC005500.GENSCAN.377-5	0.091
	306286	AA936892	EST singleton (not in UniGene) with exon hit	0.091
	305070	AA639783	EST singleton (not in UniGene) with exon hit	0.091
	304870	AA594811	Hs.119122 ribosomal protein L13a	0.091
	303856	AA968589	Hs.944 glucose phosphate isomerase	0.091

	323789	AI459612	Hs.170460	ESTs; Weakly similar to KIAA0990 protein [H.sapiens]	0.092
	334910			CH22_FGENES.455_3	0.092
	326382			CH.19_hs gi 5867327	0.092
5	332467	AA489630	Hs.119004	KIAA0665 gene product	0.092
	338534			CH22_EM:AC005500.GENSCAN.402-7	0.092
	336449			CH22_FGENES.829_6	0.092
	333709			CH22_FGENES.250_24	0.092
	336559			CH22_FGENES.842_4	0.092
	333230			CH22_FGENES.107_10	0.093
10	333133			CH22_FGENES.83_9	0.093
	334885			CH22_FGENES.451_11	0.093
	330605	X02419	Hs.77274	plasminogen activator; urokinase	0.093
	336392			CH22_FGENES.823_4	0.093
	334083			CH22_FGENES.327_38	0.093
15	325469			CH.12_hs gi 6017034	0.093
	331077	R09531	Hs.19039	ESTs	0.093
	303701	AW500732		EST cluster (not in UniGene) with exon hit	0.093
	334218			CH22_FGENES.358_3	0.093
20	336542			CH22_FGENES.840_6	0.093
	337151			CH22_FGENES.546-1	0.093
	333642			CH22_FGENES.231_2	0.093
	336863			CH22_FGENES.297-4	0.093
	334680			CH22_FGENES.419_2	0.093
25	326365			CH.18_hs gi 5867297	0.093
	338952			CH22_DJ32110.GENSCAN.23-22	0.093
	337539			CH22_FGENES.832-4	0.094
	333546			CH22_FGENES.180_2	0.094
	335258			CH22_FGENES.518_3	0.094
	336786			CH22_FGENES.168-19	0.094
30	321644	AI204177	Hs.237396	ESTs	0.094
	335943			CH22_FGENES.646_17	0.094
	327918			CH.06_hs gi 5868165	0.094
	306358	AA970548		EST singleton (not in UniGene) with exon hit	0.094
35	335671			CH22_FGENES.592_3	0.094
	335033			CH22_FGENES.475_11	0.094
	338277			CH22_EM:AC005500.GENSCAN.290-2	0.094
	332061	AA504812	Hs.192824	early B-cell factor	0.094
	305153	AA654582	Hs.77039	ribosomal protein S3A	0.094
	333880			CH22_FGENES.292_2	0.094
40	323940	AI664428	Hs.170880	ESTs	0.094
	313779	AA648796	Hs.129771	ESTs	0.095
	323109	AA169345		EST cluster (not in UniGene)	0.095
	332930			CH22_FGENES.38_4	0.095
	335368			CH22_FGENES.543_6	0.095
45	303887	R72672	Hs.193484	ESTs; Weakly similar to Similarity with yeast gene L3502.1 [C.elegans]	0.095
	336223			CH22_FGENES.727_3	0.095
	311280	AI767957	Hs.197737	ESTs; Weakly similar to Y38A8.1 gene product [C.elegans]	0.095
50	337256			CH22_FGENES.648-3	0.095
	308814	AI819263		EST singleton (not in UniGene) with exon hit	0.095
	334659			CH22_FGENES.418_7	0.095
	335895			CH22_FGENES.635_3	0.095
	321697	AW388061	Hs.4953	golgi autoantigen; golgin subfamily a; 3	0.095
55	336010			CH22_FGENES.668_8	0.096
	302624	U21260		EST cluster (not in UniGene) with exon hit	0.096
	333612			CH22_FGENES.217_7	0.096
	304823	AA584837		EST singleton (not in UniGene) with exon hit	0.096
	335665			CH22_FGENES.590_16	0.096
60	306518	AA989598		EST singleton (not in UniGene) with exon hit	0.096
	335243			CH22_FGENES.516_4	0.096
	335436			CH22_FGENES.559_5	0.096
	300243	AI420256	Hs.161271	ESTs	0.096
	332810			CH22_FGENES.7_12	0.097
65	308612	AI735634		EST singleton (not in UniGene) with exon hit	0.097
	335818			CH22_FGENES.618_6	0.097
	325838			CH.16_hs gi 6552452	0.097
	337482			CH22_FGENES.795-6	0.097
	336645			CH22_FGENES.26-1	0.097
	337293			CH22_FGENES.675-1	0.098

	329893		CH.15_p2 gij6525313	0.098
	326533		CH.19_hs gij5867441	0.098
	334905		CH22_FGENES.452_20	0.098
5	306347	AA961144	EST singleton (not in UniGene) with exon hit	0.098
	336676		CH22_FGENES.43-4	0.098
	339166		CH22_DA59H18.GENSCAN.69-7	0.098
	335774		CH22_FGENES.607_10	0.098
	339216		CH22_FF113D11.GENSCAN.6-11	0.098
10	335311		CH22_FGENES.532_4	0.098
	329632		CH.11_p2 gij6729060	0.098
	328595		CH.07_hs gij5868224	0.098
	326928		CH.21_hs gij6456782	0.098
	315234	AI079680	Hs.120770 ESTs	0.098
15	306082	AA908508	EST singleton (not in UniGene) with exon hit	0.098
	305710	AA826544	EST singleton (not in UniGene) with exon hit	0.098
	318540	T30280	EST cluster (not in UniGene)	0.099
	337553		CH22_C4G1.GENSCAN.2-1	0.099
	320951	AA344069	Hs.202699 neurexophilin 4	0.099
20	303845	T08033	EST cluster (not in UniGene) with exon hit	0.099
	338981		CH22_DA59H18.GENSCAN.2-5	0.099
	321313	R87365	Hs.26058 ESTs; Weakly similar to p532 [H.sapiens]	0.099
	328348		CH.07_hs gij5868383	0.099
	332203	H49388	Hs.102082 EST	0.099
25	301780	R07064	EST cluster (not in UniGene) with exon hit	0.099
	332095	AA608838	Hs.162681 EST	0.099
	333227		CH22_FGENES.107_5	0.099
	316442	AA760894	Hs.153023 ESTs	0.099
	326001		CH.16_hs gij5867073	0.099
30	334363		CH22_FGENES.378_11	0.099
	338895		CH22_DJ32110.GENSCAN.9-2	0.099
	327460		CH.02_hs gij6004455	0.099
	332705	T59161	Hs.76293 thymosin; beta 10	0.1
	307806	AI351739	EST singleton (not in UniGene) with exon hit	0.1
35	322800	F25037	Hs.225175 ESTs	0.1
	304918	AA602697	EST singleton (not in UniGene) with exon hit	0.1
	334327		CH22_FGENES.375_4	0.1
	318359	AI097439	Hs.135548 ESTs	0.1
	326644		CH.20_hs gij5867559	0.1
40	334454		CH22_FGENES.388_3	0.1
	327859		CH.06_hs gij5868210	0.1
	323783	AA330586	Hs.131819 ESTs	0.1
	309198	AI955915	Hs.248038 major histocompatibility complex; class I; C	0.1
	339265		CH22_BA354112.GENSCAN.10-3	0.1
45	320576	AL049977	Hs.162209 Homo sapiens mRNA; cDNA DKFZp564C122 (from clone DKFZp564C122)	0.1
	338132		CH22_EM:AC005500.GENSCAN.200-2	0.101
	333163		CH22_FGENES.91_5	0.101
	337584		CH22_C20H12.GENSCAN.5-1	0.101
50	307588	AI285535	EST singleton (not in UniGene) with exon hit	0.101
	336969		CH22_FGENES.378-2	0.101
	327535		CH.02_hs gij6525279	0.101
	328732		CH.07_hs gij5868289	0.101
	336686		CH22_FGENES.46-3	0.101
55	335777		CH22_FGENES.607_13	0.101
	332944		CH22_FGENES.47_3	0.101
	333174		CH22_FGENES.95_1	0.101
	336380		CH22_FGENES.621_8	0.101
	330571	U60800	Hs.79089 sema domain; immunoglobulin domain (Ig); cytoplasmic domain; (semaphorin) 4D	0.101
60	331789	AA398721	Hs.186749 ESTs	0.101
	338915		CH22_DJ32110.GENSCAN.12-1	0.101
	334844		CH22_FGENES.439_24	0.101
	336642		CH22_FGENES.23-4	0.101
	334906		CH22_FGENES.452_21	0.101
65	333188		CH22_FGENES.98_8	0.101
	300088	AW299993	EST cluster (not in UniGene) with exon hit	0.101
	329373		CH.X_hs gij6682537	0.102
	331120	R46576	Hs.23239 ESTs	0.102
	335856		CH22_FGENES.628_1	0.102

	331888	AA431337	Hs.98017	ESTs	0.102
	333154			CH22_FGENES.89_4	0.102
	335989			CH22_FGENES.655_2	0.102
5	304385	AA235602		EST singleton (not in UniGene) with exon hit	0.102
	338016			CH22_EM:AC005500.GENSCAN.133-1	0.102
	335190			CH22_FGENES.507_5	0.102
	318595	T39486	Hs.6137	ESTs	0.102
	333697			CH22_FGENES.250_11	0.102
10	306526	AA989713		EST singleton (not in UniGene) with exon hit	0.103
	328734			CH.07_hs gij5868289	0.103
	307294	AI205612	Hs.73742	ribosomal protein; large; P0	0.103
	327424			CH.02_hs gij5867751	0.103
	335872			CH22_FGENES.630_3	0.103
	333572			CH22_FGENES.189_1	0.103
15	334774			CH22_FGENES.430_6	0.103
	338660			CH22_EM:AC005500.GENSCAN.462-1	0.103
	326713			CH.20_hs gij5867595	0.103
	333994			CH22_FGENES.310_18	0.103
	335800			CH22_FGENES.613_4	0.103
20	318113	AI187943	Hs.132322	ESTs	0.103
	337278			CH22_FGENES.665-1	0.103
	336386			CH22_FGENES.822_6	0.103
	334790			CH22_FGENES.432_15	0.103
25	303778	AW505368		EST cluster (not in UniGene) with exon hit	0.104
	336524			CH22_FGENES.839_5	0.104
	328936			CH.08_hs gij5868500	0.104
	335102			CH22_FGENES.494_7	0.104
	300935	AA513644	Hs.222815	ESTs; Weakly similar to Wiskott-Aldrich Syndrome protein [H.sapiens]	0.104
30	307581	AI284415		EST singleton (not in UniGene) with exon hit	0.104
	317301	AW291683	Hs.226056	ESTs	0.104
	335330			CH22_FGENES.535_3	0.104
	337968			CH22_EM:AC005500.GENSCAN.103-2	0.104
	335627			CH22_FGENES.584_7	0.104
35	336274			CH22_FGENES.762_2	0.104
	334730			CH22_FGENES.424_5	0.105
	334409			CH22_FGENES.383_6	0.105
	327237			CH.01_hs gij5867544	0.105
	333321			CH22_FGENES.138_13	0.105
40	303181	AA452366		EST cluster (not in UniGene) with exon hit	0.105
	333738			CH22_FGENES.261_2	0.105
	338255			CH22_EM:AC005500.GENSCAN.276-3	0.105
	334282			CH22_FGENES.369_12	0.105
	330190			CH.05_p2 gij6165182	0.105
45	310748	AW014249	Hs.158698	ESTs	0.105
	338150			CH22_EM:AC005500.GENSCAN.207-2	0.105
	336719			CH22_FGENES.82-6	0.105
	330228			CH.05_p2 gij6013527	0.105
	327601			CH.05_hs gij5867924	0.105
50	330525	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.105
	334972			CH22_FGENES.468_2	0.105
	335111			CH22_FGENES.494_19	0.106
	334483			CH22_FGENES.395_5	0.106
	328829			CH.07_hs gij5868337	0.106
55	302753	M74299		EST cluster (not in UniGene) with exon hit	0.106
	334512			CH22_FGENES.398_10	0.106
	330024			CH.16_p2 gij6671908	0.106
	321030	AI769930	Hs.233617	Homo sapiens (clone B3B3E13) Huntington's disease candidate region	0.107
60	338410			CH22_EM:AC005500.GENSCAN.341-6	0.107
	334353			CH22_FGENES.376_5	0.107
	338276			CH22_EM:AC005500.GENSCAN.288-9	0.107
	329053			CH.X_hs gij5868574	0.107
	336560			CH22_FGENES.842_5	0.107
65	332158	AA621363	Hs.112980	EST	0.107
	336447			CH22_FGENES.829_4	0.107
	333703			CH22_FGENES.250_17	0.107
	326207			CH.17_hs gij5867222	0.107
	333232			CH22_FGENES.108_1	0.107

	334802		CH22_FGENES.435_1	0.107
	303784	AA704983	EST cluster (not in UniGene) with exon hit	0.107
	338847		CH22_DJ246D7.GENSCAN.10-2	0.107
	339407		CH22_DJ579N16.GENSCAN.1-9	0.108
5	337635		CH22_C20H12.GENSCAN.32-8	0.108
	334650		CH22_FGENES.417_17	0.108
	308511	AI687580	EST singleton (not in UniGene) with exon hit	0.108
	333382		CH22_FGENES.144_8	0.108
	325840		CH.16_hs gj 6552452	0.108
10	315044	AW205664	Hs.129568 ESTs	0.108
	333298		CH22_FGENES.133_4	0.108
	335157		CH22_FGENES.501_7	0.108
	333305		CH22_FGENES.137_2	0.108
	326379		CH.19_hs gj 5867327	0.108
15	335050		CH22_FGENES.462_1	0.108
	305185	AA663985	Hs.248038 major histocompatibility complex; class I; C	0.108
	335658		CH22_FGENES.590_9	0.108
	323040	AA336809	Hs.10862 ESTs	0.108
	337326		CH22_FGENES.699-6	0.108
20	339282		CH22_BA354I12.GENSCAN.9-6	0.108
	321202	H54052	Hs.163639 ESTs; Weakly similar to INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens]	0.109
	331792	AA398968	Hs.97548 EST	0.109
	333806		CH22_FGENES.278_2	0.109
25	321325	AB033100	EST cluster (not in UniGene)	0.109
	331373	AA435513	Hs.178170 ESTs; Weakly similar to DUAL SPECIFICITY PROTEIN PHOSPHATASE 3	0.87
	326775		CH.07_hs gj 5868309	0.109
	335105		CH22_FGENES.494_10	0.109
30	300975	AI283548	Hs.149668 ESTs	0.109
	324893	T31940	EST cluster (not in UniGene)	0.109
	333397		CH22_FGENES.144_15	0.109
	336484		CH22_FGENES.831_3	0.109
	335507		CH22_FGENES.571_22	0.109
35	336373		CH22_FGENES.820_3	0.109
	336188		CH22_FGENES.717_12	0.109
	313455	AW081702	Hs.137329 ESTs	0.109
	335185		CH22_FGENES.506_4	0.109
	306814	AI066577	EST singleton (not in UniGene) with exon hit	0.109
40	311130	AI632322	Hs.195306 ESTs	0.109
	310882	AW080339	Hs.211911 ESTs	0.109
	323383	AI346359	Hs.135209 ESTs	0.11
	300212	AW135925	Hs.184552 biphenylhydrolase-like (serine hydrolase; breast epithelial mucin-assoc.	0.11
45	325675		CH.14_hs gj 5867014	0.11
	330095		CH.19_p2 gj 6015278	0.11
	331942	AA453261	Hs.99309 ESTs	0.11
	334723		CH22_FGENES.421_34	0.11
	333614		CH22_FGENES.217_9	0.11
50	337316		CH22_FGENES.692-1	0.11
	305057	AA635626	Hs.62954 ferritin; heavy polypeptide 1	0.11
	338704		CH22_EM:AC005500.GENSCAN.480-3	0.11
	335385		CH22_FGENES.543_27	0.11
	338012		CH22_EM:AC005500.GENSCAN.128-10	0.11
55	329449		CH.Y_hs gj 5868886	0.11
	338980		CH22_DA59H18.GENSCAN.2-4	0.11
	336553		CH22_FGENES.841_10	0.111
	330021		CH.16_p2 gj 6671889	0.111
	327579		CH.03_hs gj 5867824	0.111
60	333099		CH22_FGENES.79_4	0.111
	337076		CH22_FGENES.453-4	0.111
	331388	AA456852	Hs.43543 suppressor of white apricot homolog 2	0.111
	306674	AI005542	Hs.180414 heat shock 70kD protein 10 (HSC71)	0.111
	305949	AA884409	EST singleton (not in UniGene) with exon hit	0.111
65	330748	AA419217	Hs.15911 DKFZP586E1422 protein	0.111
	333780		CH22_FGENES.273_2	0.111
	323676	AI702835	EST cluster (not in UniGene)	0.111
	308952	AI868157	Hs.224226 EST	0.111
	309338	AW026946	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.111

	329317		CH.X_hs gl 6381976	0.112
	333518		CH22_FGENES.173_3	0.112
	306982	AI127883	EST singleton (not in UniGene) with exon hit	0.112
5	336225		CH22_FGENES.728_2	0.112
	333698		CH22_FGENES.250_12	0.112
	302173	AI417947	Hs.14068 ESTs	0.112
	335510		CH22_FGENES.571_25	0.112
	328042		CH.06_hs gl 5902482	0.112
10	336512		CH22_FGENES.834_7	0.112
	328541		CH.07_hs gl 5868486	0.112
	311265	AW205118	Hs.199214 ESTs	0.112
	323218	AF131846	Hs.13396 Homo sapiens clone 25028 mRNA sequence	0.112
	302002	AF013956	Hs.123085 chromobox homolog 4 (Drosophila Pc class)	0.112
	315088	AA557351	Hs.152448 ESTs; Moderately similar to MULTIFUNCTIONAL PROTEIN ADE2	0.112
15	312581	AI937242	Hs.176590 ESTs	0.112
	322246	AW384710	Hs.125258 ESTs	0.112
	333659		CH22_FGENES.241_5	0.113
	327510		CH.02_hs gl 6117815	0.113
	336520		CH22_FGENES.839_1	0.113
20	338682		CH22_EM:AC005500.GENSCAN.472-1	0.113
	334508		CH22_FGENES.398_6	0.113
	322533	T59538	EST cluster (not in UniGene)	0.113
	306873	AI086929	EST singleton (not in UniGene) with exon hit	0.113
	336040		CH22_FGENES.679_2	0.113
25	303898	T23215	EST cluster (not in UniGene) with exon hit	0.113
	312011	AW294868	Hs.187226 ESTs	0.113
	335186		CH22_FGENES.506_5	0.113
	333607		CH22_FGENES.216_2	0.113
30	305549	AA773530	EST singleton (not in UniGene) with exon hit	0.113
	333686		CH22_FGENES.249_4	0.113
	334352		CH22_FGENES.376_3	0.113
	338195		CH22_EM:AC005500.GENSCAN.233-18	0.114
	333588		CH22_FGENES.206_2	0.114
35	339233		CH22_BA354112.GENSCAN.2-3	0.114
	337455		CH22_FGENES.777-1	0.114
	309101	AI925108	EST singleton (not in UniGene) with exon hit	0.114
	328522		CH.07_hs gl 5868477	0.114
	323999	AI537333	Hs.252782 ESTs	0.114
40	333517		CH22_FGENES.173_2	0.114
	329935		CH.16_p2 gl 6165200	0.114
	326226		CH.17_hs gl 5867230	0.114
	335890		CH22_FGENES.633_4	0.114
	336715		CH22_FGENES.77-1	0.114
45	327640		CH.04_hs gl 5867890	0.114
	338842		CH22_DJ246D7.GENSCAN.7-1	0.114
	306534	AA991487	EST singleton (not in UniGene) with exon hit	0.114
	336597		CH22_FGENES.266_1	0.114
	321010	Y17456	Hs.227150 Homo sapiens LSFR2 gene; last exon	0.114
50	302294	AA159213	Hs.5337 isocitrate dehydrogenase 2 (NADP+); mitochondrial	0.114
	324895	N44238	Hs.77515 inositol 1,4,5-triphosphate receptor; type 3	0.114
	327358		CH.01_hs gl 6552411	0.114
	308792	AI815153	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	0.115
	325886		CH.16_hs gl 5867087	0.115
	336850		CH22_FGENES.272-11	0.115
55	305858	AA863103	EST singleton (not in UniGene) with exon hit	0.115
	302569	AC004472	multiple UniGene matches	0.115
	336158		CH22_FGENES.707_2	0.115
	327866		CH.06_hs gl 5868131	0.115
	339157		CH22_DA59H18.GENSCAN.67-3	0.115
60	339258		CH22_BA354112.GENSCAN.8-3	0.115
	336129		CH22_FGENES.701_17	0.115
	333684		CH22_FGENES.249_2	0.115
	309618	AW190162	Hs.184776 ribosomal protein L23a	0.115
	312926	AA954097	Hs.127523 ESTs	0.115
65	302540	AB035698	EST cluster (not in UniGene) with exon hit	0.115
	328968		CH.08_hs gl 6458775	0.115
	327902		CH.08_hs gl 5868158	0.115
	321927	AJ223366	EST cluster (not in UniGene)	0.115
	335962		CH22_FGENES.651_4	0.115

	334927		CH22_FGENES.460_1	0.115
	330535	U11872	Human interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1	0.856
5	328591		CH.07_hs gij5868227	0.115
	334902		CH22_FGENES.452_16	0.115
	328525		CH.07_hs gij5868482	0.115
	325870		CH.16_hs gij6682482	0.116
	337522		CH22_FGENES.819-1	0.116
10	305079	AA641329	EST singleton (not in UniGene) with exon hit	0.116
	327343		CH.01_hs gij6017017	0.116
	333918		CH22_FGENES.296_7	0.116
	333600		CH22_FGENES.213_2	0.116
	335846		CH22_FGENES.623_6	0.116
15	333510		CH22_FGENES.171_4	0.116
	327629		CH.04_hs gij5867872	0.116
	333470		CH22_FGENES.161_6	0.116
	326855		CH.20_hs gij6552460	0.116
	327008		CH.21_hs gij5867664	0.117
20	337480		CH22_FGENES.795-3	0.117
	336425		CH22_FGENES.824_10	0.117
	321984	AL079687	Hs.171065 ESTs	0.117
	335651		CH22_FGENES.590_2	0.117
	308164	AI521574	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.117
25	337927		CH22_EM:AC005500.GENSCAN.80-3	0.117
	300341	H45095	Hs.153524 ESTs	0.117
	300154	AI245127	Hs.179331 ESTs	0.117
	306295	AA937331	EST singleton (not in UniGene) with exon hit	0.117
	329670		CH.14_p2 gij6272129	0.117
30	335612		CH22_FGENES.583_6	0.117
	307845	AI363450	EST singleton (not in UniGene) with exon hit	0.117
	330401	D28383	Human mRNA for ATP synthase B chain, 5'UTR (sequence from the 5'cap to the start codon)	0.117
	327127		CH.21_hs gij6682520	0.117
35	333843		CH22_FGENES.290_1	0.117
	331083	R17762	Hs.22292 ESTs	0.117
	329140		CH.X_hs gij6017060	0.117
	339338		CH22_BA354112.GENSCAN.27-3	0.117
	331974	AA464518	Hs.99616 ESTs	0.117
40	338631		CH22_EM:AC005500.GENSCAN.454-2	0.117
	330299		CH.06_p2 gij2905881	0.117
	330351		CH.09_p2 gij3056622	0.117
	305377	AA715714	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.117
	333106		CH22_FGENES.79_12	0.117
45	338514		CH22_EM:AC005500.GENSCAN.392-4	0.117
	327335		CH.01_hs gij5902477	0.117
	301970	AB028962	Hs.120245 KIAA1039 protein	0.118
	326339		CH.17_hs gij6056311	0.118
	330612	X15673	Hs.93174 Human endogenous retrovirus pHE.1 (ERV9)	0.118
50	334178		CH22_FGENES.350_6	0.118
	328008		CH.06_hs gij5902482	0.118
	329976		CH.16_p2 gij4878063	0.118
	320952	AA897432	Hs.130411 ESTs	0.118
	305621	AA789095	EST singleton (not in UniGene) with exon hit	0.118
55	337850		CH22_EM:AC005500.GENSCAN.34-3	0.118
	333626		CH22_FGENES.224_2	0.118
	337672		CH22_EM:AC000097.GENSCAN.67-1	0.118
	328803		CH.07_hs gij6004475	0.118
	325922		CH.16_hs gij5867122	0.118
60	334489		CH22_FGENES.397_1	0.118
	320638	R54766	Hs.101120 ESTs	0.118
	321932	AA569229	EST cluster (not in UniGene)	0.118
	336958		CH22_FGENES.367-1	0.118
	332082	AA600176	Hs.112345 ESTs	0.118
65	306004	AA689992	EST singleton (not in UniGene) with exon hit	0.118
	336803		CH22_FGENES.194-1	0.118
	309107	AI925823	EST singleton (not in UniGene) with exon hit	0.118
	336859		CH22_FGENES.293-9	0.118
	337835		CH22_EM:AC005500.GENSCAN.85-6	0.118
	326492		CH.19_hs gij5867422	0.118

	327289		CH.01_hs gj 5867481	0.119
	325818		CH.14_hs gj 6682490	0.119
	310787	AW262580	Hs.159040 ESTs	0.119
	330028		CH.16_p2 gj 6671908	0.119
5	325317		CH.11_hs gj 5866878	0.119
	335279		CH22_FGENES.523_7	0.119
	331720	AA192173	Hs.221530 ESTs	0.119
	329186		CH.X_hs gj 5868711	0.119
	316012	AA764950	Hs.119898 ESTs	0.119
10	338316		CH22_EM:AC005500.GENSCAN.304-2	0.119
	326033		CH.17_hs gj 5867178	0.119
	334745		CH22_FGENES.426_3	0.119
	333051		CH22_FGENES.73_5	0.119
	301763	R01279	EST cluster (not in UniGene) with exon hit	0.12
15	304502	AA454809	Hs.172928 collagen; type I; alpha 1	0.12
	335680		CH22_FGENES.584_5	0.12
	304678	AA548556	EST singleton (not in UniGene) with exon hit	0.12
	335441		CH22_FGENES.560_4	0.12
	336187		CH22_FGENES.717_11	0.12
20	309422	AW087175	EST singleton (not in UniGene) with exon hit	0.12
	336047		CH22_FGENES.679_9	0.12
	309651	AW195850	EST singleton (not in UniGene) with exon hit	0.12
	308547	AI895385	Hs.201903 EST	0.12
	304443	AA399444	EST singleton (not in UniGene) with exon hit	0.12
25	336245		CH22_FGENES.746_3	0.12
	302703	H72333	EST cluster (not in UniGene) with exon hit	0.12
	335690		CH22_FGENES.596_5	0.12
	328941		CH.08_hs gj 6456765	0.12
	333873		CH22_FGENES.291_9	0.12
30	317246	AW105092	Hs.155690 ESTs	0.12
	339288		CH22_BA354112.GENSCAN.16-6	0.12
	337966		CH22_EM:AC005500.GENSCAN.116-3	0.12
	333304		CH22_FGENES.137_1	0.121
	308332	AI591235	EST singleton (not in UniGene) with exon hit	0.121
35	329319		CH.X_hs gj 6381976	0.121
	302086	X57138	multiple UniGene matches	0.121
	333290		CH22_FGENES.129_2	0.121
	323825	AI793080	Hs.123525 ESTs; Weakly similar to NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR [R.norvegicus]	0.121
40	330575	U64105	Hs.252280 Rho guanine nucleotide exchange factor (GEF) 1	0.121
	305274	AA679990	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.121
	333647		CH22_FGENES.235_2	0.121
	302251	AA333340	EST cluster (not in UniGene) with exon hit	0.121
	329777		CH.14_p2 gj 6002090	0.121
45	333155		CH22_FGENES.89_5	0.121
	326122		CH.17_hs gj 5867194	0.121
	335310		CH22_FGENES.532_3	0.121
	335453		CH22_FGENES.562_13	0.122
50	305103	AA643329	Hs.111334 ferritin; light polypeptide	0.122
	337284		CH22_FGENES.667-2	0.122
	337418		CH22_FGENES.758-4	0.122
	313073	AI963740	Hs.46826 ESTs	0.122
	303759	AW504164	EST cluster (not in UniGene) with exon hit	0.122
	300017			0.122
55		M33197	AFFX control: GAPDH	0.122
	316725	AW135084	Hs.127264 ESTs	0.122
	330738	AA293153	Hs.120980 nuclear receptor co-repressor 2	0.122
	338466		CH22_FGENES.829_25	0.122
	335956		CH22_FGENES.647_3	0.122
60	315308	AA780564	Hs.189053 ESTs	0.122
	338925		CH22_DJ32110.GENSCAN.14-3	0.122
	334969		CH22_FGENES.466_2	0.122
	322050	AL137589	EST cluster (not in UniGene)	0.122
	339084		CH22_DA59H18.GENSCAN.38-2	0.122
65	338323		CH22_EM:AC005500.GENSCAN.306-2	0.122
	337003		CH22_FGENES.419-7	0.122
	325470		CH.12_hs gj 6017034	0.123
	336503		CH22_FGENES.833_10	0.123
	330786	D60374	Hs.258712 EST	0.123

	329446		CH.Y_hs gij5868866	0.123
	303326	AA229433	Hs.222634 ESTs; Moderately similar to ubiquitin-like protein / ribosomal protein S30	0.123
5	309067	AI916313	Hs.212788 EST	0.123
	317464	AA968472	Hs.130463 ESTs	0.123
	328755		CH.07_hs gij5868301	0.123
	326036		CH.17_hs gij5867178	0.123
	327208		CH.01_hs gij5867447	0.123
	326124		CH.17_hs gij5916395	0.123
10	327509		CH.02_hs gij6117815	0.123
	338398		CH22_EM:AC005500.GENSCAN.336-5	0.123
	304652	AA527782	Hs.84298 CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.123
15	335797		CH22_FGENES.612_6	0.124
	336714		CH22_FGENES.76-29	0.124
	327204		CH.01_hs gij5867447	0.124
	331881	AA430672	Hs.123778 ESTs	0.124
	306971	AI126509	EST singleton (not in UniGene) with exon hit	0.124
20	336174		CH22_FGENES.710_1	0.124
	336126		CH22_FGENES.701_13	0.124
	329129		CH.X_hs gij6588026	0.124
	303049	AW407562	EST cluster (not in UniGene) with exon hit	0.124
	335778		CH22_FGENES.607_14	0.124
25	336601		CH22_FGENES.369_2	0.124
	334340		CH22_FGENES.375_17	0.124
	337436		CH22_FGENES.767-1	0.124
	306013	AA896990	EST singleton (not in UniGene) with exon hit	0.124
	339213		CH22_FF113D11.GENSCAN.6-8	0.124
30	335355		CH22_FGENES.541_2	0.124
	336552		CH22_FGENES.841_9	0.124
	336384		CH22_FGENES.822_4	0.124
	310485	AI286202	Hs.149800 ESTs	0.125
	335840		CH22_FGENES.622_3	0.125
	336444		CH22_FGENES.827_10	0.125
35	315703	N36070	EST cluster (not in UniGene)	0.125
	327763		CH.05_hs gij5867961	0.125
	336383		CH22_FGENES.822_3	0.125
	333496		CH22_FGENES.168_6	0.125
40	328662		CH.07_hs gij6004473	0.125
	336986		CH22_DA59H18.GENSCAN.5-1	0.125
	328311		CH.07_hs gij5868371	0.125
	337241		CH22_FGENES.644-2	0.125
	336933		CH22_FGENES.350-7	0.125
45	313483	AW294432	Hs.144252 ESTs	0.125
	326116		CH.17_hs gij5867193	0.125
	330450	HG363-HT363	Epidermal Growth Factor Receptor-Related Protein	0.125
	307491	AI268539	EST singleton (not in UniGene) with exon hit	0.125
	331852	AA418988	Hs.98314 Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)	0.125
50	330462	HG944-HT944	Dopamine Receptor D4	0.125
	304410	AA284508	EST singleton (not in UniGene) with exon hit	0.125
	336385		CH22_FGENES.822_5	0.125
	336793		CH22_FGENES.176-3	0.125
55	326243		CH.17_hs gij5867261	0.125
	327266		CH.01_hs gij5867462	0.125
	320753	AF070579	Hs.181544 Homo sapiens clone 24487 mRNA sequence	0.125
	336960		CH22_FGENES.369-5	0.125
	329667		CH.14_p2 gij6272129	0.125
60	328168		CH.06_hs gij5868071	0.125
	336534		CH22_FGENES.839_16	0.125
	339289		CH22_BA354112.GENSCAN.16-9	0.126
	309230	AI970747	EST singleton (not in UniGene) with exon hit	0.126
	339190		CH22_FF113D11.GENSCAN.1-2	0.126
	337086		CH22_FGENES.458-14	0.126
65	319233	R21054	Hs.211522 ESTs	0.126
	339396		CH22_BA232E17.GENSCAN.6-8	0.126
	331930	AA449077	Hs.179765 Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H192)	0.126
	308069	AI475914	EST singleton (not in UniGene) with exon hit	0.126

	338477		CH22_EM:AC005500.GENSCAN.373-5	0.126
	334286		CH22_FGENES.369_16	0.126
	317245	AI025039	Hs.131732 ESTs	0.126
5	335249		CH22_FGENES.516_10	0.126
	333327		CH22_FGENES.138_20	0.126
	304240	AA009802	EST singleton (not in UniGene) with exon hit	0.126
	335464		CH22_FGENES.562_26	0.126
	335236		CH22_FGENES.515_8	0.126
	334154		CH22_FGENES.340_4	0.126
10	308257	AI984183	EST singleton (not in UniGene) with exon hit	0.126
	310015	AI220122	Hs.201981 ESTs; Weakly similar to breast carcinoma-associated antigen [H.sapiens]	0.126
	328280		CH.07_hs gi 5868352	0.126
	305744	AA831819	EST singleton (not in UniGene) with exon hit	0.126
15	327430		CH.02_hs gi 5867754	0.126
	328323		CH.07_hs gi 5868373	0.126
	333274		CH22_FGENES.123_2	0.126
	337193		CH22_FGENES.575-3	0.127
	334820		CH22_FGENES.437_2	0.127
20	328706		CH.07_hs gi 5868270	0.127
	331228	W67267	Hs.174911 ESTs	0.127
	307205	AI192479	EST singleton (not in UniGene) with exon hit	0.127
	337123		CH22_FGENES.519-3	0.127
	326201		CH.17_hs gi 5867216	0.127
25	335276		CH22_FGENES.523_2	0.127
	331202	T81115	Hs.191136 ESTs	0.127
	330532	U03187	Hs.121544 interleukin 12 receptor; beta 1	0.127
	321235	N49521	EST cluster (not in UniGene)	0.127
	301743	F12605	Hs.204529 ESTs; Weakly similar to reverse transcriptase [H.sapiens]	0.127
30	328175		CH.06_hs gi 5868073	0.127
	306407	AA971985	EST singleton (not in UniGene) with exon hit	0.127
	327145		CH.01_hs gi 5867548	0.127
	327649		CH.04_hs gi 5867899	0.127
	335142		CH22_FGENES.499_12	0.127
35	333909		CH22_FGENES.295_2	0.127
	330608	X04325	Hs.2679 gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.127
	330158		CH.21_p2 gi 6580367	0.127
	320153	AF064594	Hs.120380 phospholipase A2; group VI	0.127
40	314407	AA098835	Hs.224432 ESTs	0.127
	333383		CH22_FGENES.143_22	0.127
	320663	AI734242	Hs.244473 ESTs	0.128
	326233		CH.17_hs gi 5867232	0.128
	326596		CH.20_hs gi 5867634	0.128
45	335174		CH22_FGENES.504_4	0.128
	319843	H29920	Hs.99486 ESTs; Weakly similar to aralar1 [H.sapiens]	0.128
	335458		CH22_FGENES.562_18	0.128
	332997		CH22_FGENES.58_4	0.128
	334188		CH22_FGENES.352_3	0.128
50	329759		CH.14_p2 gi 6048280	0.128
	330348		CH.09_p2 gi 4544475	0.128
	326958		CH.21_hs gi 6469836	0.128
	305263	AA679467	EST singleton (not in UniGene) with exon hit	0.128
	337693		CH22_EM:AC000097.GENSCAN.78-14	0.128
55	326812		CH.20_hs gi 6682504	0.128
	333237		CH22_FGENES.108_7	0.128
	333699		CH22_FGENES.250_13	0.128
	311496	AI768677	Hs.209888 ESTs; Weakly similar to phosphatidylserine synthase-2 [M.musculus]	0.128
60	336499		CH22_FGENES.833_4	0.128
	320087	AF032387	Hs.113265 small nuclear RNA activating complex; polypeptide 4; 190kD	0.128
	309989	AI184186	Hs.197813 ESTs	0.128
	301490	AW298468	Hs.250461 ESTs	0.128
	337011		CH22_FGENES.427-6	0.128
65	315052	AA876910	Hs.134427 ESTs	0.128
	301611	W22172	Hs.59038 ESTs	0.128
	336497		CH22_FGENES.833_2	0.129
	302068	Y16280	Hs.132049 endothelin type b receptor-like protein 2	0.129
	334502		CH22_FGENES.397_18	0.129

	304332	AA158884	EST singleton (not in UniGene) with exon hit	0.129
	304522	AA465405	EST singleton (not in UniGene) with exon hit	0.129
	312407	R46180	Hs.153485 ESTs	0.129
5	310098	AI685841	Hs.161354 ESTs	0.129
	301119	AF142579	EST cluster (not in UniGene) with exon hit	0.129
	309268	AI985821	Hs.62954 ferritin; heavy polypeptide 1	0.129
	330989	H42142	Hs.226396 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (Dbp5; yeast; homolog)	0.129
	336949		CH22_FGENES.361-4	0.129
10	330115		CH.19_p2 gjl6015202	0.129
	339212		CH22_FF113D11.GENSCAN.6-7	0.129
	326951		CH.21_hs gjl6004446	0.129
	305165	AA662939	EST singleton (not in UniGene) with exon hit	0.129
	308238	AI559492	EST singleton (not in UniGene) with exon hit	0.129
15	337140		CH22_FGENES.537-5	0.13
	321758	U29112	EST cluster (not in UniGene)	0.13
	304619	AA515554	Hs.119598 ribosomal protein L3	0.13
	312469	AA745289	Hs.173068 ESTs	0.13
	339017		CH22_DA59H18.GENSCAN.20-6	0.13
20	330116		CH.19_p2 gjl6015202	0.13
	333312		CH22_FGENES.138_4	0.13
	338004		CH22_EM:AC005500.GENSCAN.121-1	0.13
	314141	AA232134	Hs.190028 ESTs	0.13
	300509	AI239845	Hs.128494 ESTs; Weakly similar to EG:95B7.2 [D.melanogaster]	0.13
25	338530		CH22_EM:AC005500.GENSCAN.398-11	0.13
	335968		CH22_FGENES.652_1	0.13
	314121	AI732100	Hs.187619 ESTs	0.13
	337593		CH22_C20H12.GENSCAN.6-8	0.13
	332881		CH22_FGENES.33_1	0.13
30	305836	AA858043	EST singleton (not in UniGene) with exon hit	0.13
	339059		CH22_DA59H18.GENSCAN.30-5	0.13
	305610	AA782319	EST singleton (not in UniGene) with exon hit	0.13
	305852	AA862455	EST singleton (not in UniGene) with exon hit	0.13
	327409		CH.02_hs gjl5867750	0.13
35	312751	AI613089	Hs.164178 ESTs	0.13
	308726	AI799268	Hs.209929 EST	0.13
	325961		CH.16_hs gjl5867147	0.13
	311159	AW025919	Hs.197636 ESTs	0.13
40	322715	AA057230	Hs.182135 ESTs	0.13
	336441		CH22_FGENES.827_7	0.13
	336339		CH22_FGENES.814_12	0.13
	306911	AI095365	EST singleton (not in UniGene) with exon hit	0.13
	333613		CH22_FGENES.217_8	0.13
45	338489		CH22_EM:AC005500.GENSCAN.384-17	0.131
	326904		CH.21_hs gjl5867684	0.131
	337337		CH22_FGENES.717-1	0.131
	326752		CH.20_hs gjl5867615	0.131
	303977	AW512978	EST singleton (not in UniGene) with exon hit	0.131
50	301373	AA595235	EST cluster (not in UniGene) with exon hit	0.131
	338448		CH22_EM:AC005500.GENSCAN.359-22	0.131
	333774		CH22_FGENES.272_5	0.131
	332986		CH22_FGENES.54_8	0.131
	335362		CH22_FGENES.541_12	0.131
	335896		CH22_FGENES.635_4	0.131
55	337825		CH22_EM:AC005500.GENSCAN.13-19	0.131
	325257		CH.11_hs gjl5866895	0.131
	331188	T50240	Hs.167837 ESTs	0.131
	330645	Y08302	Hs.144879 dual specificity phosphatase 9	0.131
	331760	AA292721	Hs.154434 ESTs; Weakly similar to unknown [H.sapiens]	0.131
60	322995	AA513829	Hs.29797 ribosomal protein L10	0.131
	335497		CH22_FGENES.571_5	0.131
	334824		CH22_FGENES.437_6	0.131
	319480	R06933	Hs.184221 ESTs	0.131
	334842		CH22_FGENES.439_21	0.131
65	333335		CH22_FGENES.139_4	0.131
	317252	AA905178	Hs.130124 ESTs	0.131
	329034		CH.X_hs gjl5868561	0.131
	305186	AA664230	EST singleton (not in UniGene) with exon hit	0.131
	335755		CH22_FGENES.604_4	0.131

5	302143	H15270	Hs.189847	putative neuronal cell adhesion molecule	0.131
	334939			CH22_FGENES.465_3	0.131
	318994	C15110	Hs.17802	ESTs	0.131
	334498			CH22_FGENES.397_14	0.131
	333413			CH22_FGENES.146_2	0.132
10	329676			CH.14_p2 gi 5272128	0.132
	327277			CH.01_hs gi 5867473	0.132
	305022	AA627416		EST singleton (not in UniGene) with exon hit	0.132
	336805			CH22_FGENES.196-3	0.132
	320121	T93657		EST cluster (not in UniGene)	0.132
15	334761			CH22_FGENES.428_10	0.132
	339400			CH22_BA232E17.GENSCAN.7-6	0.132
	330301			CH.06_p2 gi 2905862	0.132
	316822	AA627691	Hs.129967	ESTs; Weakly similar to neuronal thread protein	0.132
	328020			AD7c-NTP [H.sapiens]	0.132
20	325327			CH.06_hs gi 5902482	0.132
	321163	AA209530		CH.11_hs gi 5866875	0.132
	336393			EST cluster (not in UniGene)	0.132
	325905			CH22_FGENES.823_5	0.132
	305237	AA676286	Hs.2186	CH.16_hs gi 5867104	0.132
25	339046			eukaryotic translation elongation factor 1 gamma	0.132
	325375			CH22_DA59H18.GENSCAN.28-6	0.132
	333961			CH.12_hs gi 5866920	0.132
	335450			CH22_FGENES.304_7	0.132
	302286	R58438		CH22_FGENES.562_8	0.133
30	335116			EST cluster (not in UniGene) with exon hit	0.133
	327333			CH22_FGENES.496_3	0.133
	308070	AI470948		CH.01_hs gi 5902477	0.133
	308311	AI581855		EST singleton (not in UniGene) with exon hit	0.133
	320813	AW360847	Hs.208839	EST singleton (not in UniGene) with exon hit	0.133
35	323665	AW248307		ESTs	0.133
	328318			EST cluster (not in UniGene)	0.133
	320803	R51419		CH.07_hs gi 5868373	0.133
	332791			EST cluster (not in UniGene)	0.133
	314976	AA524725	Hs.162108	CH22_FGENES.3_1	0.133
40	303309	AL134164	Hs.224868	ESTs	0.133
	320581	R39753	Hs.170187	ESTs	0.133
	333944			CH22_FGENES.302_2	0.133
	317992	AI733512	Hs.130901	ESTs	0.133
	330935	F02383	Hs.26492	beta-1;3-glucuronyltransferase 3 (glucuronosyltransferase I)	0.133
45	336659			CH22_FGENES.36-5	0.133
	338887			CH22_DJ32i10.GENSCAN.6-10	0.133
	305273	AA679979	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	0.133
	333566			CH22_FGENES.183_2	0.134
	316952	AW450033	Hs.163312	ESTs	0.134
50	333818			CH22_FGENES.283_1	0.134
	328687			CH.07_hs gi 5868262	0.134
	302879	H11802		EST cluster (not in UniGene) with exon hit	0.134
	336557			CH22_FGENES.842_2	0.134
	335222			CH22_FGENES.513_5	0.134
55	338094			CH22_EM:AC005500.GENSCAN.179-3	0.134
	337384			CH22_FGENES.745-1	0.134
	327360			CH.01_hs gi 6552411	0.134
	328132			CH.06_hs gi 5868038	0.134
	323604	AI751438	Hs.182827	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	0.134
60	337591			WARNING ENTRY !!!!	0.134
	307018	AI140639		CH22_C20H12.GENSCAN.6-6	0.134
	326896			EST singleton (not in UniGene) with exon hit	0.134
	333479			CH.21_hs gi 5867680	0.134
	337915			CH22_FGENES.163_5	0.134
65	335110			CH22_EM:AC005500.GENSCAN.61-3	0.134
	333481			CH22_FGENES.494_18	0.134
	327512			CH22_FGENES.163_9	0.134
	300096	AW328639	Hs.83575	CH.02_hs gi 6117815	0.134
	330163			ESTs; Weakly similar to ZC328.3 [C.elegans]	0.134
	335752			CH.02_p2 gi 6042042	0.135
	334857			CH22_FGENES.604_1	0.135
				CH22_FGENES.443_1	0.135

	301872	H84730	EST cluster (not in UniGene) with exon hit	0.135
	337529		CH22_FGENES.823-29	0.135
	335734		CH22_FGENES.601_4	0.135
	337551		CH22_FGENES.847-8	0.135
5	309078	AI920965	Hs.77961 major histocompatibility complex; class I; B	0.135
	335513		CH22_FGENES.571_28	0.135
	339078		CH22_DA59H18.GENSCAN.37-6	0.135
	321907	N56660	Hs.148722 ESTs; Weakly similar to large tumor suppressor 1 [H.sapiens]	0.135
	337189		CH22_FGENES.571-32	0.135
10	329635		CH.12_p2 gij5302817	0.135
	308601	AI719930	EST singleton (not in UniGene) with exon hit	0.135
	305020	AA627248	Hs.2064 vimentin	0.135
	333894		CH22_FGENES.293_1	0.135
15	322465	AA137152	Hs.3784 ESTs; Highly similar to phosphoserine aminotransferase [H.sapiens]	0.135
	305601	AA780975	EST singleton (not in UniGene) with exon hit	0.135
	332186	H10781	Hs.141051 ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY	0.135
	327822		CH.05_hs gij5867968	0.135
20	310087	AI393914	Hs.160624 ESTs; Weakly similar to similar to CR16; SH3 domain binding protein	0.135
	328752		CH.07_hs gij5868298	0.135
	337611		CH22_C20H12.GENSCAN.19-4	0.135
25	334470		CH22_FGENES.394_1	0.136
	335115		CH22_FGENES.496_2	0.136
	328730		CH.07_hs gij5868289	0.136
	330350		CH.09_p2 gij3056622	0.136
	336971		CH22_FGENES.378-6	0.136
30	308258	AI565612	EST singleton (not in UniGene) with exon hit	0.136
	326745		CH.20_hs gij5867611	0.136
	335440		CH22_FGENES.560_3	0.136
	320257	AA330746	EST cluster (not in UniGene)	0.136
	328677		CH.07_hs gij5868256	0.136
	329731		CH.14_p2 gij6065783	0.136
35	315950	AA700553	Hs.206974 ESTs	0.136
	330049		CH.17_p2 gij4567182	0.136
	337070		CH22_FGENES.448-3	0.136
	304095	H11324	Hs.31059 EST	0.136
	309304	AW005527	Hs.232820 EST	0.136
40	333458		CH22_FGENES.157_7	0.136
	329639		CH.15_p2 gij6563505	0.136
	322202	AI275056	Hs.200133 ESTs	0.136
	333991		CH22_FGENES.310_15	0.136
45	318617	AW247252	Hs.75514 nucleoside phosphorylase	0.136
	310623	AI341586	Hs.195588 ESTs	0.136
	330489	M23323	Hs.3003 CD3E antigen; epsilon polypeptide (TIT3 complex)	0.136
	309646	AW194694	EST singleton (not in UniGene) with exon hit	0.136
	331068	R00071	Hs.191199 ESTs	0.136
	334285		CH22_FGENES.369_15	0.136
50	332178	F13689	Hs.100725 EST	0.136
	305724	AA827608	EST singleton (not in UniGene) with exon hit	0.136
	303158	AL138110	Hs.8594 Homo sapiens mRNA containing (CAG)4 repeat; clone CZ-CAG-7	0.136
	334543		CH22_FGENES.403_8	0.136
55	335384		CH22_FGENES.543_26	0.136
	336527		CH22_FGENES.839_8	0.136
	334951		CH22_FGENES.485_20	0.136
	325882		CH.16_hs gij5867087	0.137
	305134	AA653159	EST singleton (not in UniGene) with exon hit	0.137
	307058	AI148709	EST singleton (not in UniGene) with exon hit	0.137
60	331943	AA453418	Hs.178272 ESTs	0.137
	331116	R44780	Hs.22634 ESTs	0.137
	306094	AA908877	EST singleton (not in UniGene) with exon hit	0.137
	333561		CH22_FGENES.180_18	0.137
65	321439	H61962	EST cluster (not in UniGene)	0.137
	324594	AA497090	EST cluster (not in UniGene)	0.137
	337926		CH22_EM:AC005500.GENSCAN.77-4	0.137
	337353		CH22_FGENES.726-1	0.137
	331836	AA412295	Hs.104774 EST	0.137
	308981	AI873242	EST singleton (not in UniGene) with exon hit	0.137

	329424		CH.Y_hs gi 5868879	0.137
	325829		CH.15_hs gi 5867052	0.137
	331845	AA416863	Hs.98183 ESTs	0.137
	333854		CH22_FGENES.290_13	0.137
5	306591	AI000248	EST singleton (not in UniGene) with exon hit	0.137
	328948		CH.08_hs gi 6456765	0.137
	338935		CH22_DJ32i10.GENSCAN.18-12	0.137
	325960		CH.16_hs gi 5867147	0.137
	328377		CH.07_hs gi 5868390	0.138
10	308851	AI829820	EST singleton (not in UniGene) with exon hit	0.138
	314620	AA424352	Hs.210586 ESTs	0.138
	337592		CH22_C20H12.GENSCAN.6-7	0.138
	338684		CH22_EM:AC005500.GENSCAN.472-3	0.138
	331800	AA400498	Hs.97543 ESTs	0.138
15	304587	AA505535	EST singleton (not in UniGene) with exon hit	0.138
	333981		CH22_FGENES.310_4	0.138
	332452	AA040369	Hs.11170 SYT interacting protein	0.138
	305752	AA835278	EST singleton (not in UniGene) with exon hit	0.138
	311947	T65554	Hs.251591 EST	0.138
20	333783		CH22_FGENES.273_5	0.138
	337406		CH22_FGENES.754-14	0.138
	327976		CH.06_hs gi 5868212	0.138
	325593		CH.13_hs gi 5866992	0.138
	339425		CH22_DJ579N16.GENSCAN.14-4	0.138
25	304475	AA428879	EST singleton (not in UniGene) with exon hit	0.138
	309488	AW131104	EST singleton (not in UniGene) with exon hit	0.138
	337532		CH22_FGENES.827-6	0.138
	317234	AA904448	Hs.126368 ESTs	0.138
	312261	AA854425	Hs.144455 ESTs	0.138
30	328927		CH.08_hs gi 5868500	0.138
	336424		CH22_FGENES.824_9	0.138
	326667		CH.20_hs gi 6562455	0.138
	325988		CH.16_hs gi 5867064	0.138
	318446	AW300287	EST cluster (not in UniGene)	0.139
35	336511		CH22_FGENES.834_6	0.139
	335204		CH22_FGENES.508_13	0.139
	303244	AA147472	EST cluster (not in UniGene) with exon hit	0.139
	330870	AA115804	Hs.187593 ESTs	0.139
	329376		CH.X_hs gi 5868859	0.139
40	304703	AA563398	EST singleton (not in UniGene) with exon hit	0.139
	333653		CH22_FGENES.239_2	0.139
	306799	AI051696	EST singleton (not in UniGene) with exon hit	0.139
	304872	AA595289	EST singleton (not in UniGene) with exon hit	0.139
	330812	AA013001	Hs.60563 ESTs	0.139
45	329568		CH.10_p2 gi 3962490	0.139
	319210	AA253074	Hs.146261 ESTs	0.139
	334320		CH22_FGENES.374_5	0.139
	300860	AI916949	Hs.149748 ESTs; Weakly similar to weak similarity to collagens [C.elegans]	0.139
	305866	AA864533	EST singleton (not in UniGene) with exon hit	0.139
50	312943	AA984364	Hs.119064 ESTs	0.139
	330523	M99439	Hs.83958 transducin-like enhancer of split 4; homolog of Drosophila E(sp1)	0.139
	312708	AI076204	Hs.135440 ESTs	0.139
	309366	AW072970	EST singleton (not in UniGene) with exon hit	0.139
	303273	AA316069	EST cluster (not in UniGene) with exon hit	0.139
55	317484	AW274696	Hs.143921 ESTs	0.139
	333239		CH22_FGENES.111_1	0.139
	307126	AI184951	EST singleton (not in UniGene) with exon hit	0.139
	316813	AA826505	Hs.124517 ESTs	0.139
	331746	AA281365	Hs.121640 ESTs; Weakly similar to KIAA0366 [H.sapiens]	0.139
60	308558	AI700145	Hs.172182 poly(A)-binding protein; cytoplasmic 1	0.139
	310784	AW086142	Hs.159017 ESTs	0.139
	323831	AA335715	Hs.200299 ESTs	0.139
	307692	AI318342	EST singleton (not in UniGene) with exon hit	0.139
	310570	AI318327	EST cluster (not in UniGene)	0.139
65	327934		CH.06_hs gi 5868184	0.139
	305232	AA670052	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	0.139
	334756		CH22_FGENES.428_5	0.139
	331938	AA451867	Hs.99255 ESTs	0.139
	301393	AI474722	Hs.150898 ESTs; Weakly similar to KIAA0644 protein [H.sapiens]	0.139

	312005	T78450	Hs.13941	ESTs	0.139
	338431			CH22_EM:AC005500.GENSCAN.351-4	0.14
	331214	T90496	Hs.16757	ESTs	0.14
	333601			CH22_FGENES.213_4	0.14
5	323481	AA278449	Hs.137429	ESTs	0.14
	336911			CH22_FGENES.344-4	0.14
	338157			CH22_EM:AC005500.GENSCAN.209-5	0.14
	327845			CH.05_hs gi 5631962	0.14
	319109	Z45662	Hs.90797	Homo sapiens clone 23620 mRNA sequence	0.14
10	334763			CH22_FGENES.428_12	0.14
	329384			CH.X_hs gi 5868869	0.14
	302996	AF054663		EST cluster (not in UniGene) with exon hit	0.14
	323751	AW452656	Hs.209824	ESTs	0.14
	329916			CH.16_p2 gi 6223624	0.14
15	301993	N49826	Hs.18602	ESTs	0.14
	338129			CH22_EM:AC005500.GENSCAN.197-2	0.14
	325704			CH.14_hs gi 5867028	0.14
	335656			CH22_FGENES.590_7	0.14
	331673	W72366	Hs.40033	ESTs	0.14
20	316807	AI018331	Hs.172444	ESTs; Highly similar to transcription regulator [M.musculus]	0.14
	310743	AW449754	Hs.158665	ESTs	0.14
	326941			CH.21_hs gi 6004446	0.14
	328809			CH.07_hs gi 5868327	0.14
	323855	AI653164	Hs.128665	ESTs	0.14
25	304705	AA564064		EST singleton (not in UniGene) with exon hit	0.14
	325666			CH.14_hs gi 6469822	0.14
	333747			CH22_FGENES.265_6	0.14
	318287	AW015616	Hs.143321	ESTs	0.141
	332972			CH22_FGENES.51_5	0.141
30	305704	AA825266		EST singleton (not in UniGene) with exon hit	0.141
	315699	AW182805	Hs.189183	ESTs; Weakly similar to Nod1 [H.sapiens]	0.141
	327296			CH.01_hs gi 5867492	0.141
	336400			CH22_FGENES.823_15	0.141
35	321033	H26214	Hs.20733	ESTs; Weakly similar to !!! ALU SUBFAMILY SX WARNING ENTRY	0.141
	316522	AI475995	Hs.122910	ESTs	0.141
	335715			CH22_FGENES.599_15	0.141
	335959			CH22_FGENES.650_2	0.141
	333259			CH22_FGENES.118_7	0.141
40	337382			CH22_FGENES.744-8	0.141
	322346	AA227618	Hs.10882	HMG-box containing protein 1	0.141
	325378			CH.12_hs gi 5866920	0.141
	338500			CH22_EM:AC005500.GENSCAN.390-1	0.141
	338480			CH22_EM:AC005500.GENSCAN.362-5	0.141
45	315279	AW511138	Hs.256581	ESTs	0.141
	314439	AI539443	Hs.137447	ESTs	0.141
	333624			CH22_FGENES.222_3	0.141
	329237			CH.X_hs gi 5868729	0.141
	330117			CH.19_p2 gi 6015201	0.141
50	338017			CH22_EM:AC005500.GENSCAN.134-1	0.141
	337854			CH22_EM:AC005500.GENSCAN.38-12	0.142
	329984			CH.16_p2 gi 4646193	0.142
	305004	AA622328	Hs.162762	EST	0.142
	302815	N40373		EST cluster (not in UniGene) with exon hit	0.142
55	327823			CH.05_hs gi 5867968	0.142
	326753			CH.20_hs gi 5867616	0.142
	301201	AA904482	Hs.197775	ESTs	0.142
	334303			CH22_FGENES.373_6	0.142
	326453			CH.19_hs gi 5867399	0.142
60	311050	AI864581	Hs.215477	ESTs	0.142
	308740	AI802711	Hs.210337	EST; Weakly similar to aldolase A [H.sapiens]	0.142
	331003	H63959	Hs.142722	ESTs	0.142
	338010			CH22_EM:AC005500.GENSCAN.128-8	0.142
	336326			CH22_FGENES.812_4	0.142
65	318100	R44308	Hs.242302	ESTs	0.142
	320841	R55421		EST cluster (not in UniGene)	0.142
	325855			CH.16_hs gi 5867067	0.142
	330425	HG1728-HT1734		Non-Specific Cross Reacting Antigen (Gb:D90277), Alt. Splice Form 2	0.142

5	324583	AA425411	Hs.22581	ESTs	0.142
	326268			CH.17_hs gjl5867267	0.142
	331390	AA460341	Hs.45008	ESTs	0.142
	338904			CH22_DJ32110.GENSCAN.10-16	0.143
	333096			CH22_FGENES.79_1	0.143
10	331919	AA446869	Hs.119316	ESTs	0.143
	312214	AI248004	Hs.125187	ESTs	0.143
	323198	AW179174	Hs.7984	ESTs	0.143
	316107	AI204001	Hs.184014	ribosomal protein L31	0.143
	301335	AA885317	Hs.190511	ESTs	0.143
15	337392			CH22_FGENES.747-3	0.143
	325543			CH.12_hs gjl6682452	0.143
	305903	AA873085		EST singleton (not in UniGene) with exon hit	0.143
	332707	L35594	Hs.174185	phosphodiesterase 1/nucleotide pyrophosphatase 2 (autotaxin)	0.143
	337913			CH22_EM:AC005500.GENSCAN.59-10	0.143
20	301436	AA961061	Hs.131696	ESTs	0.143
	335078			CH22_FGENES.486_5	0.143
	338451			CH22_EM:AC005500.GENSCAN.359-39	0.143
	302777	AJ230640		EST cluster (not in UniGene) with exon hit	0.143
	330464	J03068	Hs.78223	N-acylaminoacyl-peptide hydrolase	0.143
25	330988	H41411	Hs.33855	ESTs	0.143
	328939			CH.08_hs gjl6004481	0.143
	308015	AI440174	Hs.228907	EST; Weakly similar to GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN	0.143
				12.3 [H.sapiens]	0.143
	328504			CH.07_hs gjl5868471	0.143
30	332599	AA402891	Hs.32951	solute carrier family 29 (nucleoside transporters); member 2	0.143
	335744			CH22_FGENES.601_15	0.143
	322394	AF077208		EST cluster (not in UniGene)	0.143
	323892	AL042661		EST cluster (not in UniGene)	0.143
	318443	AI939323	Hs.157714	ESTs; Weakly similar to NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN; ALPHA-5 CHAIN PRECURSOR	0.143
35				[H.sapiens]	0.143
	336568			CH22_FGENES.843_7	0.143
	330958	H08815	Hs.159824	EST	0.143
	327672			CH.04_hs gjl5867843	0.143
	335900			CH22_FGENES.635_8	0.144
40	336044			CH22_FGENES.679_6	0.144
	318845	AI815951	Hs.33183	ESTs; Weakly similar to estrogen-responsive finger protein; efp [H.sapiens]	0.144
	333483			CH22_FGENES.165_2	0.144
	333337			CH22_FGENES.139_6	0.144
	305993	AA889197		EST singleton (not in UniGene) with exon hit	0.144
45	335719			CH22_FGENES.599_22	0.144
	325682			CH.14_hs gjl6138923	0.144
	327350			CH.01_hs gjl6249563	0.144
	339291			CH22_BA354112.GENSCAN.18-1	0.144
	326358			CH.18_hs gjl5867293	0.144
50	330316			CH.08_p2 gjl6007576	0.144
	308150	AI499346	Hs.174131	ribosomal protein L6	0.144
	338065			CH22_EM:AC005500.GENSCAN.164-1	0.144
	339009			CH22_DA59H18.GENSCAN.18-7	0.144
	327776			CH.05_hs gjl5867964	0.145
55	336664			CH22_FGENES.41-8	0.145
	321921	AF070619		EST cluster (not in UniGene)	0.145
	319346	T70147	Hs.12024	ESTs	0.145
	304265	AA062892		EST singleton (not in UniGene) with exon hit	0.145
	303818	Z45986	Hs.250178	copine II	0.145
60	327498			CH.02_hs gjl6017023	0.145
	335227			CH22_FGENES.513_13	0.145
	339022			CH22_DA59H18.GENSCAN.22-1	0.145
	302597	H55661	Hs.33026	ESTs; Weakly similar to similar to Enterococcus faecalis TRAB [C.elegans]	0.145
				0.145	
65	308550	AI697008	Hs.201811	EST	0.145
	302175	AA262760	Hs.156015	Homo sapiens chromosome 19; cosmid R29381	0.145
	303252	AA156760		EST cluster (not in UniGene) with exon hit	0.145
	337414			CH22_FGENES.757-2	0.145
	310382	AI734009		EST cluster (not in UniGene)	0.145
	329333			CH.X_hs gjl5868806	0.145

	336857		CH22_FGENES.291-7	0.145
	332565	AA234896	Hs.25272 E1A binding protein p300	0.145
	318634	AI928098	Hs.156832 ESTs	0.145
5	336318		CH22_FGENES.801_1	0.145
	310960	AI923551	Hs.170843 ESTs	0.145
	335346		CH22_FGENES.537_2	0.145
	331196	T65416	Hs.12826 ESTs	0.145
	337607		CH22_C20H12.GENSCAN.17-3	0.146
10	331206	T84096	Hs.15284 ESTs	0.146
	301793	T80698	EST cluster (not in UniGene) with exon hit	0.146
	319590	AA210878	EST cluster (not in UniGene)	0.146
	311394	AI695374	Hs.256231 ESTs	0.146
	324773	AA632554	Hs.163401 ESTs	0.146
	324841	AI142359	Hs.155316 ESTs	0.146
15	332280	N70088	Hs.138467 ESTs	0.146
	329276		CH.X_hs gjl5868762	0.146
	335887		CH22_FGENES.633_1	0.146
	338294		CH22_EM:AC005500.GENSCAN.297-1	0.146
20	336993		CH22_FGENES.409-4	0.146
	334135		CH22_FGENES.336_2	0.146
	326251		CH.17_hs gjl5867263	0.146
	337396		CH22_FGENES.749-1	0.146
	339167		CH22_DA59H18.GENSCAN.69-8	0.146
25	316838	AW135418	Hs.161210 ESTs	0.146
	325313		CH.11_hs gjl586865	0.146
	331047	N66918	Hs.32205 ESTs	0.146
	323915	AL043362	EST cluster (not in UniGene)	0.146
	302747	AF062275	EST cluster (not in UniGene) with exon hit	0.146
30	306317	AA947909	EST singleton (not in UniGene) with exon hit	0.146
	334399		CH22_FGENES.382_5	0.146
	326472		CH.19_hs gjl5867404	0.146
	333061		CH22_FGENES.75_4	0.146
	337072		CH22_FGENES.448-5	0.146
35	334328		CH22_FGENES.375_5	0.146
	327039		CH.21_hs gjl6531965	0.146
	325576		CH.12_hs gjl6552443	0.147
	315935	AI075804	Hs.132660 ESTs	0.147
	319638	AA323758	EST cluster (not in UniGene)	0.147
40	334501		CH22_FGENES.397_17	0.147
	338238		CH22_EM:AC005500.GENSCAN.264-4	0.147
	308636	AI744063	EST singleton (not in UniGene) with exon hit	0.147
	336567		CH22_FGENES.843_6	0.147
	335819		CH22_FGENES.619_2	0.147
45	336950		CH22_FGENES.361-8	0.147
	307055	AI148477	EST singleton (not in UniGene) with exon hit	0.147
	315134	AW504854	Hs.126714 ESTs	0.147
	335834		CH22_FGENES.621_1	0.147
	327870		CH.06_hs gjl5868131	0.147
50	323802	AA332011	Hs.250138 protein phosphatase 2C; magnesium-dependent; catalytic subunit	0.147
	329412		CH.X_hs gjl6682553	0.147
	323791	AA333068	EST cluster (not in UniGene)	0.147
	324126	AA385315	EST cluster (not in UniGene)	0.147
	327865		CH.06_hs gjl5868130	0.147
	333445		CH22_FGENES.154_2	0.147
55	321302	AA021351	Hs.158497 KIAA0724 gene product	0.147
	336744		CH22_FGENES.118-9	0.147
	323731	AA323414	EST cluster (not in UniGene)	0.148
	320269	H07989	EST cluster (not in UniGene)	0.148
60	305468	AA749000	EST singleton (not in UniGene) with exon hit	0.148
	305592	AA780594	Hs.62954 ferritin; heavy polypeptide 1	0.148
	304094	H11295	EST singleton (not in UniGene) with exon hit	0.148
	325040	AW296368	EST cluster (not in UniGene)	0.148
	339034		CH22_DA59H18.GENSCAN.26-2	0.148
	334504		CH22_FGENES.398_2	0.148
65	334778		CH22_FGENES.431_2	0.148
	320148	U77494	Hs.119687 RAN binding protein 8	0.148
	303584	AW173759	Hs.203401 ESTs	0.148
	325826		CH.15_hs gjl5867048	0.148
	331192	T55182	Hs.152571 ESTs; Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]	0.148

	325785		CH.14_hs gi 6381957	0.148
	333166		CH22_FGENES.91_8	0.148
	336548		CH22_FGENES.841_5	0.148
	337552		CH22_C4G1.GENSCAN.1-4	0.148
5	331775	AA382742	Hs.97151 EST	0.148
	336936		CH22_DJ32110.GENSCAN.19-6	0.148
	331869	AA428554	Hs.104894 ESTs; Weakly similar to fibronectin precursor [H.sapiens]	0.148
	332865		CH22_FGENES.28_5	0.148
10	328663		CH.07_hs gi 6004473	0.148
	328436		CH.07_hs gi 5868417	0.148
	311158	AI634864	Hs.250789 ESTs; Highly similar to similar to NEDD-4 [H.sapiens]	0.148
	336942		CH22_FGENES.354-2	0.148
	302262	R53169	Hs.246091 ESTs	0.149
	333296		CH22_FGENES.132_3	0.149
15	333365		CH22_FGENES.142_2	0.149
	311706	AW452392	Hs.252854 ESTs	0.149
	337109		CH22_FGENES.489-2	0.149
	315062	AW173300	Hs.190201 ESTs	0.149
20	333454		CH22_FGENES.157_3	0.149
	334784		CH22_FGENES.432_9	0.149
	333255		CH22_FGENES.118_3	0.149
	337518		CH22_FGENES.814-7	0.149
	320651	AA489268	EST cluster (not in UniGene)	0.149
25	323437	AA287567	EST cluster (not in UniGene)	0.149
	328761		CH.07_hs gi 5868302	0.149
	328767		CH.07_hs gi 5868309	0.149
	335261		CH22_FGENES.520_2	0.149
	300827	R16689	Hs.106004 ESTs	0.149
30	339263		CH22_BA354112.GENSCAN.10-1	0.149
	337412		CH22_FGENES.756-6	0.149
	334414		CH22_FGENES.384_1	0.149
	332931		CH22_FGENES.38_5	0.149
	310801	AW270980	Hs.106346 novel centrosomal protein RanBPM	0.149
35	305216	AA669056	EST singleton (not in UniGene) with exon hit	0.149
	314779	AA470122	Hs.190261 ESTs	0.149
	338414		CH22_EM:AC005500.GENSCAN.341-27	0.149
	303342	AW247361	EST cluster (not in UniGene) with exon hit	0.149
	337509		CH22_FGENES.806-4	0.149
40	306631	AI001149	EST singleton (not in UniGene) with exon hit	0.149
	302533	L36149	Hs.248116 chemokine (C motif) XC receptor 1	0.149
	336536		CH22_FGENES.839_18	0.149
	324666	T32458	Hs.14285 ESTs	0.149
	310173	AI767433	Hs.170013 ESTs	0.149
45	333595		CH22_FGENES.211_2	0.149
	335975		CH22_FGENES.652_9	0.15
	306654	AI003654	EST singleton (not in UniGene) with exon hit	0.15
	335025		CH22_FGENES.475_3	0.15
	328711		CH.07_hs gi 5868271	0.15
50	328274		CH.07_hs gi 5868219	0.15
	325505		CH.12_hs gi 6682451	0.15
	329641		CH.14_p2 gi 6468233	0.15
	304955	AA613504	EST singleton (not in UniGene) with exon hit	0.15
	339103		CH22_DA59H18.GENSCAN.44-10	0.15
	329636		CH.12_p2 gi 5302817	0.15
55	310118	AI203293	Hs.157489 ESTs	0.15
	326056		CH.17_hs gi 5867184	0.15
	303773	AA769074	EST cluster (not in UniGene) with exon hit	0.15
	303153	U09759	Hs.8325 mitogen-activated protein kinase 9	0.15

TABLE 13A shows the accession numbers for those primekeys lacking unigeneID's for Table 13. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
20	322050 321439 321666	24275_1 1599424_1 13653_22	AL137589 AA423949 BE222949 BE222694 AI199615 AW873116 AI277950 AW044290 AW630096 H61982 W01567 N75711 BE259906 AA232518 AA013359 AL035788 AW160822 BE387134 BE002954 BE391839 AW161565 AI878841 BE616458 BE409981 BE387308 BE297436 BE315536 AA206924 R12012 AA214169 BE312812 BE387093 H11710 BE312009 BE260569 AA343566 AA219526 R34757 AA219749 BE336733 AA219751 AW411099 AA232408 BE018716 BE398089 AA206253 AA053487 AA114224 AV655868 AW732566 BE394087 AW732574 AA313442 BE336875 AA070548 BE259840 BE019828 AW732341 AA299916 BE019253 BE018238 BE387109 AA232304 BE255589 AW732585 AA181436 AA308777 AA075802 AW732521 AA314526 AA226747 BE409513 AA206168 BE388292 BE298782 BE387086 AA305310 AV652723 AA314918 BE615510 AW951763 BE398104 BE385195 BE407165 BE391336 BE390187 BE389189 BE540650 BE249684 BE385985 BE274245 BE391124 BE260080 AA182600 BE512821 BE390090 BE279398 BE279589 BE263454 BE515194 BE293569 BE272531 BE388814 BE384659 BE271685 BE561043 BE278449 BE302572 AW239076 AI750583 AA376179 AA112632 BE266324 BE266614 R13105 AA132286 BE296305 AI220355 AA205606 AA219527 AA219519 AW804310 AA083286 BE171208 T19693 AA338328 BE185868 AA903024 T92162 AA330119 BE410404 BE314668 AW576245 BE207878 AW299993 AI199558 AI285442 AW299994 AW394242 AW394184 AI357412 AI870708 AI590539 W07459 AW068287 AA310079 BE335702 AA356318 AA306059 AA346785 AW402633 AA311210 AW402909 N76879 AW402913 AW401920 AA321636 AA354474 C17297 C16938 AA311774 M29871 NM_002872 Z82188 AW405674 H94176 R89281 AA214723 AI014482 AW949347 T27749 AW804226 AW796964 AW404581 AF077208 NM_014029 W68830 W79652 AA353375 AW575218 AA552192 AA521232 AA702695 AA033975 AW407827 AA829948 N94402 AW628604 AI523308 N57605 AA641662 H42477 N52784 AI753478 AA768493 AA845729 W47391 N55270 AI090117 R89282 BE206172 AA076650 AA595650 AI218931 BE049397 AI433110 W74114 H94277 AI356627 AI085221 AI862818 AA835967 AW103905 AI640644 AA835507 AA856887 AA694392 AW337542 AI524410 BE045500 AI440060 AI358801 AW028238 AW205248 AI718264 R48618 AA357358 AI695002 AA897549 AW081065 AI433360 AI810783 AI620963 Z82188 AA360224 U29112 AI656540 AI364875 AI656246 AI690940 AA169345 AI762857 AI949997 AI809901 AI681948 AI221079 AW167404 AI347614 AI611090 AI023472 AI347683 AI027467 AW591788 AI380665 AA835735 AA836654 AI244028 AW193159 AI500112 AI918722 AI738693 AI702308 AA805365 AI766842 T59538 T59599 T59598 T59542 AF147374 AF070619 R20302 T80358 AJ223366 BE305086 AW820106 AA621983 BE305208 AI738475 AI380189 AW590847 AI127232 AA622706 AI380858 AA621975 AI587036 AA665743 AW204003 AI692234 AI002242 AI692219 AW137282 AW268783 AW295910 AI308015 AW301462 AI318288 AI318575 AI318117 AI345591 AI249650 AI246934 AI246864 AI246971 AW268311 AI249654 BE041907 AW732776 N72324 N52825 W19526 BE143464 AA376060 M83667 NM_005195 S63168 M83667 AW068039 AW630649 AI338577 AI018125 AI269878 AW242440 AI887823 AI342581 BE222416 AI582847 AI651011 AI660815 AI699574 BE550201 AI926996 AW665855 AI827752 AI761857 BE328168 BE222451 AI762201 AW000929 AW007207 BE042962 BE551843 BE465373 AI279179 AI949945 BE551862 AW051667 BE328076 BE222296 AW007229 AW772332 AI279801 AI934526 AI631938 AI770103 BE041412 AI417900 AI692655 AI689943 AW270119 AI431739 AI703347 AW770568 AW025473 AI701497 AI128026 BE328147 AW203980 BE046793 AW087704 AI674597 AI650732 AI813691 AI472092 AI695224 AI241217 AW207746 AI206840 AI271362 AI631788 AI911883 AI914619 AI380585 AI767501 AI823759 AI564116 AI190991 AI377369 AI814122 AI221623 AI354793 AI081988 AI391740 AI337435 BE467366 AI824347 AI565325 AI280038 AI640455 AI819744 BE467803 BE327524 AI149402 AI313187 BE219684 AW611948 AW665821 AI091260 AW044492 BE220366 AW025381 AW183264 AI694865 AI498474 AI129780 AI202028 AI566792 BE220659 AI928040 AI630696 AI493021 AW612488 AI913152 BE042965 AI631837 AI693873 AI498925 AI768668 AI401544 BE327023 AI693383 AI769874 AI744003 AW082273 AI686501 AI798177 AI985196 AI090033 AI432342 AI689918 AI688308 BE468080 BE219588 AI912119 BE219787 AW005392 BE326564 AI589039 AI860187 AI758143 AI338168 AI702936 BE221985 AI498727 AI918196 AI279735 AW771497 AI860133 AW237834 AW661759 AW028111 BE503416 AI360180 AW611715 AI871777 BE045447 BE326444 AI266547 AI800237 AI823315 AI478368 AI264281 AI675841 AI690041

AI498018 AI554124 AI239893 AI864054 AI280099 AI192815 AI620465 AI080201 AW002057 BE500986 AI341131 AI818991
 AI566137 AI123403 BE219192 AW183844 AI499842 AW137971 AW138720 AW015526 AW138160 AW243163 AW138705
 AW139927 AW140006 AW138810 AW137450 AW206970 AW135419 AW205974 AA043494 BE465106 AW139955 AI741112
 BE326942 AA043506 AI079957 AI942432 AI392902 AI097047 AI470599 AA514553 AA984008 N47949 AI654114 AA884832
 AI796752 AI765290 AI301155 AW470358 BE222764 AI823569 AI651188 AI692695 AI476643 BE504307 AI767573 BE219719
 AI932249 AW467075 AI913633 BE221966 AI091025 AA969215 AI799810 AA931170 BE048559 AI809606 AI138614
 AI739456 AI674605 AW772068 AI089286 AI625787 AI263418 AW008638 AI928389 AW628997 AI470010 AI914168 AI760003
 AI203050 AI334069 AI694788 BE045337 AI948659 AI912982 AI867131 AI192102 AI767583 AI347518 AI566005 AI625884
 AI215888 AI633904 AW182265 AW614357 AI128030 AI343685 AI914283 AI985003 AI623578 AI493053 AI380295 AI633895
 AI267880 AI538162 AI991552 BE219479 BE219296 AI302178 AW779296 AI913805 AI631644 AI566772 AI985498 AI942289
 AI935659 AI339092 AI247432 AI686472 AI766866 AI017228 AI333272 AW301668 AI972218 AW082027 AI632974 AI474761
 AI766127 AW236578 AW000966 AI670734 AI222399 AI871249 AI703448 BE464210 AI768037 AI871585 AI767871 AI738757
 AI220732 AI681633 AI768783 AI684463 AI307339 AI263203 AW665264 BE463969 AI768786 AI439118 AI127913 BE218324
 AI672342 BE220052 AI796163 AI221662 AW197672 AW025300 AI769681 AW612448 BE219757 AW072420 AI669980
 AI830418 AW204353 AA047011 AA913868 AI739146 AI669954 AW470507 AW614835 AW302151 AW772372 AI762427
 AW339902 AW303370 BE464775 AW299818 AW236072 AW195060 AW274737 AW263062 AW183846 AI688694 AW300493
 AW172509 AW516876 AW593773 AW299474 AW303546 AI817323 AI823624 AI694005 AI934589 AI343479 AI861825
 AI962726 AI765845 AW080318 AI640227 AI763042 AI768903 AW235386 AA738489 AW341293 AA588585 BE221732
 AI914179 AW611663 AI572789 AW194735 AW236122 AW236007 AW612789 AW197501 AW195046 AI797145 AI864423
 AI458934 AI342848 AI693227 AI912642 AI689993 AA932572 AA740269 AW470392 AW086020 AI221701 T69326 T70461
 AI765579 AI338263 AI431721 AI394249 AI186462 AI823571 AI953665 AI497954 AI761057 AI678228 AI640302 AI948742
 AA594626 AA883155 AI972682 AI804774 AI300407 AI433524 AA897341 AI401175 AI291071 AA021213 AI126509 AI948955
 AI218935 AA903938 AA502610 AI498320 AA584267 AA935285 AI476253 AA489658 AA975053 AA715326 AA557139
 AI126417 AA971455 AA557319 AI499738 AA911438 AI913637 AA494506 N90793 AI990724 AA131667 AA128164
 AA046840 AI262557 AA131729 AA594926 T59467 AA436907 AA044630 AI589177 AI279237 AI880498 AI431822 AA708934
 AW612558 AI634069 W03610 AI192272 BE550862 AI400879 AA708507 AI128003 AI375308 AI271423 AI199552 AA125977
 AI366498 AA458662 AI694362 AA044627 AI636263 AI796270 T90146 AW014724 AI870812 AI948781 AA369965 AI094721
 AW271817 AI262898 AI244680 T69252 AI934148 AA046357 W19109 AA028157 AW021924 AA253491 AI189397 AI934388
 D58282 W21323 W24288 AI682972 AA293683 AA284566 AV659511 AA434184 H87089 AA040038 N57464 AA343709
 AW805815 R89837
 BE621320 BE266806 BE276582 AW516729 AF142579 AW451687 AK000069 AA325236 BE168997 W73105 AA715365
 BE278873 AA808894 AA386371 AW517942 AW750993 BE140314 BE392384 BE621757 AA318192 BE548173 AW152607
 AW166898 AA352215 AW841506 T59802 AF147378 AA335719 AW956069 T59668 AA826362 AI961329 AI290469
 AW197375 AI805651 AA160748 AA581089 AI968889 AA581100 AA501478 AI621089 AA488534 AA503715 AA658457
 AI144504 BE387827 AA159880
 AW177009 AI381610
 AA287567 AA252404 AW967735 AA287568 AA761222 AA855644 AA831245
 BE514807 R43224 AI363450 AA450226 AF030942
 AA385315 AI627453 AI050695 AI348281
 AI340462 AI583268 AA079086 AI950777 AI301866 AI925108 AW876954 AW877000 AA525418 AA888549 AI934220
 AW380220 AA804858 AI927576 T61151 AW384053 BE391691 AA533856 AA248400 T48202 N57156 R68346 R26020
 AL050332 W30806 H61389 AA092592 AA230324 BE271217 AW372903 T48772 AA358002 AA094302 AA559656 AW373308
 AW373315 AW373297 AW373311 AW373314 AW373309 AW877055 AW770140 AW379805 AI581609 AW364144 AA078921
 AA715432 AA654210 AI004899 AA602209 W47464 AA506588 R26822 AU076528 AI535743 AI535704 AI535681
 AA402307 D60405 D61237 D59891 AW964877 AA325215 AI459739 N36070 N25658 AA083684 AW293368 AI761958
 AI741205 AI693175 AW873603 AI143269 AI187124 N25199 H19323 AI650842 AW316825 AA083842 AA935650 AW298404
 AI472001 AI648568 R17676 R41625 AI123237 R17677 AI206866 F36920 AI654713 F34084 AA618029 AI915139 AW275194
 AW514577 D80420 AW149850 Z40953 AI867861 AA927547 AA974344 AI825793 AI635565 AI652157 BE504748 AW295759
 F16800 AW839796 F01781 AA909730 AA984010
 AA595235 AW973839 T03040
 AW248307 AA313452 AW951927 AA355961 BE566080
 AI702835 AI758919 AI685405 AI952108 AI299207 AI400767 AW105389 AI952710 AA845312 AI784118 AI537315
 X57138 NM_003514 Z98744 BE253911 BE256314 AI095013 AI138475
 AA323414 AW664013 AI809377 AI276041 AW296883 AI798340
 AA333068 AA331863 AA331838 AW962531 AA331442
 AW296368 AA247632 AK002030 R15304 T08775 AW975664 AI186801 AA730688 AW190918 AI141176 AW513211
 AI275071 AA988601 BE042933 BE045713 AW087176
 AA464018 AA464079 AA468142
 AA846318 W15478 AL042661
 AW131104 BE246610
 AA333340 AW955834 R49755 U33428
 R58438 AA358612
 AL043362 AA350031 AW751972 BE549118
 AA497090 AI351879 AI350914
 AI815981 AF267269 BE260960 BE263991 AA311733 F12145 F07345 Z43604 T29948 H64102 Z43611 T35364 N40667
 AI909783 AW751045 AA160594 AI818064 AI307240 AI951554 AA641031 AA293045 AI942492 AI687077 R78689 H12368
 AA894728 AI124930 AI423498 AA777759 AA614585 AW071822 T66288 AI418558 H21480 AI335011 AI051728 AA293436
 AW302233 AW188628 N26393 AI076557 AI311022 AW451505 H62593 Z39666 H12315 AI761351 AI364142 F02935
 AW571491 T35366 AI240745 H64151 AA503793 AA831948 AI627686 AI761531 F03591 F09782

5	301763 1688575_1	R01279 R05896 T86522
	301780 18597_2	R05735 BE349600 R37388 N79751 R10115 AA702039 AA836147 AA505716 AI049661 AI499239 R54072 AI023394 AA627710 W60285 W500038 AI884786 AA827191 AA810075 AW005088 R70248 AI658560 AW078678 AA631306 H52839 AW085835 AI656182 AA737178 AW136923 AA281028 AA570316 AA722871 AA362737 AI217268 BE242373 R01113 AA628946 AI394527 AW402308 AI361110 AI917585 T99639 AA805326 N44577 AI394021 AW403385 T23949 AI497766 T96602 AA834947 AI693908 Z33450 T92127 BE541896 AI933301 BE251540 BE252269 N50968 AI695531 AW575523 AW296889 N93796 N89924 AI361804 AI085251 AA810694 BE303011 AA743784 R13478 AA358771 AA325294 AW964880 BE258953 R54116 AW881039 AW602593
10	301793 239325_1	BE265837 AA340632 T96304 T96075 T72780 H51978 R09868
	303049 102592_1	AW408042 AW407562 BE172835 BE396893 BE269184 AA045741 BE004187 AW751261 W74283
15	301863 19477_1	BE263301 AI418863 NM_005194 X52560 AW328683 BE298869 D63161
	301872 27494_4	H84730 T73262
20	301893 6561_1	T80334 BE292758 AK000854 H16996 BE253691 R88508 AA357663 AW955286 AW579550 N98864 AA595201 AI742967 BE379564 BE269460 BE397065 Z42029 BE305028 AK000549 BE536182 BE314372 AW393349 T50987 AA059735 AI560153 AW874581 N69891 AA993617 H51180 AI269042 AI281358 AW591213 AI017724 AI262859 H16997 R38991 AI804355 AI868988 AI689525 AW023081 AL047848 AI734009 AI263076 AW272255 AI792912 AA452366 AA351338 BE262590 BE262591 AA074050 AA389667 BE161346 AC004472 BE312721 BE273942 F11928 T65358 BE612432 BE261576 BE179894 AA324119 AW246199 BE395368 BE261676 BE382334 BE394701 BE304548 T31940 BE398128 BE398019 BE296693 BE379564 BE269460 BE397065 Z42029 BE305028 AK000549 BE536182 BE314372 AW393349 T50987 AA059735 BE386997 AW381699 T51050 W95025 AA477678 AA348306 AW956831 AW062919 AL040397 BE305160 AA315419 AW249929 AA295944 AI635946 AI870259 AI951125 AW028250 AI885184 AW873113 AI077544 AW025091 AI817594 AI401718 AW008245 AI499064 AA599687 AI016890 AA765638 W93340 AA588708 AW519173 R51917 AA676778 AI084871 AA687684 AI860840 AI811921 AW514730 AA477561 N78945 AA779894 AA778559 AI968953 T16188 T32828 AA991426 AI474472 AI473542 AI828972 AW247906 AA977415 AW591489 AA876008 AW191893 AA074278 AW874099 Z40196 AW083615 F01544 T55984 AI290413 AI072167 AI365049 T36028 AI042568 BE560076 W17119 AA196376 T47999 R54309 AK001269 AL354613 AA147472 AA490803 BE207628 AW816113 AA085574 AW503392 AA299910 AW750305 BE079539 BE079484 BE512838 AK001593 AW968772 AW967440 AW206280 AA251270 AI627886 AA303599 AA147473 BE206616 AA490611 AA715039 AW590866 AW590447 AI864512 AA204731 AA894480 BE001136 AA612785 AA237035 AA149960 Z44257 R12986 AA448446 AI734041 AA422167 BE220551 R66041 R32927 R32942 AA258773 AW386142 R53730 N54624 AW880296 AA253485 AW954441 H98989 AW614348 AI654838 AA779793 AW237213 N66635 AI186812 AA947479 BE158011 AI859480 AW805579 N52010 AA806305 AI628445 AW270390 AA778165 AA149949 AI650728 AA749108 AA687257 AI261661 AA747442 AA481351 AA206339 AA903407 AW473306 AI688930 AA262261 AA448310 AA748620 AI347430 BE465692 R32839 AW510564 AA436408 AA257971 AA253362 AA938330 AA513150 AA976840 AA687117 AI281547 AA046243 R32825 AI631554 AW139818 AI244536 R52946 AW235443 R40183 AA299909 AA811958 AI302918 Z40213 BE158047 BE158060 AA767245 AW748159 AW500735 AA094074 AW393348 AW393350 AW396713 AW384705 AA316069 BE274224 AL120803 BE170052 BE170039 AI906340 BE091310 AA491506 AW836675 AW863111 AW973784 AW843842 AA557573 AA578088 AI125161 AA349349 AI372794 BE312586 BE312777 T32148 AW239077 AI905357 Z42685 AW298772 R18578 AA780425 AA325971 AI372793 R10658 AA295021 AW885349 AW885288 BE271987 AW366519 AA349350 AA233207 R88464 AA434299 R02058 R00019 R54563 Z44886 R20150 AW368328 AW368321 AW802152 W79803 H12809 AA028951 AW367382 AA295247 H46355 AA905620 R54564 H12765 AW950608 AA028952 AA366908 AI085652 R43207 R77954 AI672848 T8547 AA427734 AA572853 AA769934 AI242108 R00020 R02059 R10659 AI185270 AI041890 NM_000080 X66403 F03854 AI652442 AI766431 AA976913 AI969882 AA471024 AI802727 AI824112 F02169 AI90843 BE250876 BE252859 AI157418 R78326 AW068570 AW247361 AA252638 AI751982 BE260758 BE293073 AW293303 AB040951 AK002094 AA676593 W44644 N42376 Z45942 AW841844 BE541378 AA358274 AA213391 T88771 NM_015493 AL117489 N88248 N31714 N36273 N31721 AW576263 AA449380 AI366135 AA551576 AW149789 Z17418 AW474331 AA056181 AI753611 AA046428 AA488007 AA300764 N44732 AA377697 AA346752 AA485787 AA894546 AA115295 AA299914 R88096 AA367342 AW884666 W84522 AA426325 AI983849 AA873315 AA873307 AI355170 AA534678 AA969227 AI127202 AW083323 AI338244 AW020877 AA780019 N33426 AW069314 N63079 AI926527 AA115270 AW886601 AI357402 AA599312 AI460358 AI926969 AA429402 N33197 AW886733 R88205 N52803 AW021988 AA213392 BE138656 AI142383 AA427844 AA954743 AA233622 AW073382 AA426326 AA493560 AA425133 N24819 AI419516 AI571515 AI147373 AI628677 AI214877 AA992123 H71599 AA029095 AA622262 AW117398 AW275286 AI911337 AA864950 T94173 AI475634 AI701411 AI287696 T94091 AA505746 AI184310 AI350967 AI083596 W74274 AI954381 AI832767 AI368443 AA195578 AW874416 AI005421 AW014339 AA908660 AI350791 AW241382 AI473104 AI275186 AA515528 AA194897 AA782901 AW069414 F20248 AA426011 AI305169 AI832109 AI570082 AW072984 AI492474 AA919076 AL049024 W79889 N42400 AA625435 AW983887 AA233420 AW779971 AW300287 AW152002 AW069505 AI866447 AI298231 AI146920 AI692267 AI872876 BE397032 AJ292529 N40373 N34073 AA321112 AW959902 AA258103 AW860213 BE549059 BE296027 BE296657 AA300789 AI971491 AW513665 AA909530 AI951045 AW058103 AI971506 AI061239 AA600054 AI000807 AA699975 AA281492 AW593654 AA321111 AW298633 AI278754 AI863362 AI285506 AA989727 F33114 T16079 AI762625 AI492103 AW770346 AW026763 AI468710 AI499987 AA310412 AA622784 AA642297 AI866427 H11802 T66097 AF042831 R42185 AW939055 T30280 Z43366 R54166 AA938905 AA574056 AA714466 AI805592 AI123431 AA229723 AA620759 AI004450 AW299820 AI949299 AW874308 AA626037 A974112 AA931563 AF073924 AA995769 AI766441 AI367730 AI081342 AA235800 AA235801 AI138970
50	303342 189722_1	
	302703 7075_1	
55	303252 149690_3	
	303273 67758_1	
60	302640 21194_1	
65	318446 604736_1	
	302815 42200_1	
65	302879 36555_1	
	318540 1018709_2	
	302928 22118_1	

AA719797 AA759343 X89673 AA759344 AA312909 X87825 Y10529 AC006271 AA758739 BE501015 AA909905 AF065857
 AC006271 AA970044
 304332 20696_41
 5
 AA158883 AA171835 AA187049 AA143546 BE299538 BE614280 BE621705 BE299684 BE619550 BE613099 BE619558
 BE514331 BE617716 BE612920 BE615742 BE258739 BE621539 AA434511 BE546696 BE614324 BE379359 BE250106
 BE250681 BE299592 BE300272 BE616805 BE397385 BE562024 BE271246 BE250556 BE280311 BE561995 BE618755
 BE276126 BE546275 BE311547 BE262155 BE281082 BE513087 BE546891 BE514289 BE397389 BE267442 BE545455
 BE614483 BE293447 BE270710 BE281071 BE267458 BE542095 BE262701 BE513634 BE548116 BE299546 BE619804
 BE512885 BE618638 BE266173 BE258933 BE259710 BE268569 BE563861 BE614871 BE537509 BE250108 BE515323
 BE538868 BE250081 BE277706 BE410127 BE619445 BE250753 BE304969 BE616348 BE546878 BE544952 BE410346
 10
 BE267256 X17206 NM_002952 BE304541 BE619171 BE259655 BE549186 BE314944 BE613101 BE378069 BE621110
 BE542752 BE257029 BE531315 BE619306 BE267328 BE259439 BE297093 BE280651 BE407684 BE250201 BE312819
 BE535432 BE279917 BE312626 BE531118 BE378744 BE275370 BE250195 BE409980 BE274432 BE266637 BE279321
 BE622382 BE280232 BE263816 BE378977 BE300145 BE250204 BE547609 BE264377 BE266688 BE259746 BE260829
 BE619517 BE388097 BE264025 BE618945 BE614758 BE312249 BE294359 BE531121 BE622300 BE615109 BE544354
 BE614998 BE393239 BE297520 BE393221 BE278818 BE279309 BE265476 BE618772 BE615185 BE265144 BE249837
 BE312230 BE407843 BE253884 BE407645 BE615804 BE619058 BE559512 BE383249 BE613497 BE294351 BE295062
 BE622385 BE390654 BE535436 BE563186 BE396374 BE270342 BE386110 BE260368 BE250186 BE265875 BE537229
 BE253369 BE256997 BE269482 BE264959 BE279072 AA662160 BE280733 AA858428 BE561308 BE267285 BE561422
 BE563181 BE304614 BE295437 BE619424 BE275863 BE394315 BE408109 BE541866 BE253772 BE618236 BE535261
 BE296490 BE278212 BE563154 BE257245 BE262274 BE513032 BE378567 BE394152 BE618947 BE269302 BE546516
 BE536792 BE615187 BE261186 BE615367 BE619289 BE261184 T49376 AL031671 BE273400 BE563457 BE545597
 BE615169 AA150323 AA158723 AA079033 BE313333 AA160100 BE271115 BE294302 BE273051 BE273048 BE622390
 AA837947 BE387721 AW973277 AA808731 BE280792 AA160444 BE256723 AL745420 AA643017 BE549441 BE293858
 AW975249 AL620819 AW089494 AL434549 BE305231 AA081262 BE280101 AA522507 AL950880 AA187460 BE386860
 AW859229 BE170489 BE620149 BE548218 AA316696 AA484426 AL567740 AA160605 AW939805 AA089573 BE300194
 BE391331 AW975419 H26808 BE545544 BE615974 AW800241 BE616222 W17343 BE387865 T53697 C03943 BE617637
 BE315130 T52942 T50588 N74693 AA187107 T59919 AW9797397 AA206447 AA854619 T57175 AL570296 AW517964
 AA158269 AL282220 W25297 AL580710 BE262453 AL185868 AA526485 AL288051 AL582513 AA100675 AW615567
 BE395354 AL472725 BE314881 BE621281 N99921 AL282689 AL432725 AW732011 AA872254 BE205807 T59435 AL282712
 AA650505 AL004374 AA725260 BE313161 T60173 AL371260 BE385641 AW751812 AA078827 AL491858 AL433622
 AA219118 AL002092 AA996003 AA064604 AL250287 AL304397 AL453213 AA653630 AL524573 AL440306 H48802 AA157843
 AA715629 AW973788 AA932493 AL347563 AA181309 T67880 AA643033 AW467498 AA115904 AA935410 AA483032
 AA084568 W25246 AL567588 AA155732 AA158614 AA868319 AA158568 AA188422 AL309183 AA084817 AA157955
 AL659659 AA188008 AL287379 AL540675 AA085212 AW028391 AA173297 BE256792 AA182854 BE378771 BE538571
 35
 AA079037 BE281597 AA643926 W81011 AA159344 AA320691 AA877597 T57107 AW263919 AL690413 AL619605 AL687579
 AA970560 AL368942 AL927104 AW419220 AL620051 AA128490 AA120825 AA079520 AA199648 AW188403 BE045224
 AW265533 AA074338 AA102685 AW779399 AA192451 AA182771 AW366812 BE281418 AA211094 AA131073 AA487924
 AW674848 AL568103 AA171934 F30349 AW088785 AA581370 AA205482 AW352296 AW517565 AL376249 AA158884
 AL340509 T59965 AA085193 AA071570 AL874045 AA852755 BE045217 AW189428 AA211141 AA652134 AL497729
 AA994817 AL811459 BE535857 AW769697 AW167892 AW149305 AL864981 AW272126 AW023245 AL439266 AL953196
 40
 AA160912 AL718580 BE537547 AA501448 AA069308 L07393 AA353007 AA079235 AL539140 AA740154 W58341 AA888403
 BE299000 AA196413 BE613327 BE261523 AA866599 AW844713 AL691159 AL079975 AW327479 BE180731 AA984805
 303701 1155179_1
 303759 447287_1
 45
 303773 356632_1
 303778 174437_1
 303784 414659_1
 303845 50211_2
 303898 162688_3
 50
 20121 452027_1
 319590 171338_1
 305186 17456_1
 55
 M13560 AA338951 AA161015 R72814 T69687 R75705 T61319 AA158454 R50579 T56649 AL214156 T70375 R31655
 H64997 AW800487 H49110 AA634206 H42384 H21783 AL560152 AA664230 H42302 R48708 AA013277 T61901 T92417
 AA875985 T61962 T63055 AA430725 AA458964 AA578746 AL582385 T63000 AL499875 H64998 AA022538 AL364804
 AL855211 AL439714 AL224059 AL249917 T59258 AA477806 AA715834 AA916120 R38304 R35899 R82965 H25524 H82984
 AW516728 T54642 AA079866 H27555 AA455820 T63919 R79450 AL431241 AA937349 AA127213 AA421729 H61196
 T63894 AA013050 AA079133 W96364 AA487926 AL762796 H26377 AL433386 AL865423 AW371475 R98189 AA543978
 60
 AL718204 AW381954 AL862735
 AA323758 R12731 R14082
 R17531 AW960899 AA338366 AW673294 BE047729 BE047722 AA330746 AW841797 H05030 AL142105 R12654
 H07989 AL239482 H24544 AA078369 R74153
 BE512926 BE304794 AA129140 AA052922 AA092258 BE378058 BE615391 BE615218 BE616188 AL214126 H05675
 W56857 AL028525 BE617241 BE531271 AW856227 T56489 AA322005 AW794148 AF170577 BE615738 AA005138 L76930
 L76932 L76933 X95410 AW389462 BE563092 AW897937 AA263158 AL520992 AW947350 AA522535 AW945921 AV653776
 AW884835 AW947338 AL687178 AW945799 AL905627 AW948449 AV653751 AW945924 AA563898 AW945810 AW945832
 AW371449 AW945864 AW948447 AW945910 AA643002 AA522680 AA522715 AA578840 AA523279 AA826150 AW945809
 AW405998 AA551909 R23173 AA595545 AW389497 AL933770 AL125053 AL471803 AW795856 AW796937 W30675 H70317

		H68296 T59240 AA397650 H59652 AA938072 AA978010 R35643 T89735 AW361585 AW196153 AI538069 AA604540 AI434259 R49181 T58717 AW062486 AW796966 AI648384 R77733 AI623502 BE171342 BE171303 R35858 AW974883 AW149898 AI500045 AI540710 AI540392 AW009172 AW277199 AI371312 AI500096 AI470297 AW372840 AW844562 AW844560 AW797965 AI691146 X07062 AW799199 H60666 AA837684 AF130734 T25952 AI933771 AI914660 AW391925 AW793843 AW795012 AW366709 AW750987 AW750985 R35765 AW844942 AW750986 H64920 R34651 X86703
5	321039 26338_2	BE018103 BE018083 BE293253 AW247083 BE207643 BE514793 BE183238 AA376427 AW273850 AW043786 BE439973 AL045428 AI889050 AA026496 AI422924 AI884485 W96068 AA020872 F37119 AA714378 AA021107 AA011141 AI554001 AI375841 AI469097 AA335219 AW967315 AI692177 AA410448 AI568858 AA582647 AA026419 AA281639 AW515248 AW007777 AA010840 AW188439 AI805423 AI148210 BE301590 AA744414 AA745392 AW167423 AA622659 AW000378 AI432387 AA760930 BE047189 AA021605 AV658045 AI093347 AA588594 H63143 AA639556 AI308976 AA379270 AA633407 AI874329 AI206484 AI493895 AI694103 AI249682 AA973765 AA872445 AI125446 AA287272 AW069761 AA682569 AW009712 BE542774 R50167 BE301574 AA991202 AA502006 AI219819 AW074373 AA617996 AI521242 F25241 AW515812 R16774 AA335218 AW673800 H26778 AI468557 AI886986 AI560759 AI460075 AA502968 AA503273 AA610680 AA287274 AA554020 AA284889 AA916636 AW469457 AW273250 AW673708 AW512948 AL041071 AI446042 AA903535 BE172441 AI282411 AW265021 AA810799 AI559865 AA729332 AW004611 AW129451 AA659019 BE203239 AA610825 H03511 BE383995 R16474 AA281701 AW009244 AA287424 AA558139 AW364081 F08147 AW408359 AW949429 R23785 AW247442 AA305512 T29095 AA905130 BE246361 BE244981 AA220199 BE504058 X80878 AA533727 AA608601 AW005964 AI811627 AI367037 AI277985 AI493719 AI277848 AA854982 AW247298 AI216345 AI041295 AI887378 AA781241 AI674270 AW628959 AI383083 BE504391 AA729421 AA552188 AA373387 AW880360 AW875262 AW875369 AW581540 AW875358 AW581568 R23735 AW134768 W03912 AW971410 AA506385 AA209530 H73495 H48629 W56149 H56752 AW340384 N49521 AA853680 AK001668 BE386425 BE563549 BE296124 BE298950 R51419 U46295 BE147292 AA360056 R48018 AW845348 N47383 AI817280 AI671902 AA988104 AA479464 N56996 AI192374 AI927558 AA659888 AI799903 AA548397 AI161167 AI656333 AI418829 AW592671 BE327906 AW513346 AI888579 AW469410 AW512809 D25682 AA576079 AA479354 T30342 R51307 T16044 H29063 AW079357 AI339477 R47914 AI986068 AI870065 AI868489 AI521099 AI582732 AA995540 AW957299 AA352608 AA676752 AA410510 AA358874 AI865724 AA853679 AI699265 AW188789 N47380 AA233715 BE258194 R55421 R55643 H42362 AA243884 AW886407 AA489268 R57015 R58094 BE077459 BE077423 BE546995 AW849216 T69383 AW936111 H60337 BE221073 AB033100 AA347036 BE260325 AW961669 AL047207 AA347037 AI766894 AA601045 AI559897 AW139033 AW274622 AW172884 AW089070 AA804340 AW798925 AA825266 AL137354 AL043375 AA971985 AA977992 AA989542 AA989598 AA989713 AA991487 AI000246 AI000248 AI001149 AI003654 AI041589 AI051696 AI452732 AI470948 AI475914 AI055966 AI066577 AI086929 AI095365 AI127883 AI559492 AI565612 AI571211 AI581855 AI591235 AI687580 AI719930 AI735634 AI744063 AI819263 AI829820 AI873242 AI318327 AI318328 AI318495 AA627416 AA635771 AA639783
10		
15	306051 19085_3	
20	321163 171122_1 321235 1102181_1 320603 4297_1	
25		
30	320641 185591_1 320651 58648_1 321325 28266_1	
35	305704 464759_-1 322011 23158_1 306407 306454 306516 306518 306526 306534 306590 306591 306631 306654 306786 306799 308023 308070 308099 308805 308814 308873 308911 308982 308238 308258 308289 308311 308332 308511 308601 308612 308636 308814 308851 308981	
40		
45		
50		
55		
60		
65	310570 1071946_1 305022 305060 305070	

	305079	AA641329
	305134	AA653159
	303977	AW512978
5	305216	AA669056
	305263	AA679467
	305266	AA679772
	305396	AA721052
	305403	AA723748
	305488	AA749000
10	305549	AA773530
	305601	AA780975
	305610	AA782319
	305621	AA789095
	305710	AA826544
15	305724	AA827608
	305744	AA831819
	305752	AA835278
	307018	AI140639
	307055	AI148477
20	307058	AI148709
	305801	AA845997
	305830	AA857665
	305836	AA858043
	305852	AA862455
25	305858	AA863103
	305866	AA864533
	305867	AA864572
	307126	AI184951
	305903	AA873085
30	328803	c_7_hs
	328809	c_7_hs
	305949	AA884409
	328829	c_7_hs
35	330021	c16_p2
	330024	c16_p2
	330028	c16_p2
	330049	c17_p2
	305993	AA889197
	330095	c19_p2
40	330096	c19_p2
	307205	AI192479
	307427	AI243437
	307491	AI268539
	307581	AI284415
45	307588	AI285535
	337672	CH22_6002FG_LINK_EM:AC00
	337693	CH22_6030FG_LINK_EM:AC00
	337738	CH22_6083FG_LINK_EM:AC00
	307692	AI318342
50	307806	AI351739
	309107	AI925823
	309230	AI970747
	339338	CH22_8300FG_LINK_BA35411
	309257	AI984183
55	309366	AW072970
	309422	AW087175
	325207	c10_hs
	325257	c11_hs
	309646	AW194694
60	309651	AW195850
	325313	c11_hs
	309924	AW340812
	334030	CH22_1308FG_320_2_LINK_EM
	334040	CH22_1318FG_322_8_LINK_EM
65	334083	CH22_1361FG_327_38_LINK_E
	332810	CH22_26FG_7_12_LINK_C65E1
	302747	32813_1 AF062275 L03630
	302753	33029_1 M74299 M74302 M74303
	302777	33803_1 AJ230640 AJ230648

	304094		H11295
	302824	35372_1	U21260 U21258
	302996	41196_1	AF054663 AF124197 R70292
5	325870	c16_hs	
	304240		AA009802
	304410		AA284508
	304443		AA399444
	304475		AA428879
10	304522		AA465405
	304878		AA548556
	304705		AA564064
	306004		AA889992
	306008		AA894390
	306013		AA896990
15	306082		AA908508
	336174	CH22_3567FG_710_1_LINK_DA	
	306094		AA908877
	304823		AA584837
	304872		AA595289
20	304918		AA602697
	304955		AA613504
	306249		AA933840
	306286		AA936892
	306295		AA937331
25	306317		AA947909
	306347		AA961144
	306365		AA962086
	306398		AA970548
	330401	entrez_D28383	D28383
30	330463	460_2	NM_001055 AA332948 U26309 U09031 L19955 L10819 AI366043 X84654 U71086 AV654451 AJ007418 AA053625 BE168856 AA376730 H12694 AA810348 AA621972 AI818950 AV645367 AI818966 AA910602 AW512449 H67893 AI310497 AI304330 AI339217 AW193588 AW438688 AI818970 AW316799 AA906527 AA777570 N47673 AI336428 AW945133 AI038606 R29692 AW194197 AI304748 H12639 AA053178 AA493213 AA676958 AA113154 AI313469 AI368239 R93183 W24532 U52852 U54701 AL046864 AA365795
35	330535	1374_-8	U11872
	332634	10404_2	U24488 NM_007116

TABLE 13B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 13. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	332791	Dunham, I. et.al.	Plus	72720-73315
	332792	Dunham, I. et.al.	Plus	73381-73768
	332810	Dunham, I. et.al.	Plus	304296-304384
20	332944	Dunham, I. et.al.	Plus	2414825-2414932
	332972	Dunham, I. et.al.	Plus	2572152-2572236
	333133	Dunham, I. et.al.	Plus	3360058-3360195
	333154	Dunham, I. et.al.	Plus	3615887-3616019
	333155	Dunham, I. et.al.	Plus	3616832-3617003
25	333227	Dunham, I. et.al.	Plus	3992866-3992968
	333230	Dunham, I. et.al.	Plus	3995507-3996507
	333298	Dunham, I. et.al.	Plus	4581537-4581947
	333304	Dunham, I. et.al.	Plus	4629943-4630242
	333305	Dunham, I. et.al.	Plus	4630388-4630645
30	333365	Dunham, I. et.al.	Plus	4786883-4787283
	333383	Dunham, I. et.al.	Plus	4907179-4907277
	333391	Dunham, I. et.al.	Plus	4916697-4916780
	333392	Dunham, I. et.al.	Plus	4918294-4918433
	333397	Dunham, I. et.al.	Plus	4922466-4922635
35	333403	Dunham, I. et.al.	Plus	4925140-4925256
	333413	Dunham, I. et.al.	Plus	4943824-4943974
	333445	Dunham, I. et.al.	Plus	5097827-5097885
	333479	Dunham, I. et.al.	Plus	5272855-5272939
	333481	Dunham, I. et.al.	Plus	5286358-5286505
40	333483	Dunham, I. et.al.	Plus	5297945-5298105
	333516	Dunham, I. et.al.	Plus	5570204-5570390
	333517	Dunham, I. et.al.	Plus	5570729-5570925
	333518	Dunham, I. et.al.	Plus	5571761-5572025
	333531	Dunham, I. et.al.	Plus	5622622-5622684
45	333566	Dunham, I. et.al.	Plus	5954226-5954473
	333572	Dunham, I. et.al.	Plus	6026896-6027189
	333586	Dunham, I. et.al.	Plus	6246834-6247314
	333588	Dunham, I. et.al.	Plus	6255445-6255779
	333594	Dunham, I. et.al.	Plus	6308990-6309450
50	333595	Dunham, I. et.al.	Plus	6323103-6323348
	333600	Dunham, I. et.al.	Plus	6355629-6355925
	333601	Dunham, I. et.al.	Plus	6360075-6360442
	333607	Dunham, I. et.al.	Plus	6504431-6504690
	333612	Dunham, I. et.al.	Plus	6549563-6549697
55	333613	Dunham, I. et.al.	Plus	6550643-6550748
	333614	Dunham, I. et.al.	Plus	6551227-6551389
	333624	Dunham, I. et.al.	Plus	6595146-6595244
	333626	Dunham, I. et.al.	Plus	6614174-6614467
	333635	Dunham, I. et.al.	Plus	6663683-6663973
60	333637	Dunham, I. et.al.	Plus	6674968-6675134
	333642	Dunham, I. et.al.	Plus	6708760-6709139
	333647	Dunham, I. et.al.	Plus	6772502-6772779
	333653	Dunham, I. et.al.	Plus	6811130-6811392
	333654	Dunham, I. et.al.	Plus	6816731-6816993
65	333656	Dunham, I. et.al.	Plus	6822087-6822406
	333657	Dunham, I. et.al.	Plus	6831369-6831445
	333658	Dunham, I. et.al.	Plus	6835282-6835474

	333659	Dunham, I. et.al.	Plus	6836179-6836248
	333684	Dunham, I. et.al.	Plus	7169561-7169742
	333686	Dunham, I. et.al.	Plus	7177117-7177302
	333697	Dunham, I. et.al.	Plus	7203859-7203934
5	333698	Dunham, I. et.al.	Plus	7205279-7205383
	333699	Dunham, I. et.al.	Plus	7206101-7206175
	333703	Dunham, I. et.al.	Plus	7215559-7215663
	333709	Dunham, I. et.al.	Plus	7229730-7229835
	333747	Dunham, I. et.al.	Plus	7605884-7606206
10	333774	Dunham, I. et.al.	Plus	7716509-7716636
	333775	Dunham, I. et.al.	Plus	7729983-7730149
	333806	Dunham, I. et.al.	Plus	7877475-7877666
	333843	Dunham, I. et.al.	Plus	7978762-7978887
	333854	Dunham, I. et.al.	Plus	8029446-8029524
15	333873	Dunham, I. et.al.	Plus	8133266-8133429
	333880	Dunham, I. et.al.	Plus	8151923-8152133
	333885	Dunham, I. et.al.	Plus	8154352-8154437
	333918	Dunham, I. et.al.	Plus	8307124-8307215
	333947	Dunham, I. et.al.	Plus	8579888-8579966
20	333961	Dunham, I. et.al.	Plus	8617999-8618104
	333981	Dunham, I. et.al.	Plus	8782374-8782643
	333991	Dunham, I. et.al.	Plus	8837419-8837551
	333994	Dunham, I. et.al.	Plus	8852749-8852894
	334030	Dunham, I. et.al.	Plus	9288463-9288782
25	334083	Dunham, I. et.al.	Plus	9837016-9837081
	334111	Dunham, I. et.al.	Plus	10279365-10279531
	334135	Dunham, I. et.al.	Plus	10457085-10457183
	334218	Dunham, I. et.al.	Plus	12680289-12680378
	334249	Dunham, I. et.al.	Plus	13190430-13190574
30	334262	Dunham, I. et.al.	Plus	13231452-13231581
	334264	Dunham, I. et.al.	Plus	13234447-13234544
	334327	Dunham, I. et.al.	Plus	13577413-13577486
	334328	Dunham, I. et.al.	Plus	13589868-13589936
	334340	Dunham, I. et.al.	Plus	13642407-13642522
35	334454	Dunham, I. et.al.	Plus	14326506-14326738
	334504	Dunham, I. et.al.	Plus	14510206-14510398
	334508	Dunham, I. et.al.	Plus	14514936-14515122
	334512	Dunham, I. et.al.	Plus	14545933-14546366
	334582	Dunham, I. et.al.	Plus	15026255-15026371
40	334659	Dunham, I. et.al.	Plus	15460624-15460726
	334721	Dunham, I. et.al.	Plus	15796816-15796987
	334723	Dunham, I. et.al.	Plus	15805317-15805399
	334730	Dunham, I. et.al.	Plus	15967830-15967934
	334774	Dunham, I. et.al.	Plus	16251857-16252178
45	334778	Dunham, I. et.al.	Plus	16276180-16276395
	334851	Dunham, I. et.al.	Plus	17820110-17820810
	334885	Dunham, I. et.al.	Plus	19233667-19233787
	334902	Dunham, I. et.al.	Plus	19317083-19317195
	334905	Dunham, I. et.al.	Plus	19322553-19322680
50	334906	Dunham, I. et.al.	Plus	19323493-19323590
	334910	Dunham, I. et.al.	Plus	19398155-19398684
	335018	Dunham, I. et.al.	Plus	20688288-20688415
	335025	Dunham, I. et.al.	Plus	20743941-20744050
55	335033	Dunham, I. et.al.	Plus	20753188-20753314
	335044	Dunham, I. et.al.	Plus	20842088-20842682
	335142	Dunham, I. et.al.	Plus	21465105-21465186
	335157	Dunham, I. et.al.	Plus	21543302-21544341
	335160	Dunham, I. et.al.	Plus	21573388-21573497
	335174	Dunham, I. et.al.	Plus	21631301-21631447
60	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335190	Dunham, I. et.al.	Plus	21680807-21680876
	335191	Dunham, I. et.al.	Plus	21681110-21681183
	335193	Dunham, I. et.al.	Plus	21692208-21692362
	335204	Dunham, I. et.al.	Plus	21750636-21750726
65	335222	Dunham, I. et.al.	Plus	21885542-21885608
	335226	Dunham, I. et.al.	Plus	21890838-21890930
	335227	Dunham, I. et.al.	Plus	21892145-21892289
	335309	Dunham, I. et.al.	Plus	22500158-22500276
	335310	Dunham, I. et.al.	Plus	22500714-22500831

	335311	Dunham, I. et.al.	Plus	22501602-22501676
	335355	Dunham, I. et.al.	Plus	22779222-22779516
	335362	Dunham, I. et.al.	Plus	22809167-22809461
5	335368	Dunham, I. et.al.	Plus	22843040-22843184
	335384	Dunham, I. et.al.	Plus	22918150-22918263
	335385	Dunham, I. et.al.	Plus	22919072-22919339
	335436	Dunham, I. et.al.	Plus	23427793-23427923
	335440	Dunham, I. et.al.	Plus	23458702-23459017
	335441	Dunham, I. et.al.	Plus	23460632-23460724
10	335450	Dunham, I. et.al.	Plus	23480190-23480270
	335453	Dunham, I. et.al.	Plus	23483333-23483459
	335458	Dunham, I. et.al.	Plus	23490034-23490143
	335464	Dunham, I. et.al.	Plus	23500331-23500496
	335496	Dunham, I. et.al.	Plus	24164386-24164545
15	335497	Dunham, I. et.al.	Plus	24167666-24167869
	335498	Dunham, I. et.al.	Plus	24172082-24172161
	335499	Dunham, I. et.al.	Plus	24176698-24176869
	335500	Dunham, I. et.al.	Plus	24178236-24178326
20	335507	Dunham, I. et.al.	Plus	24218973-24220039
	335510	Dunham, I. et.al.	Plus	24222975-24223118
	335513	Dunham, I. et.al.	Plus	24224272-24224496
	335627	Dunham, I. et.al.	Plus	25150005-25150061
	335651	Dunham, I. et.al.	Plus	25317560-25317696
	335655	Dunham, I. et.al.	Plus	25333211-25333369
25	335656	Dunham, I. et.al.	Plus	25333601-25333751
	335658	Dunham, I. et.al.	Plus	25336315-25336406
	335663	Dunham, I. et.al.	Plus	25342680-25342802
	335665	Dunham, I. et.al.	Plus	25344086-25344287
	335667	Dunham, I. et.al.	Plus	25345735-25345856
30	335668	Dunham, I. et.al.	Plus	25346313-25346447
	335689	Dunham, I. et.al.	Plus	25454350-25454604
	335690	Dunham, I. et.al.	Plus	25455442-25455625
	335715	Dunham, I. et.al.	Plus	25565941-25566052
	335719	Dunham, I. et.al.	Plus	25593936-25594101
35	335734	Dunham, I. et.al.	Plus	25688723-25688869
	335744	Dunham, I. et.al.	Plus	25716483-25716615
	335809	Dunham, I. et.al.	Plus	26310772-26310909
	335819	Dunham, I. et.al.	Plus	26356341-26356470
40	335822	Dunham, I. et.al.	Plus	26364067-26364196
	335872	Dunham, I. et.al.	Plus	26820760-26820943
	335885	Dunham, I. et.al.	Plus	26933436-26933534
	335968	Dunham, I. et.al.	Plus	27743843-27744029
	335971	Dunham, I. et.al.	Plus	27752808-27753017
	335975	Dunham, I. et.al.	Plus	27801321-27801391
45	335976	Dunham, I. et.al.	Plus	27809041-27809187
	335989	Dunham, I. et.al.	Plus	27983768-27983860
	335990	Dunham, I. et.al.	Plus	27988532-27988608
	336010	Dunham, I. et.al.	Plus	28570239-28570330
	336093	Dunham, I. et.al.	Plus	29556922-29557002
50	336126	Dunham, I. et.al.	Plus	30057891-30058105
	336129	Dunham, I. et.al.	Plus	30062259-30062348
	336187	Dunham, I. et.al.	Plus	30433494-30433585
	336188	Dunham, I. et.al.	Plus	30434870-30435004
	336225	Dunham, I. et.al.	Plus	30833614-30833788
55	336371	Dunham, I. et.al.	Plus	33968108-33968204
	336373	Dunham, I. et.al.	Plus	33976308-33976504
	336377	Dunham, I. et.al.	Plus	33994489-33994599
	336380	Dunham, I. et.al.	Plus	33995323-33995434
	336383	Dunham, I. et.al.	Plus	34005784-34005964
60	336384	Dunham, I. et.al.	Plus	34007429-34007559
	336385	Dunham, I. et.al.	Plus	34007879-34008159
	336386	Dunham, I. et.al.	Plus	34012965-34013115
	336441	Dunham, I. et.al.	Plus	34187606-34187663
	336444	Dunham, I. et.al.	Plus	34190585-34190718
65	336484	Dunham, I. et.al.	Plus	34237425-34237505
	336497	Dunham, I. et.al.	Plus	34267190-34267245
	336499	Dunham, I. et.al.	Plus	34267504-34267572
	336503	Dunham, I. et.al.	Plus	34271306-34271372
	336548	Dunham, I. et.al.	Plus	34353881-34354826

	336552	Dunham, I. et.al.	Plus	34356420-34356527
	336553	Dunham, I. et.al.	Plus	34356683-34356753
	336557	Dunham, I. et.al.	Plus	34428228-34428395
	336558	Dunham, I. et.al.	Plus	34428521-34428637
5	336659	Dunham, I. et.al.	Plus	1896402-1896478
	336715	Dunham, I. et.al.	Plus	3110198-3110314
	336803	Dunham, I. et.al.	Plus	6106904-6106990
	336805	Dunham, I. et.al.	Plus	6126661-6126786
10	336850	Dunham, I. et.al.	Plus	7745284-7745355
	336857	Dunham, I. et.al.	Plus	8130457-8130612
	336911	Dunham, I. et.al.	Plus	11035818-11035984
	336949	Dunham, I. et.al.	Plus	12818687-12818891
	336950	Dunham, I. et.al.	Plus	12875843-12875912
15	336958	Dunham, I. et.al.	Plus	13203550-13203973
	336993	Dunham, I. et.al.	Plus	15096270-15096324
	337076	Dunham, I. et.al.	Plus	19338177-19338679
	337109	Dunham, I. et.al.	Plus	21166580-21166650
	337123	Dunham, I. et.al.	Plus	22052874-22052942
20	337151	Dunham, I. et.al.	Plus	23106433-23106510
	337189	Dunham, I. et.al.	Plus	24225887-24225954
	337241	Dunham, I. et.al.	Plus	27280182-27280313
	337337	Dunham, I. et.al.	Plus	30395182-30395285
	337353	Dunham, I. et.al.	Plus	30804624-30804780
25	337384	Dunham, I. et.al.	Plus	31333399-31333580
	337386	Dunham, I. et.al.	Plus	31585902-31586067
	337414	Dunham, I. et.al.	Plus	31953012-31953205
	337418	Dunham, I. et.al.	Plus	32014049-32014131
	337461	Dunham, I. et.al.	Plus	32803968-32804028
	337480	Dunham, I. et.al.	Plus	33219714-33219779
30	337482	Dunham, I. et.al.	Plus	33227865-33227946
	337483	Dunham, I. et.al.	Plus	33237292-33237427
	337490	Dunham, I. et.al.	Plus	33318571-33318644
	337522	Dunham, I. et.al.	Plus	33963188-33963979
35	337532	Dunham, I. et.al.	Plus	34187269-34187366
	337552	Dunham, I. et.al.	Plus	19497-19600
	337584	Dunham, I. et.al.	Plus	945236-945452
	337611	Dunham, I. et.al.	Plus	1482883-1483016
	337672	Dunham, I. et.al.	Plus	3331236-3331313
40	337693	Dunham, I. et.al.	Plus	3575975-3576153
	337738	Dunham, I. et.al.	Plus	3865738-3865814
	337926	Dunham, I. et.al.	Plus	6286377-6286470
	337927	Dunham, I. et.al.	Plus	6343033-6343172
	337935	Dunham, I. et.al.	Plus	6534661-6534782
45	337944	Dunham, I. et.al.	Plus	6589383-6589450
	337954	Dunham, I. et.al.	Plus	6831483-6831620
	337996	Dunham, I. et.al.	Plus	7445532-7445633
	338004	Dunham, I. et.al.	Plus	7601363-7601520
	338016	Dunham, I. et.al.	Plus	7863131-7863310
50	338174	Dunham, I. et.al.	Plus	12771102-12771268
	338176	Dunham, I. et.al.	Plus	12774072-12774223
	338238	Dunham, I. et.al.	Plus	14661936-14662015
	338277	Dunham, I. et.al.	Plus	16167622-16167962
	338294	Dunham, I. et.al.	Plus	16463958-16464539
55	338316	Dunham, I. et.al.	Plus	17089711-17089988
	338323	Dunham, I. et.al.	Plus	17154655-17154792
	338324	Dunham, I. et.al.	Plus	17155309-17155574
	338386	Dunham, I. et.al.	Plus	18611213-18611407
	338398	Dunham, I. et.al.	Plus	18953492-18953581
	338410	Dunham, I. et.al.	Plus	19292807-19292916
60	338414	Dunham, I. et.al.	Plus	19345573-19345660
	338460	Dunham, I. et.al.	Plus	20233372-20233488
	338481	Dunham, I. et.al.	Plus	20942659-20942673
	338489	Dunham, I. et.al.	Plus	21142605-21143049
	338500	Dunham, I. et.al.	Plus	21253647-21253974
65	338514	Dunham, I. et.al.	Plus	21379420-21379655
	338530	Dunham, I. et.al.	Plus	21636361-21636509
	338620	Dunham, I. et.al.	Plus	23540239-23540334
	338631	Dunham, I. et.al.	Plus	23711167-23711241
	338653	Dunham, I. et.al.	Plus	24219427-24219509

	338660	Dunham, I. et.al.	Plus	24387122-24387266
	338704	Dunham, I. et.al.	Plus	25230432-25230548
	338847	Dunham, I. et.al.	Plus	27995337-27995420
5	338887	Dunham, I. et.al.	Plus	28465244-28465384
	338895	Dunham, I. et.al.	Plus	28598893-28599135
	338915	Dunham, I. et.al.	Plus	28824881-28824977
	338925	Dunham, I. et.al.	Plus	28883892-28884036
	338936	Dunham, I. et.al.	Plus	29148022-29148160
10	338952	Dunham, I. et.al.	Plus	29418831-29418968
	338980	Dunham, I. et.al.	Plus	29896789-29896874
	338981	Dunham, I. et.al.	Plus	29897917-29898008
	338986	Dunham, I. et.al.	Plus	30007287-30007415
	339009	Dunham, I. et.al.	Plus	30348477-30348598
15	339017	Dunham, I. et.al.	Plus	30420896-30421090
	339045	Dunham, I. et.al.	Plus	30744286-30744356
	339046	Dunham, I. et.al.	Plus	30746269-30746420
	339059	Dunham, I. et.al.	Plus	30814655-30814801
	339067	Dunham, I. et.al.	Plus	30869347-30869412
	339069	Dunham, I. et.al.	Plus	30880975-30881070
20	339078	Dunham, I. et.al.	Plus	30914310-30914423
	339084	Dunham, I. et.al.	Plus	30944556-30944803
	339101	Dunham, I. et.al.	Plus	31158047-31158123
	339102	Dunham, I. et.al.	Plus	31169321-31169563
25	339103	Dunham, I. et.al.	Plus	31170343-31170454
	339115	Dunham, I. et.al.	Plus	31459869-31459927
	339157	Dunham, I. et.al.	Plus	32131701-32131833
	339166	Dunham, I. et.al.	Plus	32210902-32211006
	339167	Dunham, I. et.al.	Plus	32213567-32213730
	339288	Dunham, I. et.al.	Plus	33169611-33169691
30	339289	Dunham, I. et.al.	Plus	33186756-33186903
	339291	Dunham, I. et.al.	Plus	33205057-33205247
	339407	Dunham, I. et.al.	Plus	34189461-34189620
	332865	Dunham, I. et.al.	Minus	1391482-1391218
35	332881	Dunham, I. et.al.	Minus	1563520-1563184
	332930	Dunham, I. et.al.	Minus	2022565-2022497
	332931	Dunham, I. et.al.	Minus	2023651-2023562
	332984	Dunham, I. et.al.	Minus	2632606-2632457
	332986	Dunham, I. et.al.	Minus	2635398-2635206
40	332997	Dunham, I. et.al.	Minus	2710509-2710375
	333051	Dunham, I. et.al.	Minus	2991973-2991840
	333061	Dunham, I. et.al.	Minus	3029631-3029527
	333064	Dunham, I. et.al.	Minus	3030722-3030623
	333096	Dunham, I. et.al.	Minus	3184234-3184118
45	333099	Dunham, I. et.al.	Minus	3206796-3206674
	333106	Dunham, I. et.al.	Minus	3230744-3230547
	333160	Dunham, I. et.al.	Minus	3654893-3654678
	333163	Dunham, I. et.al.	Minus	3665124-3664962
	333165	Dunham, I. et.al.	Minus	3674052-3673905
50	333166	Dunham, I. et.al.	Minus	3694664-3694567
	333170	Dunham, I. et.al.	Minus	3733394-3733299
	333174	Dunham, I. et.al.	Minus	3764284-3764210
	333188	Dunham, I. et.al.	Minus	3826990-3826863
	333214	Dunham, I. et.al.	Minus	3966559-3966437
55	333232	Dunham, I. et.al.	Minus	4001551-4001365
	333237	Dunham, I. et.al.	Minus	4003326-4003219
	333239	Dunham, I. et.al.	Minus	4095861-4094462
	333255	Dunham, I. et.al.	Minus	4297883-4297716
	333259	Dunham, I. et.al.	Minus	4305769-4306639
60	333274	Dunham, I. et.al.	Minus	4389146-4388954
	333290	Dunham, I. et.al.	Minus	4530734-4530554
	333295	Dunham, I. et.al.	Minus	4549290-4549198
	333296	Dunham, I. et.al.	Minus	4550766-4550644
	333310	Dunham, I. et.al.	Minus	4637315-4637232
65	333311	Dunham, I. et.al.	Minus	4637933-4637844
	333312	Dunham, I. et.al.	Minus	4638794-4638635
	333313	Dunham, I. et.al.	Minus	4639397-4639277
	333315	Dunham, I. et.al.	Minus	5405980-5405876
	333318	Dunham, I. et.al.	Minus	4642636-4642564
	333321	Dunham, I. et.al.	Minus	4649080-4648934

	333327	Dunham, I. et.al.	Minus	4657947-4657828
	333335	Dunham, I. et.al.	Minus	4672656-4672564
	333337	Dunham, I. et.al.	Minus	4677930-4677841
5	333454	Dunham, I. et.al.	Minus	5137007-5136880
	333458	Dunham, I. et.al.	Minus	5143942-5143806
	333459	Dunham, I. et.al.	Minus	5144548-5144344
	333470	Dunham, I. et.al.	Minus	5223319-5223088
	333483	Dunham, I. et.al.	Minus	4637315-4637232
10	333496	Dunham, I. et.al.	Minus	5404643-5404523
	333498	Dunham, I. et.al.	Minus	5405980-5405876
	333510	Dunham, I. et.al.	Minus	5557628-5557469
	333546	Dunham, I. et.al.	Minus	5886643-5886442
	333561	Dunham, I. et.al.	Minus	5903659-5903590
15	333738	Dunham, I. et.al.	Minus	7552160-7552084
	333780	Dunham, I. et.al.	Minus	7750367-7750277
	333783	Dunham, I. et.al.	Minus	7751850-7751777
	333818	Dunham, I. et.al.	Minus	7911959-7911762
	333894	Dunham, I. et.al.	Minus	8188855-8188709
20	333897	Dunham, I. et.al.	Minus	8194390-8194284
	333900	Dunham, I. et.al.	Minus	8200268-8200122
	333909	Dunham, I. et.al.	Minus	8229639-8229477
	333936	Dunham, I. et.al.	Minus	8512805-8512564
	333944	Dunham, I. et.al.	Minus	8557051-8556836
25	334040	Dunham, I. et.al.	Minus	9342995-9342934
	334154	Dunham, I. et.al.	Minus	10570714-10570572
	334178	Dunham, I. et.al.	Minus	11755052-11754971
	334188	Dunham, I. et.al.	Minus	11925963-11925834
	334273	Dunham, I. et.al.	Minus	13265608-13265522
30	334282	Dunham, I. et.al.	Minus	13285293-13285178
	334285	Dunham, I. et.al.	Minus	13289990-13289793
	334286	Dunham, I. et.al.	Minus	13291759-13291569
	334303	Dunham, I. et.al.	Minus	13454331-13454217
	334305	Dunham, I. et.al.	Minus	13456310-13456209
35	334306	Dunham, I. et.al.	Minus	13461157-13461049
	334320	Dunham, I. et.al.	Minus	13496857-13496717
	334352	Dunham, I. et.al.	Minus	13675908-13675828
	334353	Dunham, I. et.al.	Minus	13683722-13683596
	334359	Dunham, I. et.al.	Minus	13728664-13728534
40	334363	Dunham, I. et.al.	Minus	13740004-13739812
	334365	Dunham, I. et.al.	Minus	13742078-13741971
	334399	Dunham, I. et.al.	Minus	14186289-14186163
	334409	Dunham, I. et.al.	Minus	14195181-14195075
	334414	Dunham, I. et.al.	Minus	14234033-14233932
45	334470	Dunham, I. et.al.	Minus	14389581-14389442
	334483	Dunham, I. et.al.	Minus	14428355-14428281
	334489	Dunham, I. et.al.	Minus	14455428-14454288
	334498	Dunham, I. et.al.	Minus	14483789-14483700
	334501	Dunham, I. et.al.	Minus	14487509-14487356
50	334502	Dunham, I. et.al.	Minus	14488605-14488526
	334543	Dunham, I. et.al.	Minus	14834496-14834116
	334622	Dunham, I. et.al.	Minus	15191678-15191609
	334650	Dunham, I. et.al.	Minus	15371251-15371178
	334680	Dunham, I. et.al.	Minus	15520047-15519887
55	334745	Dunham, I. et.al.	Minus	16049960-16049653
	334756	Dunham, I. et.al.	Minus	16128678-16128528
	334758	Dunham, I. et.al.	Minus	16132368-16132233
	334761	Dunham, I. et.al.	Minus	16139424-16138319
	334763	Dunham, I. et.al.	Minus	16148136-16148077
60	334784	Dunham, I. et.al.	Minus	16294548-16294360
	334790	Dunham, I. et.al.	Minus	16307576-16307509
	334793	Dunham, I. et.al.	Minus	16330748-16330681
	334802	Dunham, I. et.al.	Minus	16413158-16413026
	334820	Dunham, I. et.al.	Minus	16764338-16764249
65	334824	Dunham, I. et.al.	Minus	16857777-16857674
	334832	Dunham, I. et.al.	Minus	17173957-17173760
	334842	Dunham, I. et.al.	Minus	17464352-17464181
	334844	Dunham, I. et.al.	Minus	17503891-17503768
	334857	Dunham, I. et.al.	Minus	18488368-18488242
	334927	Dunham, I. et.al.	Minus	19988711-19987653

	334939	Dunham, I. et.al.	Minus	20131162-20131054
	334951	Dunham, I. et.al.	Minus	20147708-20147502
	334969	Dunham, I. et.al.	Minus	20188176-20188020
5	334972	Dunham, I. et.al.	Minus	20294734-20294611
	335050	Dunham, I. et.al.	Minus	20884109-20883951
	335078	Dunham, I. et.al.	Minus	21059529-21059458
	335102	Dunham, I. et.al.	Minus	21313841-21313598
	335105	Dunham, I. et.al.	Minus	21320563-21320440
10	335110	Dunham, I. et.al.	Minus	21334136-21333811
	335111	Dunham, I. et.al.	Minus	21335946-21335809
	335115	Dunham, I. et.al.	Minus	21388250-21388146
	335116	Dunham, I. et.al.	Minus	21388573-21388414
	335185	Dunham, I. et.al.	Minus	21651593-21651522
15	335186	Dunham, I. et.al.	Minus	21656436-21656338
	335230	Dunham, I. et.al.	Minus	21899517-21898678
	335236	Dunham, I. et.al.	Minus	21915016-21914870
	335243	Dunham, I. et.al.	Minus	21933519-21933365
	335249	Dunham, I. et.al.	Minus	21950851-21950869
20	335258	Dunham, I. et.al.	Minus	22043431-22043262
	335261	Dunham, I. et.al.	Minus	22063937-22063772
	335276	Dunham, I. et.al.	Minus	22154036-22153937
	335279	Dunham, I. et.al.	Minus	22168834-22168638
	335330	Dunham, I. et.al.	Minus	22556589-22556422
25	335331	Dunham, I. et.al.	Minus	22556823-22556708
	335334	Dunham, I. et.al.	Minus	22560390-22560136
	335346	Dunham, I. et.al.	Minus	22641097-22640918
	335349	Dunham, I. et.al.	Minus	22661861-22661271
	335611	Dunham, I. et.al.	Minus	25070825-25070706
	335612	Dunham, I. et.al.	Minus	25072328-25072142
30	335671	Dunham, I. et.al.	Minus	25358629-25358533
	335676	Dunham, I. et.al.	Minus	25395274-25395152
	335680	Dunham, I. et.al.	Minus	25402437-25402361
	335750	Dunham, I. et.al.	Minus	25732501-25731972
35	335752	Dunham, I. et.al.	Minus	25757026-25756890
	335755	Dunham, I. et.al.	Minus	25763806-25763747
	335767	Dunham, I. et.al.	Minus	25819547-25819218
	335774	Dunham, I. et.al.	Minus	25883733-25883572
	335777	Dunham, I. et.al.	Minus	25885770-25885599
40	335778	Dunham, I. et.al.	Minus	25886469-25886334
	335797	Dunham, I. et.al.	Minus	25958182-25958030
	335800	Dunham, I. et.al.	Minus	25985373-25985280
	335818	Dunham, I. et.al.	Minus	26323886-26323744
	335834	Dunham, I. et.al.	Minus	26391707-26391530
45	335840	Dunham, I. et.al.	Minus	26420596-26420538
	335844	Dunham, I. et.al.	Minus	26433427-26433344
	335846	Dunham, I. et.al.	Minus	26436727-26436621
	335856	Dunham, I. et.al.	Minus	26662452-26662346
	335887	Dunham, I. et.al.	Minus	26939225-26938782
50	335888	Dunham, I. et.al.	Minus	26943037-26942820
	335889	Dunham, I. et.al.	Minus	26946988-26946901
	335890	Dunham, I. et.al.	Minus	26949087-26948665
	335893	Dunham, I. et.al.	Minus	26973898-26973747
	335895	Dunham, I. et.al.	Minus	26975307-26975239
55	335896	Dunham, I. et.al.	Minus	26977639-26977558
	335900	Dunham, I. et.al.	Minus	26980354-26980238
	335907	Dunham, I. et.al.	Minus	27013352-27013273
	335943	Dunham, I. et.al.	Minus	27446610-27446378
	335956	Dunham, I. et.al.	Minus	27653729-27653635
60	335959	Dunham, I. et.al.	Minus	27682313-27682145
	335962	Dunham, I. et.al.	Minus	27704276-27704144
	336040	Dunham, I. et.al.	Minus	29036458-29036300
	336044	Dunham, I. et.al.	Minus	29043828-29043727
	336047	Dunham, I. et.al.	Minus	29050617-29050466
65	336068	Dunham, I. et.al.	Minus	29252077-29251969
	336143	Dunham, I. et.al.	Minus	30135948-30135854
	336158	Dunham, I. et.al.	Minus	30163730-30163610
	336174	Dunham, I. et.al.	Minus	30241988-30241839
	336223	Dunham, I. et.al.	Minus	30816306-30816195
	336245	Dunham, I. et.al.	Minus	31420569-31420509

	336274	Dunham, I. et.al.	Minus	32085468-32085303
	336318	Dunham, I. et.al.	Minus	33364452-33364338
	336326	Dunham, I. et.al.	Minus	33567328-33567201
5	336339	Dunham, I. et.al.	Minus	33798479-33798330
	336340	Dunham, I. et.al.	Minus	33812089-33811915
	336355	Dunham, I. et.al.	Minus	33874750-33874649
	336392	Dunham, I. et.al.	Minus	34015868-34015736
	336393	Dunham, I. et.al.	Minus	34016145-34015951
10	336394	Dunham, I. et.al.	Minus	34016457-34016298
	336400	Dunham, I. et.al.	Minus	34023437-34023298
	336402	Dunham, I. et.al.	Minus	34024090-34023981
	336413	Dunham, I. et.al.	Minus	34046702-34046576
	336424	Dunham, I. et.al.	Minus	34055549-34055491
15	336425	Dunham, I. et.al.	Minus	34058544-34058446
	336437	Dunham, I. et.al.	Minus	34074154-34074090
	336447	Dunham, I. et.al.	Minus	34198207-34197996
	336449	Dunham, I. et.al.	Minus	34204707-34204577
	336466	Dunham, I. et.al.	Minus	34213195-34213046
	336492	Dunham, I. et.al.	Minus	34255578-34255437
20	336511	Dunham, I. et.al.	Minus	34277480-34277351
	336512	Dunham, I. et.al.	Minus	34278373-34278275
	336520	Dunham, I. et.al.	Minus	34319184-34319101
	336522	Dunham, I. et.al.	Minus	34320169-34320056
25	336524	Dunham, I. et.al.	Minus	34321055-34320921
	336527	Dunham, I. et.al.	Minus	34322071-34321966
	336534	Dunham, I. et.al.	Minus	34326797-34326620
	336536	Dunham, I. et.al.	Minus	34327678-34327538
	336542	Dunham, I. et.al.	Minus	34331316-34331183
30	336556	Dunham, I. et.al.	Minus	34375244-34374907
	336557	Dunham, I. et.al.	Minus	34375443-34375341
	336558	Dunham, I. et.al.	Minus	34375825-34375698
	336559	Dunham, I. et.al.	Minus	34376430-34376261
	336560	Dunham, I. et.al.	Minus	34376814-34376596
35	336561	Dunham, I. et.al.	Minus	34377168-34376928
	336597	Dunham, I. et.al.	Minus	7627912-7627757
	336601	Dunham, I. et.al.	Minus	13265853-13265654
	336642	Dunham, I. et.al.	Minus	1304281-1304212
	336645	Dunham, I. et.al.	Minus	1351268-1351168
40	336662	Dunham, I. et.al.	Minus	2158060-2157993
	336664	Dunham, I. et.al.	Minus	1993558-1993481
	336676	Dunham, I. et.al.	Minus	2022565-2022497
	336684	Dunham, I. et.al.	Minus	2158060-2157993
	336686	Dunham, I. et.al.	Minus	2160698-2160486
45	336714	Dunham, I. et.al.	Minus	3094026-3093871
	336719	Dunham, I. et.al.	Minus	3331631-3331503
	336736	Dunham, I. et.al.	Minus	4093128-4093041
	336744	Dunham, I. et.al.	Minus	4333001-4332848
	336786	Dunham, I. et.al.	Minus	5419973-5419873
50	336793	Dunham, I. et.al.	Minus	5631345-5631237
	336859	Dunham, I. et.al.	Minus	8201756-8201561
	336863	Dunham, I. et.al.	Minus	8396673-8396425
	336933	Dunham, I. et.al.	Minus	11760045-11759981
	336942	Dunham, I. et.al.	Minus	12027537-12027455
55	336960	Dunham, I. et.al.	Minus	13267243-13267172
	336969	Dunham, I. et.al.	Minus	13725722-13725643
	336971	Dunham, I. et.al.	Minus	13732308-13732221
	337003	Dunham, I. et.al.	Minus	15523541-15523422
	337011	Dunham, I. et.al.	Minus	16106423-16106080
60	337070	Dunham, I. et.al.	Minus	19034423-19034321
	337072	Dunham, I. et.al.	Minus	19077452-19077323
	337086	Dunham, I. et.al.	Minus	19657011-19656881
	337140	Dunham, I. et.al.	Minus	22649450-22649388
	337193	Dunham, I. et.al.	Minus	24594969-24594874
65	337256	Dunham, I. et.al.	Minus	27659956-27659876
	337278	Dunham, I. et.al.	Minus	28429017-28428848
	337284	Dunham, I. et.al.	Minus	28491414-28491094
	337293	Dunham, I. et.al.	Minus	28846334-28845873
	337316	Dunham, I. et.al.	Minus	29657129-29656997
	337326	Dunham, I. et.al.	Minus	30017199-30017069

	337382	Dunham, I. et.al.	Minus	31233666-31233579
	337392	Dunham, I. et.al.	Minus	31442311-31442229
	337406	Dunham, I. et.al.	Minus	31864840-31864588
5	337412	Dunham, I. et.al.	Minus	31916487-31916312
	337419	Dunham, I. et.al.	Minus	32021496-32021170
	337438	Dunham, I. et.al.	Minus	32257869-32257739
	337455	Dunham, I. et.al.	Minus	32434517-32434425
	337509	Dunham, I. et.al.	Minus	33414613-33414498
10	337518	Dunham, I. et.al.	Minus	33796750-33796647
	337529	Dunham, I. et.al.	Minus	34043668-34043546
	337533	Dunham, I. et.al.	Minus	34193388-34193261
	337539	Dunham, I. et.al.	Minus	34254490-34254322
	337551	Dunham, I. et.al.	Minus	34524446-34524362
15	337553	Dunham, I. et.al.	Minus	24230-24160
	337591	Dunham, I. et.al.	Minus	1006414-1006184
	337592	Dunham, I. et.al.	Minus	1007791-1007634
	337593	Dunham, I. et.al.	Minus	1009460-1009291
	337607	Dunham, I. et.al.	Minus	1355719-1355637
20	337612	Dunham, I. et.al.	Minus	1570235-1570142
	337635	Dunham, I. et.al.	Minus	2169690-2169569
	337824	Dunham, I. et.al.	Minus	4559540-4559266
	337825	Dunham, I. et.al.	Minus	4567155-4567005
	337850	Dunham, I. et.al.	Minus	5077143-5076943
25	337854	Dunham, I. et.al.	Minus	5153435-5153272
	337913	Dunham, I. et.al.	Minus	6149843-6149786
	337915	Dunham, I. et.al.	Minus	5922748-5922690
	337968	Dunham, I. et.al.	Minus	7095797-7095680
	338010	Dunham, I. et.al.	Minus	7754282-7754184
30	338012	Dunham, I. et.al.	Minus	7761421-7761351
	338017	Dunham, I. et.al.	Minus	7864521-7864401
	338065	Dunham, I. et.al.	Minus	7235048-7234950
	338094	Dunham, I. et.al.	Minus	9595602-9595440
	338129	Dunham, I. et.al.	Minus	10915338-10915237
35	338132	Dunham, I. et.al.	Minus	10989617-10989530
	338150	Dunham, I. et.al.	Minus	11478551-11478355
	338157	Dunham, I. et.al.	Minus	11731444-11731375
	338195	Dunham, I. et.al.	Minus	13484103-13483972
	338255	Dunham, I. et.al.	Minus	15242294-15242231
40	338276	Dunham, I. et.al.	Minus	16109555-16109398
	338431	Dunham, I. et.al.	Minus	19747608-19747496
	338448	Dunham, I. et.al.	Minus	20151152-20151054
	338451	Dunham, I. et.al.	Minus	20174286-20174193
	338477	Dunham, I. et.al.	Minus	20821897-20821838
45	338534	Dunham, I. et.al.	Minus	21771238-21771170
	338682	Dunham, I. et.al.	Minus	24800712-24800461
	338684	Dunham, I. et.al.	Minus	24827522-24827428
	338689	Dunham, I. et.al.	Minus	24893073-24892972
	338695	Dunham, I. et.al.	Minus	25104153-25104016
50	338825	Dunham, I. et.al.	Minus	27664798-27664712
	338842	Dunham, I. et.al.	Minus	27824238-27824079
	338893	Dunham, I. et.al.	Minus	28491807-28491631
	338904	Dunham, I. et.al.	Minus	28766345-28766253
	338935	Dunham, I. et.al.	Minus	29071537-29071461
55	339022	Dunham, I. et.al.	Minus	30523414-30523289
	339034	Dunham, I. et.al.	Minus	30621603-30621422
	339190	Dunham, I. et.al.	Minus	32403103-32402985
	339212	Dunham, I. et.al.	Minus	32494335-32494210
	339213	Dunham, I. et.al.	Minus	32496590-32496440
60	339216	Dunham, I. et.al.	Minus	32504250-32504109
	339233	Dunham, I. et.al.	Minus	32751331-32751238
	339258	Dunham, I. et.al.	Minus	32934756-32934615
	339262	Dunham, I. et.al.	Minus	32971258-32971090
	339263	Dunham, I. et.al.	Minus	32974634-32974452
	339265	Dunham, I. et.al.	Minus	32975943-32975806
65	339338	Dunham, I. et.al.	Minus	33468728-33468606
	339396	Dunham, I. et.al.	Minus	34017306-34017205
	339400	Dunham, I. et.al.	Minus	34045024-34044940
	339425	Dunham, I. et.al.	Minus	34407911-34407798
	325207	6552430	Plus	140049-140170

	329568	3962490	Plus	36331-36750
	329517	3983513	Minus	53197-53269
	325313	5866865	Minus	27385-28192
5	325327	5866875	Plus	75189-75264
	325317	5866878	Minus	156551-156649
	325257	5866895	Plus	10867-10955
	329632	6729060	Plus	192813-193017
	325371	5866920	Minus	1035422-1035536
	325375	5866920	Minus	1165503-1165810
10	325378	5866920	Minus	1187981-1188167
	325469	6017034	Plus	286823-286991
	325470	6017034	Plus	287578-287663
	325576	6552443	Minus	137769-137894
	325505	6682451	Minus	240852-240946
15	325543	6682452	Plus	151873-152057
	329635	5302817	Minus	62522-62622
	329636	5302817	Minus	64969-65078
	325593	5866992	Minus	469726-469860
	325675	5867014	Plus	955517-955711
20	325704	5867028	Plus	156198-156397
	325682	6138923	Plus	370618-370763
	325785	6381957	Plus	61849-62003
	325666	6469822	Plus	16769-16857
	325818	6682490	Minus	120278-120559
25	329777	6002090	Minus	191389-191479
	329768	6015501	Plus	118315-118422
	329759	6048280	Minus	37647-37730
	329731	6065783	Plus	158772-158900
	329687	6117856	Minus	22165-22288
30	329676	6272128	Minus	142207-142359
	329667	6272129	Plus	101355-101745
	329669	6272129	Plus	131223-131291
	329670	6272129	Plus	131351-131495
	329641	6468233	Minus	105995-106107
35	329791	6469354	Minus	131982-132089
	325826	5867048	Minus	46361-46458
	325829	5867052	Plus	232674-233060
	329888	6067149	Minus	37227-37473
	329993	6525313	Minus	166123-166791
40	329899	6563505	Minus	111058-111783
	325988	5867064	Plus	17349-17606
	325855	5867067	Plus	276141-276251
	325999	5867073	Plus	149115-149192
	326001	5867073	Plus	155223-155348
45	325886	5867087	Plus	194694-194915
	325882	5867087	Minus	8178-8347
	325905	5867104	Plus	78779-78876
	325922	5867122	Minus	329063-329134
	325937	5867132	Minus	152633-152902
50	325960	5867147	Minus	162506-162635
	325961	5867147	Minus	165106-165209
	325838	6552452	Plus	171451-171532
	325839	6552452	Plus	181964-182037
	325840	6552452	Plus	184380-184547
55	325844	6552453	Minus	14188-14332
	325870	6682492	Plus	228209-228297
	329984	4646193	Minus	139780-139890
	329976	4878063	Minus	62584-62691
	329935	6165200	Minus	69059-69127
60	329916	6223624	Plus	36396-37195
	330021	6671989	Plus	120938-121032
	330024	6671908	Minus	1005-1270
	330028	6671908	Minus	30015-30144
	326033	5867178	Plus	37261-37333
65	326036	5867178	Minus	120215-120273
	326056	5867184	Minus	181553-181690
	326116	5867193	Plus	45548-45604
	326122	5867194	Plus	144397-144683
	326138	5867203	Minus	179374-179436

	326145	5867204	Minus	52599-52814
	326180	5867211	Minus	182758-183222
	326201	5867216	Minus	166168-166959
5	326207	5867222	Plus	48139-48219
	326226	5867230	Plus	52644-52705
	326233	5867232	Plus	124788-124863
	326238	5867260	Plus	64282-64338
	326241	5867260	Minus	181648-181916
	326243	5867261	Plus	123638-123978
10	326251	5867263	Minus	82716-82822
	326268	5867267	Plus	122114-122765
	326124	5916395	Plus	407102-407580
	326339	6056311	Minus	164637-165251
15	330049	4567182	Minus	314662-315210
	326358	5867293	Plus	9122-9195
	326365	5867297	Minus	96630-96764
	326379	5867327	Plus	32299-32402
	326382	5867327	Minus	50420-50503
	326390	5867340	Minus	108814-110592
20	326424	5867389	Minus	168329-168409
	326453	5867399	Plus	86222-86423
	326472	5867404	Plus	293739-293940
	326492	5867422	Plus	120768-120991
	326533	5867441	Minus	532153-532280
25	330117	6015201	Minus	7340-7680
	330115	6015202	Plus	11403-11677
	330116	6015202	Plus	12109-12418
	330095	6015278	Plus	15343-15814
	330096	6015278	Plus	49370-49458
30	326644	5867559	Plus	42684-42819
	326713	5867595	Plus	121511-121798
	326745	5867611	Plus	127130-127318
	326752	5867615	Minus	1214-1562
	326753	5867616	Plus	12454-12511
35	326598	5867634	Plus	68955-69014
	326667	6552455	Plus	142311-142441
	326855	6552460	Minus	111390-111463
	326812	6682504	Plus	189811-189941
	327005	5867664	Plus	610847-610907
40	327008	5867664	Plus	928737-928811
	326896	5867680	Minus	12032-12122
	326904	5867684	Minus	9280-9606
	326951	6004446	Plus	193812-193998
	326941	6004446	Plus	62018-62896
45	326943	6004446	Minus	89242-89427
	326928	6456782	Minus	291007-291219
	326958	6469836	Minus	42952-43082
	326959	6469836	Minus	43159-43301
	327039	6531965	Plus	694486-694998
50	327127	6682520	Plus	41925-42083
	330158	6580367	Plus	81966-82456
	327204	5867447	Plus	165135-165239
	327208	5867447	Plus	180805-180864
	327266	5867462	Minus	82400-82615
55	327277	5867473	Minus	165616-165715
	327289	5867481	Plus	49296-49536
	327296	5867492	Plus	7627-8166
	327237	5867544	Minus	59702-59813
	327145	5867548	Minus	40482-40551
60	327333	5902477	Minus	141448-141609
	327335	5902477	Minus	142979-143124
	327343	6017017	Minus	12288-12395
	327350	6249563	Minus	41890-41985
	327358	6552411	Minus	3802-3950
65	327360	6552411	Minus	6255-6422
	327409	5867750	Minus	52949-53011
	327424	5867751	Plus	160442-160598
	327430	5867754	Plus	1320-1403
	327470	5867772	Plus	150910-150973

5	327460	6004455	Plus	175245-175343
	327498	6017023	Minus	42178-42283
	327509	6117815	Minus	54882-55053
	327510	6117815	Minus	56824-56944
	327512	6117815	Plus	176256-176325
10	327535	6525279	Plus	19105-19175
	330163	6042042	Minus	20321-20385
	330171	6648220	Plus	110889-111575
	327579	5867824	Minus	37229-38335
	327672	5867843	Minus	69649-69740
15	327629	5867872	Plus	49592-49811
	327640	5867890	Plus	9448-9566
	327649	5867899	Plus	205871-205927
	327612	6525283	Plus	2747-2924
	327718	6525284	Plus	86123-86186
20	327801	5867924	Plus	23239-23348
	327762	5867961	Minus	50303-50439
	327763	5867961	Plus	229347-229476
	327776	5867964	Minus	164308-164486
	327822	5867968	Minus	168886-169633
25	327823	5867968	Minus	170359-170433
	327807	5867968	Plus	33745-33811
	327845	6531962	Plus	193402-193549
	330228	6013527	Minus	3719-3787
	330190	6165182	Plus	36103-36243
30	328122	5868031	Plus	158474-158656
	328132	5868038	Minus	126737-126839
	328159	5868065	Minus	52957-53162
	328168	5868071	Plus	60321-60479
	328175	5868073	Plus	208-271
35	328217	5868096	Minus	3742-4362
	327865	5868130	Plus	61503-62205
	327866	5868131	Minus	2893-3046
	327870	5868131	Plus	53558-53757
	327879	5868142	Minus	77722-77793
40	327902	5868158	Minus	133339-133467
	327918	5868165	Plus	547530-547591
	327934	5868184	Plus	41830-42036
	327959	5868210	Minus	46497-46682
	327976	5868212	Minus	349301-349409
45	328020	5902482	Minus	556386-556652
	328042	5902482	Minus	1985085-1986626
	328008	5902482	Plus	296663-297151
	330301	2905862	Minus	4420-5781
	330299	2905881	Minus	1020-1362
50	328274	5868219	Minus	31244-31439
	328595	5868224	Plus	148738-148967
	328591	5868227	Minus	237647-237726
	328668	5868254	Minus	10888-10984
	328677	5868256	Minus	58708-58950
55	328687	5868262	Plus	624479-624585
	328706	5868270	Plus	165501-165614
	328711	5868271	Minus	97797-97990
	328730	5868289	Plus	8068-8214
	328732	5868289	Plus	37437-37550
60	328734	5868289	Plus	50559-50747
	328752	5868298	Minus	114911-115087
	328755	5868301	Minus	145959-146446
	328761	5868302	Minus	239308-239412
	328775	5868309	Plus	12845-12920
65	328784	5868309	Minus	74523-74604
	328787	5868309	Plus	135772-135963
	328809	5868327	Plus	91792-91849
	328829	5868337	Plus	36309-36630
	328280	5868352	Plus	160563-160631
	328311	5868371	Minus	170560-170826
	328318	5868373	Plus	414945-415620
	328323	5868373	Minus	1080089-1080235
	328348	5868383	Minus	260272-260379

	328377	5868390	Plus	16947-17023
	328436	5868417	Plus	203760-203904
	328504	5868471	Plus	47064-47217
5	328506	5868471	Plus	60716-60830
	328522	5868477	Plus	1972307-1972452
	328525	5868482	Plus	12387-14313
	328541	5868486	Plus	130956-131050
	328662	6004473	Plus	1184773-1184855
	328663	6004473	Plus	1185279-1186634
10	328803	6004475	Minus	291716-291948
	328304	6004478	Minus	3884-3952
	328927	5868500	Minus	428829-428893
	328936	5868500	Minus	1352202-1352259
	328939	6004481	Minus	131139-131320
15	328941	6456765	Minus	9817-9885
	328948	6456765	Plus	28227-28413
	328958	6456775	Plus	117442-118283
	330316	6007576	Minus	119761-119931
	330350	3056622	Minus	26413-26820
20	330351	3056622	Minus	27522-27614
	330348	4544475	Minus	19855-19962
	329034	5868561	Minus	32819-32939
	329046	5868569	Plus	18971-19030
	329053	5868574	Plus	426453-426541
25	329186	5868711	Minus	13108-13225
	329237	5868729	Plus	133238-133339
	329276	5868762	Minus	222629-222709
	329333	5868806	Plus	392666-392746
	329376	5868859	Plus	52356-52694
30	329384	5868869	Minus	116524-116662
	329140	6017060	Plus	290842-290905
	329317	6381976	Plus	614823-615209
	329319	6381976	Plus	721390-721470
	329129	6588026	Plus	144568-144712
35	329373	6682537	Minus	38950-39301
	329412	6682553	Minus	68948-69041
	329424	5868879	Plus	362196-362344
	329446	5868886	Plus	84776-84889
	329449	5868886	Plus	97697-97771

TABLE 14: shows genes, including expression sequence tags, down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Background subtracted normal prostate : prostate tumor tissue			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	331328	AA261133	Hs.88808	ESTs	18.53
	320875	D60641	Hs.131921	ESTs	14.55
	300994	AI251936	Hs.146298	ESTs	12.17
	323461	AA418762	Hs.190044	ESTs	10.55
20	301015	AA947682	Hs.217173	ESTs; Weakly similar to Chain A; Cdc42hs-Gdp Complex [H.sapiens]	10.17
	319419	AA543096	Hs.13648	ESTs; Highly similar to mitogen-induced [M.musculus]	9.2
	323486	C05278	Hs.166800	ESTs; Moderately similar to [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR [H.sapiens]	8.87
	324882	AW419080	Hs.250645	ESTs	8
25	330569	U57796	Hs.57679	zinc finger protein 192	7.88
	330126			CH.21_p2 gil6093735	7.8
	316265	AA737400	Hs.142230	ESTs	7.7
	323045	AA148950	Hs.188836	ESTs	7.64
	320668	R58399	Hs.146217	ESTs	7.4
30	330769	AA465192	Hs.16514	ESTs	7.15
	312614	AI766732	Hs.201194	ESTs	7
	314790	AW341754	Hs.189305	ESTs	6.83
	309979	AW452118	Hs.257533	EST	6.74
	314236	AA743396	Hs.189023	ESTs	6.49
35	329192			CH.X_hs gil5868716	6.1
	324307	AA627642	Hs.4994	transducer of ERBB2; 2 (TOB2)	5.99
	303685	AW500106		EST cluster (not in UniGene) with exon hit	5.82
	314921	AW452382	Hs.257564	ESTs	5.8
	315840	AA679001	Hs.192221	ESTs	5.68
40	332776	AA034364	Hs.256551	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	5.43
	313533	AW298141	Hs.157975	ESTs	5.4
	303494	F30712		EST cluster (not in UniGene) with exon hit	5.35
	317490	AI627358	Hs.148367	ESTs	5.31
45	332546	D84454	Hs.21899	solute carrier family 35 (UDP-galactose transporter); member 2	5.25
	334719			CH22_FGENES.421_30	5.25
	300679	AA813958	Hs.207727	ESTs; Moderately similar to KIAA0071 [H.sapiens]	5.22
	311811	AI625304	Hs.190312	ESTs	5.22
	315310	AW511298	Hs.256067	ESTs	5.19
	312871	H86747	Hs.227602	KIAA1116 protein	5.11
50	324715	AI739168		EST cluster (not in UniGene)	4.97
	313870	AW206435	Hs.146057	ESTs	4.97
	321453	N50080	Hs.117827	ESTs	4.78
	316160	AW197887	Hs.253353	ESTs	4.63
	313833	AA766825		EST cluster (not in UniGene)	4.58
55	315850	AW270550	Hs.116957	ESTs	4.53
	303124	AF161350		EST cluster (not in UniGene) with exon hit	4.46
	323346	AL134932	Hs.143607	ESTs	4.4
	301383	AA913591	Hs.126480	ESTs	4.35
	324513	AW501678	Hs.164577	ESTs	4.28
60	303480	AA331906		EST cluster (not in UniGene) with exon hit	4.25
	323591	AA301270		EST cluster (not in UniGene)	4.22
	313803	AW468119		EST cluster (not in UniGene)	4.2
	317863	AI733395	Hs.129124	ESTs	4.1
	312381	R42049	Hs.195473	ESTs	4.08
65	317514	AW451570	Hs.126850	ESTs	4.03
	319750	AA621606	Hs.117956	ESTs	4.03

	322520	T55958	EST cluster (not in UniGene)	4
	314754	AW026761	Hs.134374 ESTs	4
	316088	AI990652	Hs.208973 ESTs	4
	316473	AI939339	Hs.146883 ESTs	3.96
5	307848	AI364186	EST singleton (not in UniGene) with exon hit	3.95
	300730	AW449204	Hs.257125 ESTs	3.94
	303034	W60843	Hs.31570 ESTs	3.93
	324668	AI679131	Hs.201424 ESTs	3.9
10	324674	AA541323	Hs.115831 ESTs	3.88
	300547	N53442	Hs.143443 ESTs	3.83
	316100	AW203986	Hs.213003 ESTs	3.79
	314801	AA481027	Hs.127336 ESTs; Weakly similar to ORF YGR245c [S.cerevisiae]	3.75
	320856	D59945	EST cluster (not in UniGene)	3.74
15	313188	AI039702	Hs.179573 collagen; type I; alpha 2	3.73
	314187	AA804409	Hs.118920 ESTs	3.73
	311826	AA765470	Hs.122826 ESTs	3.7
	302358	D81150	EST cluster (not in UniGene) with exon hit	3.68
	311441	Z38720	Hs.151014 ESTs	3.66
	321914	AA011603	EST cluster (not in UniGene)	3.59
20	332216	H95082	Hs.102332 EST	3.52
	324771	AA631739	EST cluster (not in UniGene)	3.5
	323691	AA317561	EST cluster (not in UniGene)	3.49
	303525	AW518519	Hs.115130 ESTs	3.47
25	309709	AW242630	EST singleton (not in UniGene) with exon hit	3.46
	300038		AFX control: MurlL4	3.38
	316526	AI088192	Hs.135474 ESTs; Weakly similar to ATP-DEPENDENT RNA HELICASE A [H.sapiens]	3.36
	313029	AA731520	Hs.170504 ESTs	3.35
	304356	AA196027	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	3.34
30	314610	AI948688	Hs.191805 ESTs	3.33
	329815		CH.14_p2 gjl5624868	3.32
	314949	AI745387	Hs.239124 ESTs	3.31
	300598	N53574	Hs.158932 ESTs	3.3
	329218		CH.X_hs gjl5868726	3.28
35	315706	AW440742	Hs.155556 ESTs	3.28
	303751	AW503637	EST cluster (not in UniGene) with exon hit	3.25
	307763	AI347274	EST singleton (not in UniGene) with exon hit	3.25
	321414	AA324975	Hs.128993 ESTs; Weakly similar to KIAA0465 protein [H.sapiens]	3.25
	312187	AA700439	Hs.188490 ESTs	3.25
40	334061		CH22_FGENES.327_14	3.23
	336036		CH22_FGENES.678_7	3.23
	321477	H67818	Hs.222059 ESTs	3.21
	315760	AW138383	Hs.245437 ESTs	3.2
	316733	AA811713	Hs.163222 ESTs	3.2
	300355	AW235248	Hs.79828 ESTs	3.2
45	323611	AA304986	Hs.145704 ESTs	3.19
	314138	AA740616	EST cluster (not in UniGene)	3.17
	316774	AA814859	EST cluster (not in UniGene)	3.16
	308884	AI833131	Hs.179100 ESTs	3.11
50	331317	AA258222	Hs.87757 ESTs	3.1
	317221	AI989538	Hs.191074 ESTs	3.08
	316386	AA749062	Hs.180285 ESTs	3.08
	321040	H26953	EST cluster (not in UniGene)	3.08
	308828	AI824829	EST singleton (not in UniGene) with exon hit	3.08
55	300778	AA236233	Hs.188716 ESTs	3.07
	316667	AW015940	Hs.232234 ESTs	3.07
	324614	AW503101	EST cluster (not in UniGene)	3.07
	316468	AW293046	Hs.255158 ESTs	3.07
	300671	AI239706	Hs.189886 ESTs	3.06
60	314301	AW297967	Hs.188181 ESTs	3.05
	312335	AW043620	Hs.236993 ESTs	3.03
	322957	AA247755	EST cluster (not in UniGene)	3.01
	316848	AA830053	Hs.126798 ESTs	3.01
	313473	AA009660	Hs.251948 ESTs; Moderately similar to T07D3.7 [C.elegans]	2.99
65	318518	T27119	EST cluster (not in UniGene)	2.98
	313383	AI076370	Hs.134037 ESTs	2.97
	331389	AA458637	Hs.152207 ESTs	2.96
	304257	AA053294	EST singleton (not in UniGene) with exon hit	2.95
	309917	AW340014	EST singleton (not in UniGene) with exon hit	2.95
	318661	H08035	Hs.21398 ESTs; Moderately similar to PUTATIVE GLUCOSAMINE-6-PHOSPHATE	2.95

		ISOMERASE [H.sapiens]	2.95
	321253 AI699484	EST cluster (not in UniGene)	2.93
	321193 AA149508	Hs.103288 ESTs	2.93
	332864	CH22_FGENES.28_4	2.92
5	300027		
	M11507	AFFX control: transferrin receptor	2.91
	324330 AA884766	EST cluster (not in UniGene)	2.88
	320014 AA137114	Hs.170291 ESTs	2.88
	333916	CH22_FGENES.296_5	2.88
10	318885 Z43272	EST cluster (not in UniGene)	2.87
	318146 AI040125	Hs.150521 ESTs	2.87
	323348 AA233056	Hs.191518 ESTs	2.85
	305703 AA825148	Hs.21229 F-box protein Fbw1b	2.84
	335862	CH22_FGENES.629_7	2.83
15	317672 AW205409	Hs.127748 ESTs	2.82
	323416 AI610397	Hs.159560 ESTs	2.81
	312652 AI419909	Hs.160994 ESTs	2.81
	324094 AA382603	EST cluster (not in UniGene)	2.81
	319761 R84237	EST cluster (not in UniGene)	2.8
20	317013 AA864468	Hs.135646 ESTs	2.8
	317383 AA913887	Hs.126511 ESTs	2.78
	314659 AW277121	Hs.254881 ESTs	2.78
	312479 AI950844	Hs.128738 ESTs; Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]	2.77
	332808	CH22_FGENES.7_10	2.75
25	311824 AW293826	Hs.250610 ESTs	2.75
	321992 C06003	Hs.116456 ESTs	2.73
	316074 AW517542	Hs.208382 ESTs	2.73
	309839 AW296076	EST singleton (not in UniGene) with exon hit	2.73
	312071 AA683529	Hs.143119 ESTs	2.73
30	312684 AW294020	Hs.117721 ESTs	2.72
	332668 AA062971	Hs.181161 ESTs; Weakly similar to INHIBITOR OF APOPTOSIS PROTEIN 1 [M.musculus]	2.72
	322139 H53744	EST cluster (not in UniGene)	2.72
	304168 H77679	EST singleton (not in UniGene) with exon hit	2.72
	325602	CH.13_hs gi 5866994	2.71
35	319885 R59096	Hs.136698 ESTs	2.71
	300611 N75450	EST cluster (not in UniGene) with exon hit	2.71
	316854 AA831215	Hs.159066 ESTs; Weakly similar to predicted using Genefinder [C.elegans]	2.69
	318208 AI091458	Hs.134559 ESTs	2.68
	331623 R38715	Hs.153529 Homo sapiens clone 24540 mRNA sequence	2.68
40	324616 AI623999	Hs.162000 ESTs	2.68
	304968 AA614308	EST singleton (not in UniGene) with exon hit	2.67
	314912 AI431345	Hs.161784 ESTs	2.67
	300767 AW193466	Hs.136525 ESTs	2.67
	313463 AI057369	Hs.122536 ESTs	2.65
45	320600 AA135565	Hs.250739 ESTs	2.65
	301180 AI308989	Hs.156939 ESTs	2.65
	324825 AA704457	Hs.255738 ESTs; Moderately similar to gag [H.sapiens]	2.65
	300336 AW292417	Hs.255074 ESTs; Moderately similar to high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha [H.sapiens]	2.64
50	317850 N29974	EST cluster (not in UniGene)	2.64
	339047	CH22_DA59H18.GENSCAN.28-7	2.64
	324580 AA492588	EST cluster (not in UniGene)	2.63
	321142 AI817933	Hs.209584 ESTs	2.62
	319478 R06841	EST cluster (not in UniGene)	2.62
55	300793 AI248571	Hs.186837 ESTs	2.61
	313733 AA836116	EST cluster (not in UniGene)	2.6
	326505	CH.19_hs gi 5867435	2.6
	314987 AW015506	Hs.130730 ESTs	2.6
	303114 AF090948	EST cluster (not in UniGene) with exon hit	2.59
60	318709 H24244	Hs.240763 ESTs; Weakly similar to /prediction	2.58
	312878 AI209108	Hs.143946 ESTs	2.57
	329224	CH.X_hs gi 5868728	2.56
	328018	CH.06_hs gi 5902482	2.56
	323231 AA324437	Hs.177230 ESTs	2.55
65	312887 AW157377	Hs.132910 ESTs	2.55
	315183 AW136134	Hs.220277 ESTs	2.55
	300259 AI479011	Hs.170783 ESTs	2.54
	313240 AI743261	Hs.131860 ESTs	2.54
	316897 AW293174	Hs.252627 ESTs	2.53

	313966	AI807551	Hs.189061	ESTs	2.53
	331263	AA015718		ze31a12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:36574 3', mRNA sequence	2.51
	310683	AW055233	Hs.160870	ESTs	2.5
5	302566	AA085996	Hs.248572	Human PAC clone DJ404F18 from Xq23	2.5
	302697	AJ001408		EST cluster (not in UniGene) with exon hit	2.5
	308362	AI613519		EST singleton (not in UniGene) with exon hit	2.49
	322347	AF086538		EST cluster (not in UniGene)	2.49
10	316240	AA974253	Hs.120319	ESTs	2.49
	323208	AA203415	Hs.136200	ESTs	2.48
	321643	W76005	Hs.32094	ESTs	2.48
	330723	AA243617	Hs.31082	ESTs; Highly similar to db83 [R.norvegicus]	2.48
	323455	AA256675	Hs.200438	ESTs; Weakly similar to atypical PKC specific binding protein [R.norvegicus]	2.47
15	308383	AI624497		EST singleton (not in UniGene) with exon hit	2.47
	328744			CH.07_hs gjl5868290	2.47
	332344	W45574	Hs.252497	ESTs	2.47
	328121			CH.06_hs gjl5868031	2.47
	321915	AI670955	Hs.200151	ESTs	2.46
20	314954	AA521381	Hs.187726	ESTs	2.45
	302821	AA188868	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1/X [H.sapiens]	2.45
	329454			CH.Y_hs gjl5868887	2.45
	336605			CH22_FGENES.420_4	2.45
	300664	AI444628	Hs.256809	ESTs	2.44
25	323362	AL135067	Hs.117182	ESTs	2.44
	300024	M10098		AFFX control: 18S ribosomal RNA	2.44
	325026	AI671168	Hs.12285	ESTs	2.43
	324510	AI148353	Hs.120849	ESTs	2.43
	313389	AI765182	Hs.119903	ESTs	2.43
30	301309	M78276	Hs.255917	ESTs	2.43
	313570	AA041455	Hs.209312	ESTs	2.43
	316504	AW135854	Hs.132458	ESTs	2.42
	319401	R01342		EST cluster (not in UniGene)	2.42
	312827	AI744361	Hs.205591	ESTs; Weakly similar to zinc finger protein Png-1 [M.musculus]	2.42
35	327871			CH.06_hs gjl5868131	2.41
	337173			CH22_FGENES.565-3	2.41
	302948	AA465635		EST cluster (not in UniGene) with exon hit	2.41
	324303	AL118754		EST cluster (not in UniGene)	2.4
	315527	AI791138	Hs.116768	ESTs	2.4
40	315979	AA830515	Hs.222917	ESTs	2.4
	331310	AA253351	Hs.44439	STAT induced STAT inhibitor-4	2.4
	321095	AA017595	Hs.32844	ESTs	2.4
	308561	AI701559		EST singleton (not in UniGene) with exon hit	2.39
	313035	N36417	Hs.144928	ESTs	2.37
45	322114	AA643791	Hs.191740	ESTs	2.37
	313671	W49823	Hs.145553	ESTs	2.37
	303211	AA099548	Hs.191436	ESTs; Highly similar to dJ1118D24.4 [H.sapiens]	2.37
	301256	AA932948		EST cluster (not in UniGene) with exon hit	2.36
	338165			CH22_EM:AC005500.GENSCAN.212-3	2.36
50	324692	AA557952		EST cluster (not in UniGene)	2.35
	318587	AA779704	Hs.168830	ESTs	2.35
	312378	R41582	Hs.109219	retinal degeneration B beta	2.35
	318625	T48446	Hs.193162	ESTs	2.35
	305181	AA663726	Hs.116922	EST	2.35
	300815	AA286678		EST cluster (not in UniGene) with exon hit	2.34
55	324063	AW292740	Hs.254815	ESTs	2.34
	315859	AA682305	Hs.133268	ESTs	2.33
	305092	AA642912		EST singleton (not in UniGene) with exon hit	2.33
	306598	AI000320		EST singleton (not in UniGene) with exon hit	2.33
60	300307	AI651016	Hs.246311	ESTs	2.33
	321348	Z49979		EST cluster (not in UniGene)	2.33
	325112	AI903770	Hs.124344	ESTs	2.32
	336679			CH22_FGENES.43-7	2.32
	321383	AJ002574		EST cluster (not in UniGene)	2.32
65	337357			CH22_FGENES.730-6	2.31
	300680	AW468066	Hs.257712	ESTs; Weakly similar to KIAA0986 protein [H.sapiens]	2.31
	327120			CH.21_hs gjl6531970	2.31
	302761	AW250553		EST cluster (not in UniGene) with exon hit	2.3
	312132	AI475490	Hs.170577	ESTs	2.3
	315639	AA827652		EST cluster (not in UniGene)	2.3

	312189	T95594	Hs.187435	ESTs	2.3
	306537	AA991705		EST singleton (not in UniGene) with exon hit	2.3
	327061			CH.21_hs gj 5531965	2.3
5	315391	AA759098	Hs.192007	ESTs	2.3
	322384	AI968646	Hs.33862	ESTs	2.29
	323206	AA203339	Hs.220750	ESTs	2.29
	318110	AI680915	Hs.201379	ESTs	2.28
	335250			CH22_FGENES.516_11	2.28
10	331696	Z38907	Hs.91662	KIAA0888 protein	2.28
	318327	AW294013	Hs.200942	ESTs	2.28
	324980	AA969121	Hs.254296	ESTs	2.28
	319429	AI608881	Hs.11482	ESTs; Highly similar to junctional adhesion molecule [H.sapiens]	2.28
	310601	AI970543	Hs.192605	ESTs	2.28
	318905	Z43395		EST cluster (not in UniGene)	2.28
15	323442	AA252753	Hs.164039	ESTs	2.27
	304428	AA342250	Hs.99819	ubiquitin specific protease 16	2.27
	313352	AW292127	Hs.144758	ESTs	2.27
	316491	AA766025	Hs.238794	EST	2.27
20	317751	AI697688	Hs.202241	ESTs	2.26
	314136	AA229781	Hs.221962	ESTs	2.26
	306665	AI004614	Hs.130577	EST	2.26
	303946	AW474196	Hs.221604	ESTs	2.25
	313435	AA769123		EST cluster (not in UniGene)	2.25
25	317679	AA968799	Hs.150289	ESTs	2.25
	322370	AA330095		EST cluster (not in UniGene)	2.25
	306620	AI000929		EST singleton (not in UniGene) with exon hit	2.24
	329109			CH.X_hs gj 5868626	2.24
	311043	AI871209	Hs.177128	ESTs	2.24
30	300228	AI458372	Hs.158748	ESTs; Weakly similar to synapsin Ib [M.musculus]	2.24
	307223	AI193698	Hs.184776	ribosomal protein L23a	2.24
	309023	AI888045		EST singleton (not in UniGene) with exon hit	2.23
	310749	AI493675	Hs.170332	ESTs	2.23
	316769	AI914939	Hs.212184	ESTs	2.22
35	320409	AA356195		EST cluster (not in UniGene)	2.21
	333149			CH22_FGENES.87_8	2.21
	324951	M86125	Hs.137487	ESTs	2.21
	321939	AI791617	Hs.145068	ESTs	2.2
	320594	AI863952	Hs.169436	arginyltransferase 1	2.2
40	320722	R67430	Hs.172787	ESTs	2.2
	321781	D78667		EST cluster (not in UniGene)	2.2
	328903			CH.08_hs gj 5868514	2.2
	303889	T19204		EST cluster (not in UniGene) with exon hit	2.2
	325045	T08845		EST cluster (not in UniGene)	2.2
45	312828	AI865455	Hs.211818	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	2.19
	335109			CH22_FGENES.494_15	2.18
	330878	AA131471	Hs.71440	ESTs	2.18
	311289	AI971362	Hs.231945	ESTs	2.18
	304608	AA513456		EST singleton (not in UniGene) with exon hit	2.18
50	337393			CH22_FGENES.747-4	2.18
	332812			CH22_FGENES.7_14	2.18
	327665			CH.04_hs gj 5867839	2.18
	314581	AW504859	Hs.237849	ESTs	2.17
	326508			CH.19_hs gj 6682496	2.17
55	301242	AW161535	Hs.258803	ESTs	2.17
	312780	AI765651	Hs.172900	ESTs	2.17
	315954	AW276810	Hs.254859	ESTs	2.16
	311179	AI880843	Hs.223333	ESTs	2.16
	315320	AI084182	Hs.186895	ESTs	2.16
60	313017	AI015203	Hs.118015	ESTs	2.16
	312430	AW139117	Hs.117494	ESTs	2.15
	300864	AA406539	Hs.190958	ESTs	2.15
	314753	AA463262		EST cluster (not in UniGene)	2.15
	322574	AF156548		EST cluster (not in UniGene)	2.15
65	321409	C03864		EST cluster (not in UniGene)	2.15
	321205	AA002047		EST cluster (not in UniGene)	2.14
	320406	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	2.14
	337646			CH22_EM.AC000097.GENSCAN.11-2	2.13
	303084	AF174008		EST cluster (not in UniGene) with exon hit	2.13
	312185	AA654772	Hs.186564	ESTs	2.13

	306813	AI066544	EST singleton (not in UniGene) with exon hit	2.13	
	314465	AA602917	Hs.156974 ESTs	2.12	
	318168	AI821782	Hs.220587 ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	2.12	
5	315990	AI800041	Hs.190555 ESTs	2.11	
	320712	R68867	EST cluster (not in UniGene)	2.11	
	318487	AI167877	Hs.143716 ESTs	2.11	
	317462	AW015206	Hs.178784 ESTs	2.11	
	304384	AA235482	Hs.62954 ferritin; heavy polypeptide 1	2.11	
10	314544	AA399018	Hs.250835 ESTs	2.1	
	319881	T72744	EST cluster (not in UniGene)	2.1	
	328078		CH.06_hs gil5868008	2.1	
	317354	AW090770	Hs.192271 ESTs	2.1	
	308617	AI738720	EST singleton (not in UniGene) with exon hit	2.09	
15	311558	AW439969	Hs.218177 ESTs	2.09	
	313605	AI761786	Hs.204674 ESTs	2.09	
	314289	AA848118	Hs.221216 ESTs	2.08	
	332933		CH22_FGENES.38_7	2.08	
	325498		CH.12_hs gil5866967	2.08	
20	313659	AW296067	Hs.124106 ESTs	2.08	
	324596	AW149321	Hs.105411 ESTs	2.08	
	324783	AA840770	EST cluster (not in UniGene)	2.07	
	302696	AA347452	EST cluster (not in UniGene) with exon hit	2.07	
	313418	AW450874	Hs.114696 ESTs	2.06	
25	326920		CH.21_hs gil6456782	2.06	
	327574		CH.03_hs gil5867818	2.06	
	323207	AI052795	Hs.192201 ESTs	2.06	
	303753	AW503733	Hs.170315 ESTs	2.05	
	305235	AA670480	EST singleton (not in UniGene) with exon hit	2.05	
30	316055	AA693880	EST cluster (not in UniGene)	2.05	
	317194	AW445167	Hs.126036 ESTs	2.05	
	319565	AW408683	Hs.32922 ESTs	2.05	
	335146		CH22_FGENES.499_2	2.05	
	301475	AI678183	Hs.170917 prostaglandin E receptor 3 (subtype EP3)	2.04	
35	312442	AA120970	Hs.143199 ESTs	2.04	
	322502	R62925	Hs.243665 ESTs	2.04	
	303693	AA290875	Hs.30120 ESTs	2.04	
	310179	AI215643	Hs.171381 ESTs	2.03	
	321121	W23285	EST cluster (not in UniGene)	2.03	
40	331330	AA282197	Hs.89002 ESTs; Highly similar to CGI-07 protein [H.sapiens]	2.03	
	306557	AA694530	EST singleton (not in UniGene) with exon hit	2.03	
	317865	AI298794	Hs.129130 ESTs	2.03	
	318667	AI493742	Hs.165210 ESTs	2.02	
	318042	AW294522	Hs.149931 ESTs	2.02	
45	323818	AW245528	Hs.134754 ESTs	2.02	
	331286	AA137062	Hs.103853 ESTs	2.01	
	311262	AI989942	Hs.232150 ESTs	2.01	
	335601		CH22_FGENES.581_41	2.01	
	311351	AI682303	Hs.201274 ESTs	2.01	
50	312996	AA249018	EST cluster (not in UniGene)	2.01	
	328190		CH.06_hs gil5868077	2	
	338030		CH22_EM:AC005500.GENSCAN.148-16	2	
	333940		CH22_FGENES.301_6	2	
	328227		CH.06_hs gil5868105	2	
55	331481	N27448	Hs.43944 EST	2	
	335288		CH22_FGENES.527_1	2	
	307513	AI274307	EST singleton (not in UniGene) with exon hit	2	
	323316	AL134620	EST cluster (not in UniGene)	2	
	319479	R21945	Hs.256153 ESTs	2	
60	303482	AA502583	Hs.197271 ESTs	2	
	327489		CH.02_hs gil6004459	1.99	
	323935	AW175841	Hs.192183 ESTs	1.99	
	309575	AW168096	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	1.99	
	337043		CH22_FGENES.439-19	1.98	
65	312897	AI828174	Hs.227049 ESTs	1.98	
	307881	AI370434	EST singleton (not in UniGene) with exon hit	1.98	
	328656		CH.07_hs gil6004473	1.98	
	314569	AA813784	Hs.123001 ESTs	1.98	
	332783	W45302	Hs.87889 helicase-mol	1.98	
	315259	AA701499	Hs.148115 ESTs	1.98	

	313171	N67879	Hs.157695	ESTs	1.97
	318060	AI241421	Hs.132236	ESTs	1.97
	332256	N66393	Hs.102754	ESTs	1.97
	312110	AI962180	Hs.226803	ESTs	1.97
5	335864		CH22_FGENES.629_9		1.97
	320389	W00545	Hs.171785	ESTs	1.97
	314065	AA868267	Hs.85524	ESTs	1.96
	323086	H15474	Hs.12214	Homo sapiens clone 23716 mRNA sequence	1.96
	323919	AA862973	Hs.220704	ESTs	1.96
10	310750	AI373163	Hs.170333	ESTs	1.96
	309435	AW090537		EST singleton (not in UniGene) with exon hit	1.96
	300129	AW028820		EST cluster (not in UniGene) with exon hit	1.96
	320130	AI820675	Hs.203804	ESTs	1.95
	323787	AW373448	Hs.169885	ESTs; Weakly similar to cDNA EST EMBL:T02216 comes from this gene [C.elegans]	1.95
15	336112		CH22_EM:AC005500.GENSCAN.185-24		1.95
	313625	AW468402	Hs.254020	ESTs	1.95
	325240		CH.10_hs gi 5866848		1.95
	331833	AA412102	Hs.250911	interleukin 13 receptor; alpha 1	1.95
	332252	N63882	za21f9.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293225 3', mRNA sequence		1.95
20	300279	AW237425	Hs.253817	ESTs	1.95
	326023		CH.17_hs gi 5867245		1.95
	321609	H86021	Hs.198800	ESTs; Weakly similar to hMmTRA1b [H.sapiens]	1.94
	324183	AA402453	Hs.113011	ESTs	1.94
25	336276		CH22_FGENES.762_5		1.94
	334913		CH22_FGENES.456_3		1.94
	325417		CH.12_hs gi 5866925		1.94
	318489	AW043590	Hs.225023	ESTs	1.94
	318455	AI148763		EST cluster (not in UniGene)	1.94
30	306890	AI092235		EST singleton (not in UniGene) with exon hit	1.94
	315073	AW452948	Hs.257631	ESTs	1.94
	321289	R84687	Hs.226306	ESTs	1.94
	308521	AI689808		EST singleton (not in UniGene) with exon hit	1.93
	306382	AA968967		EST singleton (not in UniGene) with exon hit	1.93
35	331320	AA262999	Hs.42788	ESTs	1.93
	324279	AA501412	Hs.191688	ESTs; Weakly similar to Pro-Pol-dUTPase polypeptide [M.musculus]	1.93
	309577	AW168753		EST singleton (not in UniGene) with exon hit	1.93
	327014		CH.21_hs gi 5867664		1.93
	303488	AW025860		EST cluster (not in UniGene) with exon hit	1.93
40	306561	AA995223	Hs.129559	EST	1.92
	330694	AA019806	Hs.108447	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	1.92
	313083	N50545	Hs.159200	ESTs	1.92
	327752		CH.05_hs gi 5867949		1.92
	318874	AA295490		EST cluster (not in UniGene)	1.92
45	301267	AW297762	Hs.255690	ESTs	1.91
	332092	AA608787	Hs.112590	ESTs	1.91
	323509	AL036947		EST cluster (not in UniGene)	1.91
	321452	AA317554		EST cluster (not in UniGene)	1.91
	311483	AI765013	Hs.209128	ESTs	1.91
50	300976	AI246374	Hs.185861	ESTs	1.91
	323715	AA322155		EST cluster (not in UniGene)	1.91
	313600	AW296132	Hs.166674	ESTs	1.91
	332029	AA489697	Hs.145053	ESTs	1.91
	304013	AW518573	Hs.156110	Immunoglobulin kappa variable 1D-8	1.91
55	322019	AA354549	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (from clone DKFZp727C191)	1.91
	334150		CH22_FGENES.339_1		1.9
	310094	AW450967	Hs.235240	ESTs	1.9
	316218	AW207642	Hs.174021	ESTs	1.9
	324774	AI031771	Hs.132586	ESTs	1.9
60	326507		CH.19_hs gi 5867435		1.9
	314570	AA405696		EST cluster (not in UniGene)	1.9
	336268		CH22_FGENES.758_2		1.9
	315278	AI985544	Hs.116429	ESTs	1.9
	325824		CH.15_hs gi 5867048		1.9
65	316277	AA737780	Hs.213392	ESTs	1.9
	323181	AA418583	Hs.143621	ESTs	1.89
	301438	AA961643	Hs.127716	ESTs	1.89
	307050	AI147341	Hs.146734	EST	1.89
	306830	AI075803		EST singleton (not in UniGene) with exon hit	1.89

	302426	AL049925	Hs.225964	DKFZP547G0910 protein	1.89
	320127	H72615	Hs.17268	ESTs	1.89
	337736			CH22_EM:AC000097.GENSCAN.100-2	1.89
5	331319	AA262755	Hs.194264	ESTs	1.88
	310767	AI377505	Hs.158835	ESTs	1.88
	314880	AI732169	Hs.105429	ESTs	1.88
	312539	AI004377	Hs.200360	ESTs	1.88
	309674	AW205604	Hs.168034	ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	1.88
	314621	AI627478	Hs.187670	ESTs	1.88
10	319495	AI972146	Hs.192756	ESTs	1.88
	313472	AA007374		EST cluster (not in UniGene)	1.88
	302705	UC9060		EST cluster (not in UniGene) with exon hit	1.88
	329511			CH.10_p2 gj 3983514	1.88
	317140	AI699412	Hs.201925	ESTs	1.87
15	302598	AI815985	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5)	1.87
	301153	AA725670	Hs.120485	ESTs; Weakly similar to serine/threonine kinase with SH3 domain; leucine zipper domain and proline rich domain [H.sapiens]	1.87
	332222	N28271	Hs.176618	ESTs	1.87
	330703	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.87
20	318470	AI159863	Hs.143713	ESTs	1.87
	314014	AW291847	Hs.121715	ESTs; Weakly similar to HP protein [H.sapiens]	1.87
	300370	AI827817		EST cluster (not in UniGene) with exon hit	1.86
	312329	R84768	Hs.13399	Homo sapiens clone 25032 mRNA sequence	1.86
	325587			CH.12_hs gj 6682462	1.86
25	310237	AI884313	Hs.158906	ESTs	1.86
	318872	R13085		EST cluster (not in UniGene)	1.86
	303431	AA317915		EST cluster (not in UniGene) with exon hit	1.86
	338427			CH22_EM:AC005500.GENSCAN.349-1	1.86
	300452	AI352293	Hs.191098	ESTs	1.85
30	321279	H85330	Hs.146060	ESTs	1.85
	301690	F05865	Hs.249180	ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)	1.85
	307932	AJ230822		EST singleton (not in UniGene) with exon hit	1.85
	318292	AI679966	Hs.150603	ESTs	1.85
	310254	AI239811	Hs.157491	ESTs	1.85
35	311790	AW016437	Hs.233462	ESTs	1.84
	314248	AA278347	Hs.126078	ESTs	1.84
	335586			CH22_FGENES.581_25	1.84
	339209			CH22_FF113D11.GENSCAN.6-4	1.84
	307954	AI419692		EST singleton (not in UniGene) with exon hit	1.84
40	302549	AF055136	Hs.248162	tectorin alpha	1.84
	321629	H87213	Hs.158092	ESTs	1.84
	301239	AA807558		EST cluster (not in UniGene) with exon hit	1.84
	332434	N75542	Hs.75356	transcription factor 4	1.84
	327192			CH.01_hs gj 5867445	1.83
45	310214	AI220072	Hs.165893	ESTs	1.83
	320516	R33857	Hs.181479	ESTs; Weakly similar to E-SELECTIN PRECURSOR [H.sapiens]	1.83
	324231	W80827		EST cluster (not in UniGene)	1.83
	336616			CH22_FGENES.613_5	1.83
	328799			CH.07_hs gj 5868316	1.83
50	324661	AW504161		EST cluster (not in UniGene)	1.83
	313190	AA766707	Hs.153039	ESTs	1.83
	301979	L28168	Hs.121495	potassium voltage-gated channel; Isk-related family; member 1	1.82
	302099	AL021397	Hs.137576	ribosomal protein L34 pseudogene 1	1.82
	320187	T99949		EST cluster (not in UniGene)	1.82
55	320791	R78808	Hs.93961	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]	1.82
	305733	AA829535	Hs.84298	CD74 antigen (invariant polypept of MHC; class II antigen-associated)	1.82
	308280	AI569349	Hs.180920	ribosomal protein S9	1.81
	321533	W78877	Hs.40111	ESTs	1.81
	312946	AI915122	Hs.204087	ESTs; Weakly similar to F33D11.9b [C.elegans]	1.81
60	319474	H90265	Hs.100636	ESTs	1.81
	329519			CH.10_p2 gj 3983510	1.81
	324685	AA220982		EST cluster (not in UniGene)	1.81
	320697	N62937	Hs.139181	ESTs	1.81
	329246			CH.X_hs gj 5868732	1.81
65	332000	AA481271	Hs.193945	ESTs	1.81
	310811	AI420990	Hs.161303	ESTs	1.81
	325866			CH.16_hs gj 5867076	1.81
	322064	Z78343		EST cluster (not in UniGene)	1.8
	333712			CH22_FGENES.251_1	1.8

	313457	AA576052	Hs.193223	ESTs	1.8
	321591	H85687	Hs.117927	ESTs	1.8
	330260			CH.05_p2 gi 6671884	1.8
5	311080	AI656320	Hs.197711	ESTs	1.8
	329522			CH.10_p2 gi 3983507	1.8
	322889	AA081924	Hs.211417	ESTs	1.8
	300175	AI275011	Hs.204877	ESTs	1.8
	330976	H20560	Hs.244624	ESTs	1.8
10	300208	AI341180	Hs.196115	ESTs; Weakly similar to FIBRILLIN 1 PRECURSOR [H.sapiens]	1.79
	319635	R17531		EST cluster (not in UniGene)	1.79
	313454	AA730673	Hs.188634	ESTs	1.79
	303093	AI400310	Hs.148958	ESTs	1.79
	309815	AW292760		EST singleton (not in UniGene) with exon hit	1.79
	326506			CH.19_hs gi 5867435	1.79
15	319845	AA649011	Hs.187902	ESTs	1.79
	300290	AI623739	Hs.186387	ESTs	1.79
	312180	AI248285	Hs.118348	ESTs	1.79
	313058	D81015	Hs.125382	ESTs	1.79
20	330120			CH.19_p2 gi 6671864	1.78
	328412			CH.07_hs gi 5868405	1.78
	302345	NM_000565		EST cluster (not in UniGene) with exon hit	1.78
	308100	AI475949		EST singleton (not in UniGene) with exon hit	1.78
	311386	AW205705	Hs.207514	ESTs	1.78
	330282			CH.05_p2 gi 6671910	1.78
25	318856	Z43011	Hs.21169	ESTs	1.78
	312486	AA845630	Hs.117904	ESTs	1.78
	325450			CH.12_hs gi 5866941	1.78
	321206	H54178	Hs.226469	ESTs	1.78
	330977	H20826	Hs.31783	ESTs	1.78
30	303487	AA333666		EST cluster (not in UniGene) with exon hit	1.77
	310398	AI264671	Hs.164166	ESTs	1.77
	313230	AI540166	Hs.129563	ESTs	1.77
	317747	AI683782	Hs.128245	ESTs	1.77
	303381	AL038841	Hs.163313	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	1.77
35	336123			CH22_FGENES.701_8	1.77
	300185	AI286182	Hs.208484	ESTs	1.77
	316002	AW451733	Hs.119824	ESTs	1.77
	319850	AA001811	Hs.83722	ESTs	1.77
40	329941			CH.16_p2 gi 6165199	1.77
	328329			CH.07_hs gi 5868375	1.77
	322934	AI493054	Hs.158968	ESTs	1.77
	325902			CH.16_hs gi 5867101	1.76
	322239	W01813	Hs.12109	WD40 protein C1a01	1.76
45	303530	AI274851	Hs.258744	ESTs	1.76
	300980	AI025527	Hs.222097	ESTs	1.76
	331909	AA437300	Hs.178210	ESTs	1.76
	321553	H92449	Hs.118406	ESTs	1.76
	301618	T52760		EST cluster (not in UniGene) with exon hit	1.76
50	319592	AA627356	Hs.163315	ESTs	1.76
	318511	T26528	Hs.227175	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.76
	327183			CH.01_hs gi 5867442	1.76
	313516	AA029058	Hs.135145	ESTs	1.76
	318644	AI752482		EST cluster (not in UniGene)	1.76
55	321632	AA419617		EST cluster (not in UniGene)	1.76
	324657	AW451142	Hs.255628	ESTs	1.76
	300437	AW449374	Hs.257149	ESTs	1.75
	319775	AA504429	Hs.6211	methyl-CpG binding domain protein 1	1.75
	314775	AI149880	Hs.188809	ESTs	1.75
	337460			CH22_FGENES.780-5	1.75
60	309849	AW297444		EST singleton (not in UniGene) with exon hit	1.75
	301471	AA995014	Hs.129544	ESTs; Weakly similar to ORF YLL027w [S.cerevisiae]	1.75
	312739	AI318426	Hs.155925	ESTs	1.75
	319995	H15355	Hs.60887	ESTs	1.75
65	326495			CH.19_hs gi 5867423	1.75
	337497			CH22_FGENES.801-4	1.75
	322633	AA004534	Hs.153981	ESTs	1.75
	332177	F10812	Hs.101433	ESTs	1.75
	326930			CH.21_hs gi 6456782	1.75
	316893	AA837332		EST cluster (not in UniGene)	1.75

	324826	AA704806	Hs.143842	ESTs	1.75
	311269	AI656924	Hs.174257	ESTs	1.75
	309375	AW075342		EST singleton (not in UniGene) with exon hit	1.75
5	314171	AI821895	Hs.193481	ESTs	1.75
	311684	AI990741	Hs.252809	ESTs	1.75
	334387			CH22_FGENES.380_1	1.75
	312195	AI300101	Hs.252222	ESTs	1.75
	315707	AI418055	Hs.161160	ESTs	1.74
	324349	AW501470		EST cluster (not in UniGene)	1.74
10	300724	AI762929	Hs.206134	ESTs; Weakly similar to similar to reverse transcriptase [C.elegans]	1.74
	309906	AW339340		EST singleton (not in UniGene) with exon hit	1.74
	303714	AW501336		EST cluster (not in UniGene) with exon hit	1.74
	318704	Z24981		EST cluster (not in UniGene)	1.74
	303027	AF111178		EST cluster (not in UniGene) with exon hit	1.74
15	322601	W92924		EST cluster (not in UniGene)	1.74
	319382	H93199	Hs.33665	ESTs	1.74
	315858	AA737345		EST cluster (not in UniGene)	1.74
	332243	N55484	Hs.220540	ESTs; Highly similar to ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR [H.sapiens]	1.74
20	330951	H02566	Hs.191268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.74
	324044	AL045752	Hs.211519	ESTs	1.73
	320630	AA199847		EST cluster (not in UniGene)	1.73
	327288			CH.01_hs gi 5867481	1.73
	314986	AI201367	Hs.142860	ESTs	1.73
25	319078	H17255	Hs.144515	ESTs	1.73
	326278			CH.17_hs gi 5867269	1.73
	302552	H49792		EST cluster (not in UniGene) with exon hit	1.73
	322322	AF086431		EST cluster (not in UniGene)	1.73
	327075			CH.21_hs gi 6531965	1.73
30	317392	AI797588	Hs.145459	ESTs	1.73
	300810	AI076890	Hs.186949	ESTs	1.73
	315978	AA830893	Hs.119769	ESTs	1.73
	323903	AA773580	Hs.193598	ESTs	1.73
	330803	AA004699	Hs.150590	putative translation initiation factor	1.73
35	309845	AW296802	Hs.255580	EST	1.73
	314963	AI689617	Hs.200934	ESTs	1.73
	311710	F09774	Hs.175971	ESTs	1.73
	315315	AI984592	Hs.15088	ESTs	1.73
	300378	AA663560	Hs.235873	ESTs; Weakly similar to K11C4.2 [C.elegans]	1.73
40	316141	AW303457		EST cluster (not in UniGene)	1.72
	319826	T71739	Hs.75442	albumin	1.72
	312961	AI033922	Hs.122517	ESTs	1.72
	334379			CH22_FGENES.379_11	1.72
	305854	AA862733		EST singleton (not in UniGene) with exon hit	1.72
45	313031	N34927	Hs.186566	ESTs	1.72
	329728			CH.14_p2 gi 6065785	1.72
	312090	N57692	Hs.118064	ESTs	1.72
	323341	AL134875	Hs.192386	ESTs	1.72
	302077	AA310580	Hs.132898	Homo sapiens chromosome 11; BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene	1.71
50	310766	AI971438	Hs.158824	ESTs	1.71
	311450	AI809985	Hs.203340	ESTs	1.71
	311792	AW238064	Hs.253909	ESTs	1.71
	321500	H71999		EST cluster (not in UniGene)	1.71
55	311948	T78791	Hs.241569	ESTs; Moderately smlr to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.71
	302270	R56151		EST cluster (not in UniGene) with exon hit	1.71
	329089			CH.X_hs gi 5868614	1.71
	322331	AF086467		EST cluster (not in UniGene)	1.71
	318235	AI080361	Hs.134217	ESTs	1.71
60	304561	AA489792		EST singleton (not in UniGene) with exon hit	1.71
	312681	AI028149	Hs.193124	pyruvate dehydrogenase kinase; isoenzyme 3	1.71
	310250	AI478629	Hs.158465	ESTs	1.71
	338176			CH22_EM:AC005500.GENSCAN.219-6	1.71
	336910			CH22_DJ32110.GENSCAN.11-2	1.71
65	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (from clone DKFZp564B1462)	1.7
	322289	AA534550	Hs.539	ribosomal protein S29	1.7
	319802	AI701489	Hs.202501	ESTs	1.7
	314022	AW452420	Hs.248678	ESTs	1.7
	314937	AA515602	Hs.152330	ESTs	1.7

5	300580	AA761322	Hs.220538	ESTs	1.7
	304398	AA262785		EST singleton (not in UniGene) with exon hit	1.7
	313421	AW339515	Hs.163700	ESTs	1.7
	309763	AW270182		EST singleton (not in UniGene) with exon hit	1.7
	322092	AF085833		EST cluster (not in UniGene)	1.7
10	315603	AA764768	Hs.121158	ESTs	1.7
	325031	T08597		EST cluster (not in UniGene)	1.7
	327157			CH.01_hs gi 5866841	1.7
	314809	AI741461	Hs.161904	ESTs	1.7
	320361	H67220	Hs.146406	nitrilase 1	1.69
15	324721	AW402302	Hs.43618	ESTs	1.69
	328624			CH.07_hs gi 5868246	1.69
	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjugating enzyme [M.musculus]	1.69
	328960			CH.08_hs gi 6456775	1.69
	315702	AA657501	Hs.146315	ESTs	1.69
20	302385	AJ224172	Hs.204096	lipophilin B (uteroglobin family member); prostatein-like	1.68
	319699	R14537		EST cluster (not in UniGene)	1.68
	309506	AW137700		EST singleton (not in UniGene) with exon hit	1.68
	330417	D64424	Hs.57697	hyaluronan synthase 1	1.68
	315296	AA876905	Hs.125286	ESTs	1.68
25	328538			CH.07_hs gi 5868485	1.68
	323923	AA354146		EST cluster (not in UniGene)	1.68
	320303	AL079289	Hs.137154	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 35971	1.68
	302987	AJ927068	Hs.110853	ESTs; Weakly similar to R10D12.12 [C.elegans]	1.68
	310696	AI472124	Hs.157757	ESTs	1.68
30	307512	AI273815	Hs.242463	keratin 8	1.68
	338506			CH22_EM:AC005500.GENSCAN.390-10	1.68
	331722	AA195405	Hs.110347	Homo sapiens mRNA for alpha integrin binding protein 80; partial	1.68
	301431	R05385		EST cluster (not in UniGene) with exon hit	1.68
	318853	Z42977	Hs.21062	ESTs	1.68
35	323032	AW244073	Hs.145946	ESTs	1.68
	317538	AW137772	Hs.185980	ESTs	1.68
	325780			CH.14_hs gi 6381953	1.67
	321739	AL080280		EST cluster (not in UniGene)	1.67
	319808	T58960		EST cluster (not in UniGene)	1.67
40	313443	AA249037		EST cluster (not in UniGene)	1.67
	331366	AA424754	Hs.43149	ESTs	1.67
	316443	AI797592	Hs.207407	ESTs	1.67
	322878	AA081820		EST cluster (not in UniGene)	1.67
	330320			CH.08_p2 gi 5932415	1.67
45	329081			CH.X_hs gi 5868602	1.67
	334026			CH22_FGENES.318_3	1.67
	317791	AI801500	Hs.128457	ESTs	1.67
	322235	AF086106		EST cluster (not in UniGene)	1.66
	331148	R73816	Hs.17385	ESTs	1.66
50	325452			CH.12_hs gi 5866941	1.66
	315106	AW452184	Hs.232100	ESTs	1.66
	326014			CH.16_hs gi 5867160	1.66
	307130	AI185234		EST singleton (not in UniGene) with exon hit	1.66
	300943	AA524545	Hs.224630	ESTs	1.66
55	319402	W21298		EST cluster (not in UniGene)	1.66
	310889	AI457946	Hs.170437	ESTs; Weakly similar to hyperpolarization-activated; cyclic nucleotide-gated channel 2 [H.sapiens]	1.66
	323371	AL135118		EST cluster (not in UniGene)	1.66
	335568			CH22_FGENES.581_4	1.66
	320654	AW263086	Hs.118112	ESTs	1.66
60	338983			CH22_DA59H18.GENSCAN.3-1	1.65
	330002			CH.16_p2 gi 6623963	1.65
	315343	AW205477	Hs.179891	ESTs	1.65
	334487			CH22_FGENES.395_9	1.65
	312169	AI064824	Hs.193385	ESTs	1.65
65	309668	AW204480	Hs.253414	EST	1.65
	309518	AW148928	Hs.248895	EST	1.65
	307965	AI421841		EST singleton (not in UniGene) with exon hit	1.65
	316787	AW369770	Hs.130351	ESTs	1.65
	300835	AA401858	Hs.224843	ESTs	1.65
	338763			CH22_EM:AC005500.GENSCAN.517-16	1.65
	303327	AA232729	Hs.154302	ESTs	1.65
	313231	AW139993	Hs.163682	ESTs	1.65

	334073		CH22_FGENES.327_28	1.65
	319901 T77136	Hs.8765	RNA helicase-related protein	1.65
	326530		CH.19_hs gjl5867441	1.65
5	301126 AI802877	Hs.210843	ESTs; Weakly similar to dJ1039K5.2 [H.sapiens]	1.65
	314043 AA827082		EST cluster (not in UniGene)	1.65
	304387 AA236027		EST singleton (not in UniGene) with exon hit	1.65
	322932 AA099732		EST cluster (not in UniGene)	1.65
	337272		CH22_FGENES.660-1	1.64
10	332694 AA262768	Hs.243901	KIAA1067 protein	1.64
	318996 Z44266		EST cluster (not in UniGene)	1.64
	315336 AW342028	Hs.256112	ESTs	1.64
	313329 AW293704	Hs.122658	ESTs	1.64
	318088 AW295409	Hs.137945	ESTs	1.64
	313835 AI538438	Hs.159087	ESTs	1.64
15	320035 AA378974	Hs.130720	ESTs; Weakly similar to CELLULAR NUCLEIC ACID BINDING PROTEIN [H.sapiens]	1.64
	309372 AW074330		EST singleton (not in UniGene) with exon hit	1.63
	324157 AW402236		EST cluster (not in UniGene)	1.63
	323929 AA354940	Hs.145958	ESTs	1.63
	302490 AA885502	Hs.187032	ESTs	1.63
20	333942		CH22_FGENES.301_8	1.63
	327469		CH.02_hs gjl5867772	1.63
	301918 AA476777		EST cluster (not in UniGene) with exon hit	1.63
	315664 AI744068	Hs.160712	ESTs	1.63
	304405 AA282572		EST singleton (not in UniGene) with exon hit	1.63
25	310624 AI341594	Hs.157522	ESTs; Moderately similar to env protein [H.sapiens]	1.63
	319250 F11623		EST cluster (not in UniGene)	1.63
	310608 AI962234	Hs.196102	ESTs	1.63
	317348 AI348076	Hs.831	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	1.63
	306513 AA989230		EST singleton (not in UniGene) with exon hit	1.63
30	320807 AA086110	Hs.188536	Homo sapiens clone 24836 mRNA sequence	1.63
	303710 AI269069	Hs.250652	ESTs; Highly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	1.63
	328291		CH.07_hs gjl5868363	1.63
	304236 W93278		EST singleton (not in UniGene) with exon hit	1.63
	317683 AI791700	Hs.127893	ESTs	1.63
35	311960 AW440133	Hs.189690	ESTs	1.62
	312834 AI028309	Hs.114246	ESTs	1.62
	325326		CH.11_hs gjl5866875	1.62
	313663 AI953261	Hs.169813	ESTs	1.62
	327526		CH.02_hs gjl6381882	1.62
40	300429 AW449679	Hs.158739	ESTs; Highly similar to XG GLYCOPROTEIN PRECURSOR [H.sapiens]	1.62
	305169 AA663131		EST singleton (not in UniGene) with exon hit	1.62
	316621 AI021996	Hs.122138	ESTs	1.62
	329666		CH.14_p2 gjl6272129	1.62
	318035 AI744130	Hs.131201	ESTs	1.62
45	300492 AL031709		multiple UniGene matches	1.62
	316532 AI307229	Hs.184304	ESTs	1.62
	332048 AA496019	Hs.201591	ESTs	1.62
	307113 AI183686		EST singleton (not in UniGene) with exon hit	1.62
	319127 N49476		EST cluster (not in UniGene)	1.62
50	331155 R87650	Hs.33439	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.61
	338220		CH22_EM:AC005500.GENSCAN.246-9	1.61
	315763 AW515270	Hs.118342	ESTs	1.61
	323571 AA984133	Hs.153260	c-Cbl-interacting protein	1.61
	312240 R28628	Hs.203669	ESTs	1.61
55	304569 AA490934		EST singleton (not in UniGene) with exon hit	1.61
	313179 AI076101	Hs.131704	ESTs	1.61
	326858		CH.20_hs gjl6552462	1.61
	317276 AI823847	Hs.129986	ESTs	1.61
	312572 AA350125	Hs.187499	ESTs	1.61
60	311932 AW451654	Hs.257482	ESTs	1.61
	302103 AA452310	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	1.61
	308413 AI636253	Hs.196511	EST	1.61
	310077 AI620617	Hs.148565	ESTs	1.61
	337780		CH22_EM:AC000097.GENSCAN.121-2	1.61
65	327796		CH.05_hs gjl5867962	1.61
	308352 AI610791		EST singleton (not in UniGene) with exon hit	1.61
	324539 AI378032	Hs.125892	ESTs	1.61
	303232 AA437414		EST cluster (not in UniGene) with exon hit	1.61
	337884		CH22_EM:AC005500.GENSCAN.54-2	1.61

5	303620	AA397546	Hs.119151	ESTs	1.61
	303481	AA336839		EST cluster (not in UniGene) with exon hit	1.61
	314481	AA548589	Hs.105846	ESTs	1.61
	300327	AI908894	Hs.245893	ESTs	1.6
	323473	AA262442		EST cluster (not in UniGene)	1.6
10	326154			CH.17_hs gij5867170	1.6
	331920	AA446865	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.6
	323827	AW406878		EST cluster (not in UniGene)	1.6
	322452	W56710		EST cluster (not in UniGene)	1.6
	310597	AI739071	Hs.158515	ESTs	1.6
15	307871	AI388665		EST singleton (not in UniGene) with exon hit	1.6
	322215	AF088005		EST cluster (not in UniGene)	1.6
	318420	AI139857	Hs.143837	ESTs	1.6
	332217	H98987	Hs.102383	EST	1.6
	324937	M79230	Hs.182398	ESTs	1.6
20	320543	AF052176	Hs.158529	Homo sapiens clone 24457 mRNA sequence	1.6
	300674	AW467388		EST cluster (not in UniGene) with exon hit	1.6
	315193	AI241331	Hs.131765	ESTs	1.6
	319713	R24204		EST cluster (not in UniGene)	1.6
	301210	AI379982	Hs.158944	ESTs	1.6
25	309365	AW072861		EST singleton (not in UniGene) with exon hit	1.6
	321403	AW451454	Hs.247568	adenylate kinase 3	1.6
	321908	AA376936	Hs.20998	ESTs	1.6
	303349	AA382661		EST cluster (not in UniGene) with exon hit	1.6
	324338	AL138357	Hs.247514	ESTs	1.6
30	310599	AW300144		EST cluster (not in UniGene)	1.6
	333193			CH22_FGENES.98_15	1.6
	336433			CH22_FGENES.825_12	1.6
	312097	AI352096	Hs.157169	ESTs	1.6
	311445	AW204237	Hs.192703	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.59
35	317736	AI361722	Hs.192410	ESTs	1.59
	308147	AI498991		EST singleton (not in UniGene) with exon hit	1.59
	313489	AA017492	Hs.135655	ESTs	1.59
	316289	AA902488	Hs.122952	ESTs	1.59
	326983			CH.21_hs gij5867657	1.59
40	314781	AW205298	Hs.202372	ESTs	1.59
	328397			CH.07_hs gij5868397	1.59
	331970	AA461084	Hs.187677	ESTs	1.59
	321744	N91419	Hs.12028	ESTs	1.59
	310509	AI292181	Hs.150036	ESTs	1.59
45	315921	AI147545	Hs.114172	ESTs	1.59
	322049	AI928242	Hs.144383	ESTs	1.59
	301161	AA731518		EST cluster (not in UniGene) with exon hit	1.59
	300548	AI026836	Hs.114689	ESTs	1.59
	319142	F07366		EST cluster (not in UniGene)	1.59
50	313526	AW152263	Hs.249243	ESTs	1.59
	305937	AA883238		EST singleton (not in UniGene) with exon hit	1.58
	330123			CH.19_p2 gij5671869	1.58
	327819			CH.05_hs gij5867988	1.58
	318250	AI478814	Hs.134603	ESTs	1.58
55	306760	AI034094	Hs.169476	tubulin; alpha; ubiquitous	1.58
	322358	AA220235	Hs.246836	ESTs	1.58
	317866	AI690269	Hs.201345	ESTs	1.58
	320725	AA703319	Hs.120967	ESTs	1.58
	311332	AW292247	Hs.255052	ESTs	1.58
60	334893			CH22_FGENES.452_7	1.58
	318730	AA398215		EST cluster (not in UniGene)	1.58
	315889	AW271639	Hs.221744	ESTs	1.58
	303702	AW500748	Hs.224961	ESTs; Weakly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	1.57
	315086	AI492660	Hs.170935	ESTs	1.57
65	332514	AA156499	Hs.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.57
	335549			CH22_FGENES.576_10	1.57
	329532			CH.10_p2 gij3983505	1.57
	323140	AA180467		EST cluster (not in UniGene)	1.57
	313166	AI801098	Hs.151500	ESTs	1.57
	337896			CH22_EM:AC005500.GENSCAN.56-3	1.57
	330658	AA319514	Hs.211093	ESTs	1.57
	324585	AI823969	Hs.132678	ESTs	1.57

	317151	AW298195	Hs.255735	ESTs	1.57
	308818	AI819700	Hs.208231	EST	1.57
	326547			CH.19_hs gij5867307	1.57
5	318833	H06234	Hs.24888	ESTs	1.57
	320488	R31386		EST cluster (not in UniGene)	1.57
	306929	AI124514		EST singleton (not in UniGene) with exon hit	1.57
	338083			CH22_EM:AC005500.GENSCAN.174-1	1.57
	316868	AI660898	Hs.195602	ESTs	1.57
10	310937	AI472880	Hs.170480	ESTs	1.57
	328638			CH.07_hs gij6004473	1.57
	310074	AI651039	Hs.148559	ESTs	1.56
	327058			CH.21_hs gij6531965	1.56
	320076	AI653733	Hs.204079	ESTs	1.56
	322345	AF086529		EST cluster (not in UniGene)	1.56
15	314731	AI745498	Hs.204579	ESTs	1.56
	318687	H49619	Hs.127301	ESTs	1.56
	303841	AI934464		EST cluster (not in UniGene) with exon hit	1.56
	302370	AA009849	Hs.199297	Homo sapiens GNAS1 gene encoding NESP55	1.56
	322571	AF156271		EST cluster (not in UniGene)	1.56
20	318050	AI052093	Hs.133132	ESTs	1.56
	303388	AL039604		EST cluster (not in UniGene) with exon hit	1.56
	323758	AA833858		EST cluster (not in UniGene)	1.56
	328369			CH.07_hs gij5868388	1.56
	329415			CH.Y_hs gij5868874	1.56
25	303915	AW468839	Hs.257767	EST	1.56
	338794			CH22_EM:AC005500.GENSCAN.528-1	1.56
	303074	AA243481	Hs.127320	ESTs; Weakly similar to KIAA0346 [H.sapiens]	1.56
	318807	F08434		EST cluster (not in UniGene)	1.56
	334287			CH22_FGENES.369_17	1.56
30	311928	AW024798	Hs.233374	ESTs	1.55
	304582	AA505833	Hs.162017	EST	1.55
	300785	AA682913	Hs.247179	ESTs; Weakly similar to KIAA0319 [H.sapiens]	1.55
	304921	AA603092		EST singleton (not in UniGene) with exon hit	1.55
35	324605	AW502851	Hs.249978	ESTs	1.55
	324473	AW501163		EST cluster (not in UniGene)	1.55
	300566	H86709	Hs.21371	son of sevenless (Drosophila) homolog 1	1.55
	314165	AA761265	Hs.221281	ESTs	1.55
	302868	AA157392		EST cluster (not in UniGene) with exon hit	1.55
40	314034	AI299137	Hs.154214	ESTs	1.55
	325389			CH.12_hs gij5866921	1.55
	331849	AA417078	Hs.193767	ESTs	1.55
	320536	AA331732	Hs.137224	ESTs	1.55
	303347	AA258033		EST cluster (not in UniGene) with exon hit	1.55
45	315769	AA744875	Hs.189413	ESTs	1.55
	317031	AA973297	Hs.126101	ESTs	1.55
	300203	AI827065	Hs.224877	ESTs	1.55
	304037	T26438		EST singleton (not in UniGene) with exon hit	1.55
	322613	AW160507		EST cluster (not in UniGene)	1.54
50	317987	AW138174	Hs.130651	ESTs	1.54
	322313	AF086386		EST cluster (not in UniGene)	1.54
	323992	AW411383	Hs.169688	ESTs	1.54
	325303			CH.11_hs gij5866908	1.54
	312701	AI457663	Hs.128127	ESTs	1.54
55	304787	AA582678		EST singleton (not in UniGene) with exon hit	1.54
	305849	AA861571		EST singleton (not in UniGene) with exon hit	1.54
	314557	AA401367	Hs.128647	ESTs	1.54
	316507	AI381515	Hs.158381	ESTs	1.54
	315023	AA533505	Hs.185844	ESTs	1.54
60	314920	AA513406	Hs.152307	ESTs	1.54
	323097	Z44354	Hs.180950	guanine nucleotide binding protein (G protein); q polypeptide	1.54
	325043	W27919	Hs.32944	inositol polyphosphate-4-phosphatase; type I; 107kD	1.54
	307892	AI376086	Hs.158759	EST	1.54
	324573	AA491600	Hs.161942	ESTs	1.54
	313092	AI923673	Hs.212827	ESTs	1.54
65	324696	AA641092	Hs.257339	ESTs	1.54
	303019	AF098363		EST cluster (not in UniGene) with exon hit	1.54
	317158	AI459140	Hs.129109	ESTs	1.54
	309536	AW151933		EST singleton (not in UniGene) with exon hit	1.54
	301568	AI146423	Hs.146709	ESTs	1.53

	315674	AA651923	Hs.191850	ESTs	1.53
	321861	N79341		EST cluster (not in UniGene)	1.53
	310690	AI184510	Hs.143728	ESTs	1.53
5	330036			CH.17_p2 gl 6042048	1.53
	316907	AA843868	Hs.190567	ESTs	1.53
	312299	AA972712	Hs.174818	ESTs	1.53
	331128	R51361	Hs.23423	ESTs	1.53
	305177	AA663591		EST singleton (not in UniGene) with exon hit	1.53
10	337685			CH22_EM:AC000097.GENSCAN.77-1	1.53
	335290			CH22_FGENES.527_3	1.53
	308896	AI858667		EST singleton (not in UniGene) with exon hit	1.53
	307944	AI418246		EST singleton (not in UniGene) with exon hit	1.53
	300867	AW340374	Hs.121033	neural precursor cell expressed; developmentally down-regulated 1	1.53
15	335320			CH22_FGENES.534_7	1.53
	329841			CH.14_p2 gl 6672062	1.53
	317916	AI565071	Hs.159983	ESTs	1.53
	332901			CH22_FGENES.36_2	1.53
	305413	AA724659		EST singleton (not in UniGene) with exon hit	1.53
20	316707	AI016387	Hs.184406	ESTs	1.53
	313693	AW469180	Hs.170651	ESTs	1.53
	316101	AA922236	Hs.221037	ESTs	1.53
	320796	AF038966	Hs.184543	secretory carrier membrane protein 1	1.53
	307451	AI248615		EST singleton (not in UniGene) with exon hit	1.53
25	323648	AI679968	Hs.152060	ESTs	1.53
	331482	N27515	Hs.40296	ESTs	1.53
	318059	AI023175	Hs.167022	ESTs	1.53
	325958			CH.16_hs gl 5867142	1.53
	315736	AA664265	Hs.230213	ESTs	1.53
30	314740	AW015667	Hs.119427	ESTs	1.52
	314117	AA224368	Hs.185164	ESTs	1.52
	301648	AA313954		EST cluster (not in UniGene) with exon hit	1.52
	338752			CH22_EM:AC005500.GENSCAN.513-10	1.52
	309314	AW009312		EST singleton (not in UniGene) with exon hit	1.52
35	301445	AI208364	Hs.128233	ESTs; Weakly similar to REGULATOR OF CHROMOSOME CONDENSATION [H.sapiens]	1.52
	308501	AI885263	Hs.201150	EST	1.52
	312330	AA635305	Hs.121574	ESTs	1.52
	318040	AI018150	Hs.148781	ESTs	1.52
40	336205			CH22_FGENES.719_10	1.52
	325701			CH.14_hs gl 5867028	1.52
	315009	AW189460	Hs.208358	ESTs	1.52
	303121	AW407585	Hs.27769	ESTs; Weakly similar to mCAC [M.musculus]	1.52
	309271	AI986221		EST singleton (not in UniGene) with exon hit	1.52
45	328385			CH.07_hs gl 5868395	1.52
	307700	AI318545		EST singleton (not in UniGene) with exon hit	1.52
	314591	AW103292	Hs.245328	ESTs	1.52
	304484	AA432067	Hs.258373	ESTs	1.52
	304382	AA232873		EST singleton (not in UniGene) with exon hit	1.52
	304232	W52674		EST singleton (not in UniGene) with exon hit	1.52
50	309853	AW298169	Hs.57553	tousled-like kinase 2	1.52
	312504	AW207346	Hs.143202	ESTs	1.52
	313134	N63406	Hs.258697	ESTs	1.52
	330391	AF015950	Hs.115256	telomerase reverse transcriptase	1.52
	314342	AI873046	Hs.258775	ESTs	1.51
55	305977	AA887293		EST singleton (not in UniGene) with exon hit	1.51
	301165	N85789	Hs.224155	ESTs; Weakly similar to PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE [H.sapiens]	1.51
	300613	AI932294	Hs.249604	ESTs; Weakly similar to B-CELL LYMPHOMA 6 PROTEIN [H.sapiens]	1.51
60	324124	AI554212	Hs.185664	ESTs; Weakly similar to SERINE/THREONINE-PROTEIN KINASE NRK2 [H.sapiens]	1.51
	308037	AI458207	Hs.174181	ESTs	1.51
	323909	AL043148	Hs.186257	ESTs	1.51
	315464	AW139500	Hs.116135	ESTs	1.51
	308700	AI022056		EST singleton (not in UniGene) with exon hit	1.51
65	337976			CH22_EM:AC005500.GENSCAN.107-1	1.51
	306855	AI083982		EST singleton (not in UniGene) with exon hit	1.51
	311045	AI568399	Hs.174746	ESTs	1.51
	315010	AA531082	Hs.240049	ESTs	1.51
	310205	AW025248	Hs.202445	ESTs	1.51
	310759	AW135924	Hs.224883	ESTs	1.51

	310954	AW449044	Hs.171298	ESTs	1.51
	312019	T77046	Hs.188750	ESTs	1.51
	334773			CH22_FGENES.430_5	1.51
5	332043	AA490831	Hs.125056	ESTs	1.51
	322950	AA296219		EST cluster (not in UniGene)	1.51
	337920			CH22_EM:AC005500.GENSCAN.67-3	1.51
	328993			CH.09_hs gij5868536	1.51
	309245	AI972447		EST singleton (not in UniGene) with exon hit	1.51
10	312172	AI222168	Hs.191168	ESTs	1.51
	304039	T47349		EST singleton (not in UniGene) with exon hit	1.5
	301329	AI149653	Hs.190496	ESTs	1.5
	313376	AI949246	Hs.200381	ESTs	1.5
	324248	AW504918		EST cluster (not in UniGene)	1.5
15	308771	AI809301		EST singleton (not in UniGene) with exon hit	1.5
	334935			CH22_FGENES.464_3	1.5
	319764	AA019827		EST cluster (not in UniGene)	1.5
	318519	T27135		EST cluster (not in UniGene)	1.5
	332807			CH22_FGENES.7_9	1.5
20	322310	AF086376		EST cluster (not in UniGene)	1.5
	324557	AA489166	Hs.156933	ESTs	1.5
	332118	AA609585	Hs.162689	EST	1.5
	319539	R09027		EST cluster (not in UniGene)	1.5
	313149	AW291092	Hs.201058	ESTs	1.5
25	329722			CH.14_p2 gij6065785	1.5
	323514	AA861209		EST cluster (not in UniGene)	1.5
	308078	AI472621		EST singleton (not in UniGene) with exon hit	1.5
	337965			CH22_EM:AC005500.GENSCAN.100-10	1.5
	335905			CH22_FGENES.635_13	1.5

TABLE 14A shows the accession numbers for those primekeys lacking unigeneID's for Table 14. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Pkey	CAT number	Accession
	322064	234514_1	BE261397 Z78343 BE176419 AA383657 N90640 AA334052 AW955761 BE536232 AA374087 AA584776
20	321409	197898_1	N71838 AA282003 T54072 AA761419 H92966 AI831371 AI095435 AI690247 R99331 AW964110 AA975590 AA346128 H94196 C03864
	322092	46678_1	AF085833 R69689 AW341677 AA923375 BE327566 AW630415 R69601 AW615339
	321452	212379_2	AW962489 H64300 AA329527
	313603	199797_1	AA284333 AW468119 AA284334 AA810992
25	320856	36098_1	AB040928 T94673 AI289313 AI536039 Z44366 BE141499 D60116 D61488 D59945 AA419503 R28090 R72986 H03255 AI189112 AI912312 AW511018 AI401349 AW470144 C14624 AI335797 Z40300 AI014456 D60269 D60115 T16722 AI370673 D60270
	322139	46806_1	H53744 AF075088 H53797
	321500	552826_1	BE004271 AI248023 AI022157 H71999
30	313733	441212_1	AA766346 AA809877 AA836116 AW469598 AW977404
	322215	47002_1	AF088005 N51816 N51731
	322235	47070_1	AF086106 AI193589 AW665594 N71795 AA722627 AW665373 AI300251
	321632	286374_1	AW812795 AA419617 H87827 AW299775 AW382168 AW382133 BE171659 AW392392 BE171641 AA541393
	313833	120893_1	AA766825 AA811180 AA085906 AI762946 AW977820
	322310	47376_1	AF086376 W77804 W72689 AA837735
35	322313	47386_1	AF086386 W77947 W72708
	322322	47434_1	AF086431 AA886756 AI557237
	322331	47467_1	AF086467 W81444 W81445
	322345	47537_1	W95298 AF086529 AI912190 AW294159 AI458747 W94782
40	322347	47545_1	AF086538 W95969 AI631911 W95835
	322370	187612_1	AA330095 W25112 AA249401
	321739	43998_1	AL080280 T73124 H02689 AL080281
	321781	1511778_1	D78667 D78871 C18258
	314570	280469_1	AA904776 AA405695 AA405962
	300129	635249_1	AW028820 AI219068
45	322452	497108_2	AI147202 W56755 W56710
	321861	1651920_1	N79341 N99082 N47551
	323140	159551_1	AA180467 AA449184 AA464831 AA505048
	322520	38916_1	T55958 T57205 AF147346
50	321914	85114_1	AA011603 N58604 N58611
	322571	22297_1	NM_016102 AF156271 AA781868 AW152318 AW770403 AA909463 AA482996 AA758672
	322574	39412_1	AF156548 AA639797 AI675267 AI825497 AI823355
	314753	311451_1	AA463262 AA463615 AW160405 AW407583
	300370	3910_2	AW136181 AA581939 AK001221 AA694538 AA424043 AI016272 AA098960 AA884473 AI356180 BE391633 AA437086 AI277866 AA098827 AA992680 BE172624 AA424101 AA320776 AW962967 N77431 AW858960 AW858897 T85649 AA357743 AI827817 AI905672
55	322601	577912_1	AI082395 W92924 BE048524 AW005302 AI084474 AI369330 AI827710 AW135506 AW298694
	322613	34330_1	AW160507 NM_013367 AF191338 AA384939 AI445790 AA730309 BE397003 BE267753 AI979163 N50386 AW583671 AW583608 BE074466 BE074479 BE074471 AW976283 AA604393 AW162122 W73648 AI823475 N75898 W73713 AW470099 AW513236 AW025055 AW613115 AI923379 W58081 AW664525 AW196795 AI143619 AI565152 AA025406 AA505846 AI685494 AA829984 N59156 N59163 R15442 AA826919 AI610221 AI200120 AA603279 AW150822 AI189513 AI807122 AI016368 AI335868 AW583389 AI193892 AI956157 AI628879 AW591589 AW583446 AI955406 AW148396 AI340255 AI667942 AA748525 AA876991 Z38516 AI874002 AI869474 N63100 AA429094 AA082443
	316055	409389_1	AW105663 AA693880 AW517398 AI768507 BE220851 AW978538 AA831489
	323316	981459_1	BE219300 BE327455 AI134620 R36741 R17996
65	300492	25768_1	AL031709 AI249061 AA907658 AI20444

316141	423880_2	AW303457 AA972713 AA724265
323371	117336_2	N45114 N51465 BE087338 AI083551 AL135118 BE395609
307700	30923_11	BE280998 BE254670 BE294951 BE564879 AW405364 AA069256 AA129837 AI559667 BE281405 AW410850 BE041153
5		AI254811 AW301340 AI613335 AW301411 AI609469 AI611607 AI611616 AI377623 AI335509 AI613544 BE043165 AI371663
		AI340452 AI612066 AW072890 AI254558 AI349884 AI370095 AI613383 AI611946 AI613353 AI307414 AI318229 AI612685
		AW305327 AW268924 AI370063 AI349292 BE049068 AI369098 AW274098 AI344845 AW075187 AI053401 AI345220
		BE138515 AI613386 AI583302 AW301955 AI349661 AI307432 AI054168 AI223913 AI612081 AI348942 AI334539 AI309366
10		AI370098 AI252360 AW086316 AW268911 AW073482 AI379802 AI224284 AI053661 AI334538 AI309369 AI309688 AI310023
		AI492709 AI335418 AI053999 AI366989 AW073478 AI247058 AI249584 AI305875 AI308585 AW071272 AI271487 AI340719
		AI366995 AI223673 AW271066 AI611936 AW071296 AI270796 AI254385 AI251393 AI252562 AW268236 AI254858
		AW071317 AI309102 AI609897 AW268971 AI583267 AI792484 AW075168 BE138443 AI254126 AI309622 AI310872
		AI611953 AI251054 AW276658 AI335405 AW075039 AI311768 AI612028 AW271895 AI612005 AI312240 AW271082
		AI371642 AI334879 AI310194 AI310772 AI345419 AI334675 AI223914 AI284707 AI284813 AI349140 AI254853 AI313094
15		AI310170 AI309499 AI312476 AI376484 AI335467 AI340802 AI309815 AI310168 AI611446 AI345824 BE327775 AI318545
		F17185 AW614950
	308362 792518_1	AW998989 AI613519
	307783 697809_1	AI347274 AW844024
	301161 427238_1	AA731518 AA765714
	324094 270098_1	BE395109 AW663898 AW237041 AI492154 BE046906 AI651285 AI983290 AW002590 AI201040 F32424 AA992272
20		AW271836
	309023 4737_1	AF180681 NM_015313 AA229509 AA225792 AA216413 AI888045 BE005205 AB002360 T55518 BE276097 AW380669
		BE142836 AW370976 AA479384 R96425 AI680999 AA595138 H54582 AI022709 T55440 AI041769 AA861144 AW392028
		AA479287 AA824634 AI638446 H54691 R96382 AA770352 AI640467 AW293491 AA779138 R28298 AA970562 C15590
25		R64455 AA020769 AL036394 H80566 BE548861 AA301207 AW959414 AI284253 AA043173 W52429 BE544571 R24852
		Z42603 F13120 R24340 R24326 T75305 H70110 N56255 AA334210 F11453 AW947285 H80345 AA298992 AW380931
		AI267175 Z45421 AW380981 W86113 AA663590 AA167577 BE566760 BE169166 AA449904 AA459205 N31126 W03564
		N31208 AW993277 N44765 AW605275 D61449 W68572 AA258190 D60496 AW992964 U46277 H04097 AA370360
		AW957211 AA159775 AI631243 H83367 H21671 D61077 AW392712 N21112 H98522 N45298 N83629 AI93509 AW022043
30		AA744886 AI580482 AA723286 AI422244 AI423984 D62804 AI088349 AA587890 AI144172 N33275 BE074397 H03399
		D62578 AI056639 AI829918 AA579584 AI089460 AI350124 W68573 AI580828 H98897 AI570468 H83715 W86114 AA923123
		D57446 AA043174 AW337721 AI266551 AI140017 AW022356 D79855 D79650 D79393 D60495 AA788666 AA693443
		AW516977 W60139 AI628156 AW473223 AI608892 AA159670 AW440366 AI421529 T50751 AI174374 AA912234 AA724248
		AW780400 AA907218 H80514 D57452 AA863419 AA552618 D29614 R44556 T16452 R44935 Z41132 D29188 H69692
35		AI250176 AI078860 AA370359 AW183108 H74200 AA258183 F10723 C00323 R86148 AA860570 AW130073 AL079946
		AA410327 AA532614 AA234500 AI151507 AA410288 AW969639 AA483232 AI383200 AA236540 AI807672 H73441
	323473 193878_1	AA262442 AA768862 AA262443
	315639 392767_1	AA827650 AA827652 AW629526 BE044585 AW974451 AA761439 AA648505 AA765803
	322878 117013_1	AA081820 AA082191 AA079811
	301239 457668_1	AA807558 AA827117 AW629567
40	301256 16720_1	NM_016603 AF251038 AI124624 AA776579 AW298470 AI304868 AW082724 AI348442 BE218336 N20641 AI018013
		AW858832 AW978157 AA815187 AA932948 AF157316 AI444958 W00848 W02935 AI434933 N26335 AA428681 AW371059
		AI651612 AW134937 AW968911 AA488815 AL157523 W48766 AW936954 AW936941 AW579205 AW936886 AW936889
		N74541 AW936953 AW578421 AW604352 AW367088 AW849258 AW849453 AW371606 AI554921 W49785 H99814
		AA805957 AA904606 AW206696 BE169229 AA333951 AA190704 AW936944 AA463219 AA430306 AW805704 N48503
45		BE222307 AI638612 BE550045 AI605304 AI690987 AA776841 H12890 AW183731 AI380760 AI636261 AA812641
		AW592656 AI686132 AA843424 H99220 AW084996 AW128879 AI800871 AA610135 AA191524 AI150076 AI474530
		AA748461 N29013 AA746372 N59606
	300611 337193_1	N75450 AA877636 AW137945 W05248 AA514763 AW972399 AI758397 AW195051
	324157 247225_2	AW402931 BE393099
50	323509 967739_1	AL036947 T93676 T85475
	323514 197787_1	AA641735 AA281881 AA861209 AA934756 AA835887 AA641795 AA748822 AW295703
	300674 466093_1	AW467388 AA826954
	322932 39838_1	AF168711 AA098732 BE019157 AI380212 BE299159 AA249097 AA305112 AW962349 AW962353 AW401801 BE292961
		AI439469 AA442919 AI630537 AA724473 AI814288 AW966815 AI376871 AI860202 AI683132 AA099733 AW627633
55		AI754022 BE206347 AW183349 AI378222 BE178926 AI473282 W52944 AW752469 AW966817
	323591 209807_1	AA301270 AA301379 AA301366
	322950 10774_1	R85652 AA114024 AA296219 AA375304 AW963796 AW885952 AW020969 AA114025 AI804930 BE350971 AI765355
		AW317067 AW974763 H85930 AW172600 AI310231 AW612019 D62908 D62864 AA652738 AI674617 AI494064 AW138666
60		AI147620 AI147629 AW611793 AI668922 AI971005 AI864742 AA174171
	322957 29014_1	AK001701 AA134337 AA356202 BE163251 AW875175 AW875181 AW875177 BE163389 AK000741 AA247755 AA120819
		AW868040 AA309118 AW962348 AA471267 AW996843 AK001452 BE005344 BE617899 AA186588 AA120820 AW363311
		AA648105 N71529 BE168417 AW673900 AI858160 AA134338 AA659697 N22162 AI335437 AI311237 AI343171 AI336661
		AW268074 AW274348 AA935005 AW576295 AW262628 AW593153 AA730055 AA662650 AA782687 AW894855 AI933533
65		AW193002 AW899448 AW890142 AW812670 AA085664 AA334191 BE178085 BE180553 AA389680 AA984772 AA442527
		W26560 BE384359 AA847210 AW304931 AI669606 AA085613 AW197240 AI632828 AA581646 AW129348 AI017643
		AW089030 D20893 AI382955 AI557148 AW499979
	324231 975669_1	W60827 AL079868 AL047234
	324248 977901_1	AW504918 N55410 AL118594 AW839266
	323691 221757_1	AA317561 AI793000 AW235111 AI793178 AA767397 AI263113 AA719462

5	315858	406384_1	AA737345 AA682286 AI799378
	301431	569736_1	R05385 AI061251
	324303	233842_1	AL118754 AA333202 H38001
	324330	300543_1	AA884766 AW974271 AA582975 AA447312
	300815	41537_2	BE152396 BE152395 AA287515 BE001834 AA286678 AW406477
10	324349	1154015_1	AW501470 AW502931 AW499500
	323715	225129_1	AA322155 AA326396 AA326538
	309314	23273_3	AW009312
	323758	229624_1	AA833858 AW978090 AA327679 AA810438
	309375	127_1	AF286598 AW075342 AB028994 AL043713 AW378914 AA340650 N57166 AW956914 R17961 AA336481 BE393734
15			AW977867 AW294638 AA927857 AA961627 AW303969 AW894416 AA812119 AA912758 AA424355 AA490582 W30941
			AA476693 AA131029 AA127777 AL043714 AA496984 T51117 AA127722 AA594012 AI492876 N76483 AW119061 BE464926
			AW303419 AI972370 AI768172 AI826550 AI435432 AI379516 AA778421 AI276089 AA424521 N59361 AA723153 AA723176
			AI867487 AA090677 AI827221 AI351027 W02732 AI810729 AA142848 AI082110 N59379 N29744 AI283747 AI148665
			AW779845 AI382967 F34319 AI369934 AI282438 AW183449 AA863467 AA813469 AI092645 AI870701 AA863119
20	325031	266373_2	T65475 R07576 T17017 F08143 Z43546
	325045	1534945_1	T08845 Z43538 F06691
	324473	38795_1	BE560824 BE513941 AW238907 AA580852 AW501176 BE241846 AW501163 AW751433 AW501340 BE241715 AI910774
	323827	235506_1	AW406878 AW966560 AW966151 AW966496 AA336174 AA335376 AA335537
	302270	1734192_1	R56151 W91936
25	301618	10967_5	T52761 T52760
	301646	42154_1	AI277841 AI630669 AI804370 Z41939 AW751251 AA299456 Z44739 AW860471 Z30158 AW105391 H56997 W84688
			AA491201 W84636 AA706815 AI131055 AA483636 AI005075 AW340034 AI332372 AW118195 AI338932 AI191968
			AA693932 AI189982 AI193225 AA884163 AA594562 W37747 AA249754 AA746131 AI916540 AI832188 AW946555
			AA833838 Z40564 AA861563 F01447 AA887937 AI933559 AW973250 AA566018 AA313954
30	323923	249295_1	AA354146 AI184230 AA643525
	324580	328264_1	AA492588 AA492498 AA492571
	316774	463723_1	AA814859 AA814857 AI582623
	309577	6483_6	AW902251 AW168753
	302345	29533_1	X12830 NM_000565 AW503691 X58298 S72848 AA193347 AW503481 AW177946 AW178192 AW178188 AA285233
35	302358	1064753_1	AA410577 AA193465 AW177939 AW365459 BE221693
	324614	215437_1	AW207734 D60164 D81150 D81078 D61356 AW998604
	324661	385257_1	AW503101 AA309184 N56323 R70998
	324665	41003_1	AW504161 AW503601 AW505509
			AF226667 AA207032 AA100804 AA121287 AA488316 AI808218 AW419048 AI911097 AW132123 AA502311 AW089948
40	324692	351987_1	AA100952 AI075431 AW083432 AI990554 BE466029 F28643 AF086422 W79581 AW439007 F37179 W79780 AW439035
	316893	473541_1	AA731381 AW750380 AA251012 AW589846 AA730238 AA329792 AW087255 AA220982 AA082469 AA877260 AA232380
	303027	21796_1	BE298910
			AA557952 AA677593 AA618150
			AW979189 AA837332 AA856946 AA876935
45	324715	290035_2	AF111178 NM_005708 AF105267 AW590040 AI979280 AA001322 BE146329 AA702430 AA702429 AA694221 AI206348
			AI206285 AW770197 AA923032 AI379586 AA701165 AW594643 AA001909 AW002368
			AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682
			AI928140 AA731438 AI092404 AI085630 AA731340
			AA631739 AA768584 AW134477
50	324783	389615_1	AA640770 AI683112 AA913009
	303114	37417_1	AF090948 AI064898 AI111182
	303124	21112_1	AB018257 BE148640 AA081832 AK001915 AF150217 AF161350 AI219174 AW074664 D60040 AA346065 H28750
			AW151783 BE613360 BE612628 BE502031 AW183790 AA992580 AA505815 AI310432 AI678015 AW592679 AA879181
			AA806708 AI744110 H24681 C16064 D62900 AI285033 AA346064 AI865123 AW467798 BE221231 AL120676 N89877
55	302552	82290_1	AI928370 AI358387 AA748486 AV647478 AV647460 AA312313 AI279340 AW505099
	301918	316229_1	AA005122 H49792
	303232	20474_1	AA476777 T86049
			AA437414 AA131479 AA086182 AB037775 AW161063 AW514393 AA332331 AW136197 BE150789 AA425533 AA249605
			N88308 AI016201 BE004662 AA291027 R57587 AA424277 AA476391 W07532 T97036 AA218898 AW162629 R57770
60			W01278 W90204 W90156 AL119197 R84513 AA280103 AA334994 AW965504 AA460868 AA447470 AW138594 W38898
			W90028 AI078353 W90078 AA699696 N35523 AA704225 AA035059 AW134892 AA115140 AI142854 H90084 AA826342
			AA460694 N46339 AA425344 N56953 AA035569 AI761083 AI658696 AI524818 AI338965 AW069249 AW299871 BE464061
			AI189720 AW340682 AI423380 AI275122 H17532 N80735 AA826343 AI039694 BE328398 AI192947 AW271286 AI623122
			AI922802 AW293087 N22141 AA730657 AW316610 N26473 F06683 Z43610 H14783 R59761 H11540 AI265915 AI681773
65	302696	33570_1	AI091748 BE220636 AW841861 AI702181 AI468447 AA907544 AI273941 AW244034 R37769 AA446663 T96929 BE045884
			AA476341 H89994 H29043 AW051211 N49522 AA306977
			AK000738 AA347452 AW961713 H70832 AI750643 AA362887 AW955588 W44974 AA279599 AW298762 AA452666
			AA443355 AI337273 AA446931 AI752977 AA661554 W42674 AI292172 R41163 AA621381 AI244157
			AJ001409 AJ001410
	309917	57485_2	AW340014 AW866993 AV651649
	303347	192210_1	AA258033 AA459485
	303349	193138_1	AA382661 AW958642 AA259088
	310599	690880_1	AW300144 AI338491 AI798381 BE220076

5	303388	869232_1	AL039604 AL039497
	302761	45074_1	AW250553 L07876 Z36843 R30693 AI190087 AW965317
	318455	606341_1	AI148763 AI903763 AI903753 AI903762 AI903800 AI903801
	317850	363835_1	AI681545 AI951714 AI570397 AW873588 AA836396 AI359986 AI499790 AA773477 AI951615 T07547 AW304709 AF114041
	303431	32082_1	BE176629 Z44580 T30422 T32690 AW953065 H10602
10			NM_000539 AA019013 AA019367 AA056154 H38735 AA057003 AA021051 H38102 AA015774 AA059291 AA019439 H84843
			H83375 AA019914 AA017288 R84449 W26519 H38258 AA018736 H84147 AA018577 AA059353 U49742 H38767 AA318341
			AA317553 H86646 H91989 AA317398 AA317378 W29024 W23034 T27877 AW950059 AA017195 R84262 AA057177
			H89941 AA019904 H84662 AA015775 AA019368 AA020976 H37900 C20733 H38682 H85197 AA018578 AA017252
			AA019440 AA059059 H38651 H84148 AA018560 W25754 C20752 AA317915 AW952115 AA317369 AA019845 R85402
15			AA019492 AA017196 AA056093 AA056094 AA058836 AA056155 W25957 W23027 AA056159 W23043 W21890 W28951
			AA317978 W26459 AA317265
	319127	1653640_1	N49476 Z45911 R21061
	303480	232749_1	AA331908 AA332484
	303481	31534_1	AK001952 AA336839 AW249271 BE247287 AF182002 BE613472 AW962673 AA332235 AW849937 AW849814 H49893
20			AA477148 AW968944 AF182003 AW007897 BE246145 W76100 AI480141 AW410205 AA609339 AI209111 W0000979
			AA330280 AW961554 W72865 H49894 AA514317 AA620407 AA504522 AW472833 AA716609 AW129282 AA347351
			AA628378 AW598960 AI636696 AA464632 AA464533 AW874189 AA757076 AA479654 AW517910 AW292357 AW872638
			AW262288 AI910666 AW513749 AW238771 AA215797 BE387073
	303487	20890_1	BE143533 AW850432 AK000042 AA333666 AA385314 AW966616 AW793068 AW793414 AA361103 AW390841 AA040095
25			AW385058 AW799162 AI383115 AI990745 AI653703 BE503693 AW150758 AI949919 AW190450 AW512348 AI625970
			AW501057 N52954 AI281378 AI401710 AI648409 AW002659 AI687639 AI093943 R33960 AA040062 AI926267 AI240425
			AI520911 AI093428 R52943
	303488	36085_1	AI040372 AB040915 W40569 BE158910 BE158914 D63226 AW025860 AW583088 AA334307 AA210942 AW753212
			AW805322 AA362635 BE158911 AW891225 AW994862 AA605451 R28541 AA229347 N48266 AI377788 R28682 R36122
30			AA811941 AI240742 AI632001 T99965 W01976 AW891205 AW891177 T97433 C15571 AA346850 AA504293 W07500
			AI694503 AA489216 AA327725 AW959917 AA694146 N68514 AI076285 AW016246 T07783 AA642400 AA716133 AA805332
			R00312 AA705021 AW498605 AW891723 AW891906 AA808025 N29039 N74897 W60393 AA810184 AI627460 AW057516
			AA807436 AA760966 AI359295 N78642 N20682 AA830300 W81705 AA832258 AW891718 AI811796 AW515523 Z41735
			AA449978 AW891714 AI684539 AW891896 AW071701 AI890916 AI924994 AI039743 AA888524 AA244214 AI015736
35			AI270105 AI865077
	303494	236389_1	F30712 F35665 AW263888 AI904014 AI904018 AA336927 AA336502
	319142	164820_1	H08370 Z46168 F07366 AA193168 AA193138
	302868	12593_1	AK000290 AI476034 AA465309 BE148761 AW303607 AW958665 AW469635 AI819365 AI243857 AW469326 AA157110
			AA278626 AA496257 AA306658 F29732 AA831859 AA312210 AA564476 AA579065 AA769522 AA740386 AI205635
40			AA491643 AA810400 AA417708 AI567332 AA157392 N53817 AA374229
	318518	1205335_1	R68545 T27119 R25687 AW750672
	318519	434741_1	H13364 T27135 R61679 AA746905
	304168	72494_-10	H77679
	302948	21445_1	AB038995 NM_016530 AK001111 AA465635 AW968716 U66624 AA885459 AA703019 AI040266 AI018689 AI692886
45			AI125372 AI376796 AI192040 N58161 AL133607 AW503673 AW505479 AA362265 AJ404671
	319250	244351_1	F11623 H17552 AA347728
	318644	17700_1	BE311816 AK000916 AW868037 AW868039 AF228527 AI752482 AW868041 AA077049 AI201537 W55873 AA206019
			AA077918 AW968729 AI978828 AW139620 AI093053 AW204025 AI418805 AA598928 AA586345 AA045669 BE314455
			AA045668
50	318674	204968_1	W01166 AW996900 BE184300 Z44887 T34535 R51495 AW888575 AA295490 AA295162 AA295163 AW937125 T56951
	304232	20640_2	BE386106 W52674
	303685	8088_1	AW500106 BE241915 AW503971 NM_016542 AB040057 AA313812 AK000556 W16504 AI822088 AA259107 AA191319
			BE085957 AA309584 BE122687 AW952435 T84469 BE088194 BE088132 AA328562 BE092674 AA263102 T39634
			AW992380 R79391 R24392 H03060 AW675066 AI299952 AW020325 D25953 N75199 AA361425 AW612302 AW236333
55			AW673897 AW953686 N22323 AA649166 AI377099 H03061 AI660072 AW276405 AA809779 AI803430 AW297484
			AW510384 AA814816 AA371522 D63035 AA953567 R79392 R24282 AA876831 AW297542 AI699023 AA992652 AI041436
	318704	799152_1	AI631602 AW589676 Z28684 Z24981
	318730	275116_1	Z32887 BE349923 AA398215 AA399231
	303714	1155758_1	AW501336 AW501337
60	304387	183612_1	AA236027 BE003275
	304398	10169_1	AA195509 BE394661 AV660757 AA489161 BE165972 AW503705 AA262785 AF123320 Z78357 NM_014171 AF161488
			AA248971 BE568575 AA461410 AA165108 AI637731 H75454 AA372934 AW339334 BE568754 BE564697 BE567299
			AI631606 BE537269 AW197204 AA290890 AI189393 AW292463 AW470227 F27399 AW611942 BE566888 AW301701
			AI675761 AI628429 AA164711 AI797753 AI656879 AI912690 AI675277 AI695099 AI094095 AW014158 BE091059 AI201748
65			AW236961 AI038003 AI083606 AA401606 AI079405 AI073516 AI655537 AA401475 AI814532 AI079862 AI093789 AI422084
			AI216476 AI392760 AA926998 AA781782 Z25198 AI086377 AI185511 AI185539 Z26843 AI223792 AI379563 AA706253
			AI433798 AI921885 H75455 AW025269 AI224100 AI083611 AI225057 AW196334 AI572254 AA761628 AI472801 AA283784
	303751	468554_1	AA830149 AW978407 M85983 AW503637
	319401	1323199_1	W00973 N56457 AW992226 T84921 R01342
	319402	1003489_1	R68913 R68901 H25352 R01370 H43764 AW044451 W21298
	318807	1536467_1	F08434 Z42573 H28810
	319478	765461_1	AI524124 R06841 R06842
	318872	1534581_1	Z43108 F06295 R13085

	318885	94880_2	AA742999 Z43272 AA345258 AW956677 AA031942
	303841	79133_1	W19657 BE616760 BE259848 BE382680 BE615587 AI934464 AA322745 T07155 AW961174 AA307302 Z41888 AA621992
			AA188400 AW770608 AI147458 AI148408 AI696291 AA972591
5	303889	1777183_1	T19204 T36109 T36107
	319539	63198_1	R09027 AA344892 AA329574 AW955648 AW978708 AI567804 AI378935 AW014657 AI804134 R08922 N92947 BE546788
	318905	1536408_1	F08365 Z43395 R54298
	320187	396254_1	T99949 AA654769 AA664550 AW975264
	318996	65715_1	Z44266 H06384 AV655948
10	319635	163534_1	R17531 AW960899 AA338366 AW673294 BE047729 BE047722 AA330746 AW841797 H05030 AI142105 R12654
	319699	747196_1	AI458682 H24240 R14537 R18426 AW867082
	319713	1699356_1	R24204 R15712 T84695
	319761	75324_2	AW630974 BE005208 R84237 AA724997 AA334867 AW955777 R18816
	319764	88596_1	AA019827 R18947 H46852
	319808	7069_3	T58960 AA609180 AA621130 AI927236 AA431075
15	321040	193331_1	AA261830 AW967855 H26953 AA262478
	320409	43709_1	AA226869 AA296516 AW959753 AA186390 AL359619 AA356195 AA148427 R22748 AI033624 BE548853 H95327
			AW579751 BE561649 AA397533 BE617136 AA236444 T89946 AA247450 N55777 W38725 AI743846 AI808406 AA922229
			AI051464 W04713 R11251 W19656 AI042319 AA489276 AI224533 H95274 AW269958 T89311 AI890088 AI862754
			AI830968 AI669336 AI589780 AA534557 AW273839 AI338155 AI126632 N83542 BE046048 AA807028 AA848107
20			AW167978 AA976930 AA148428 AI289304 AI524262 AI625961 AA773469 AI222288 AI280054 AI242371 AA227222
			AA973329 AA298517 AA829436 AA234526 AI149769 AI567865 AA936939 AI590681 AW469308 AI689531 AA486419
			AI422051 AI057252 AA626941 AI475352 AW247913 AI222370 AA670122 AW198034 AA486418 AI363794 AA380739
	319681	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
25	320488	368456_1	AI817336 R32883 AA595590 AI743065 R31386
	321121	1545647_1	W23285 H42714 F25381 F37215
	321205	81249_1	AA002047 N72537 H54142 H81580
	321253	375160_1	AA610649 AI689484 H59558
	314043	155125_1	AA827082 AA732246 AA167611 AA830741
	320630	17685_2	AA199847 AA410224 R53323 AW936567 AW936568 AW936571
30	313435	443527_1	AA769123 AA831715 AW977666 W92553
	313443	82292_1	AA005125 W95019 W93335 AA249037
	313472	82811_1	AA007374 AA007468 AI816886
	321348	41762_1	Z49979 D61703 U30168
	314138	179960_1	AA740616 AA654854 AA229923
35	320712	57156_2	R66867 R65678 R82673 W73128 R83101
	321383	41924_1	AW968556 AJ236555 AW968731 AJ002574 AA459446 H70260 AW977657 AA767351 AW268572 AA810719 AI698677
			AI300460 AA907450 AA649224 T07415 AI536896 BE018515 AI279865 BE047421
			AW368634 AI702169 AI245179 AW368646 BE545574 AA249018 AW368633 N27553
40	312996	187327_1	AA989230
	306513		AA991705
	306537		AA994530
	306557		AI000320
	306598		AI000929
	306620		AI022056
45	306700		AI472621
	308078		AI068544
	306813		AI075803
	306830		AI083982
	306855		
50	329722	c14_p2	
	329728	c14_p2	
	306890		AI092235
	308100		AI475949
	308147		AI498991
	306929		AI124514
55	308352		AI610791
	308383		AI624497
	308521		AI689808
	308561		AI701559
	308617		AI738720
60	308771		AI809301
	308828		AI824829
	308896		AI858667
	303019	41850_1	AF098363 AF098365
	303084	44211_1	AF174008 AF174027 AF174106
65	305092	AA642912	
	305169		AA663131
	305177		AA663591
	305235		AA670480
	305413		AA724659

	305849	AA861571
	305854	AA862733
	307113	AI183686
5	307130	AI185234
	305937	AA883238
	305977	AA887293
	307451	AI248615
	307513	AI274307
10	307848	AI364186
	307871	AI368665
	307881	AI370434
	307932	AJ230822
	307944	AI418246
	307954	AI419692
15	307965	AI421641
	309245	AI972447
	309271	AI966221
	309365	AW072861
	309372	AW074330
20	309435	AW090537
	309506	AW137700
	309536	AW151933
	309709	AW242630
25	325417 c12_hs	
	325450 c12_hs	
	325452 c12_hs	
	309815	AW292760
	309839	AW296076
	309849	AW297444
30	309906	AW339340
	302705 31765_1	U09060 U09061
	304037	T26438
	304039	T47349
	304236	W93278
35	304257	AA053294
	304382	AA232873
	304405	AA262572
	304561	AA489792
	304569	AA490934
40	304787	AA582678
	304921	AA603092
	327819 c_5_hs	
	304968	AA614308
	306382	AA968967
45	331263 47479_1	AW760192 AA015718 W02571
	332252 1663967_1	N63882 T91174

TABLE 14B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332807	Dunham, I. et.al.	Plus	297686-297808
332808	Dunham, I. et.al.	Plus	298277-298360
332812	Dunham, I. et.al.	Plus	309688-310561
332901	Dunham, I. et.al.	Plus	1841954-1842090
333149	Dunham, I. et.al.	Plus	3574317-3574413
333916	Dunham, I. et.al.	Plus	8298994-8299169
334026	Dunham, I. et.al.	Plus	9196549-9196681
334061	Dunham, I. et.al.	Plus	9686941-9687077
334073	Dunham, I. et.al.	Plus	9792201-9792374
334150	Dunham, I. et.al.	Plus	10529221-10529854
334379	Dunham, I. et.al.	Plus	13908356-13908467
334719	Dunham, I. et.al.	Plus	15778859-15779026
334773	Dunham, I. et.al.	Plus	16235169-16235328
334893	Dunham, I. et.al.	Plus	19302753-19302881
334935	Dunham, I. et.al.	Plus	20108247-20108373
335146	Dunham, I. et.al.	Plus	21491292-21491457
335320	Dunham, I. et.al.	Plus	22542132-22542246
335568	Dunham, I. et.al.	Plus	24935021-24935655
335586	Dunham, I. et.al.	Plus	24990333-24990497
335601	Dunham, I. et.al.	Plus	25044923-25045157
336036	Dunham, I. et.al.	Plus	29019796-29019877
336123	Dunham, I. et.al.	Plus	30051089-30051186
336268	Dunham, I. et.al.	Plus	31997555-31998040
337173	Dunham, I. et.al.	Plus	23624127-23624224
337460	Dunham, I. et.al.	Plus	32536159-32536395
337685	Dunham, I. et.al.	Plus	3547161-3547245
337736	Dunham, I. et.al.	Plus	3850500-3850643
337780	Dunham, I. et.al.	Plus	4113793-4113990
337965	Dunham, I. et.al.	Plus	7034267-7034392
337976	Dunham, I. et.al.	Plus	7166011-7166119
338030	Dunham, I. et.al.	Plus	8072708-8072827
338112	Dunham, I. et.al.	Plus	10391398-10391600
338165	Dunham, I. et.al.	Plus	12205719-12205875
338178	Dunham, I. et.al.	Plus	12800037-12800181
338427	Dunham, I. et.al.	Plus	19685043-19685354
338506	Dunham, I. et.al.	Plus	21221871-21221953
338794	Dunham, I. et.al.	Plus	27114697-27114763
338910	Dunham, I. et.al.	Plus	28795375-28795551
339047	Dunham, I. et.al.	Plus	30760793-30760968
332864	Dunham, I. et.al.	Minus	1390386-1390296
332933	Dunham, I. et.al.	Minus	2035790-2035681
333193	Dunham, I. et.al.	Minus	3832993-3832494
333712	Dunham, I. et.al.	Minus	7286177-7286073
333940	Dunham, I. et.al.	Minus	8523830-8523671
333942	Dunham, I. et.al.	Minus	8552629-8552330
334287	Dunham, I. et.al.	Minus	13294116-13293871
334387	Dunham, I. et.al.	Minus	13946021-13945781
334487	Dunham, I. et.al.	Minus	14432191-14432132
334913	Dunham, I. et.al.	Minus	19463909-19463815
335109	Dunham, I. et.al.	Minus	21325792-21325667
335250	Dunham, I. et.al.	Minus	21952922-21952826

	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335290	Dunham, I. et.al.	Minus	22309950-22309891
	335549	Dunham, I. et.al.	Minus	24666203-24666128
5	335862	Dunham, I. et.al.	Minus	26690300-26690125
	335864	Dunham, I. et.al.	Minus	26694537-26694382
	335905	Dunham, I. et.al.	Minus	26988888-26988719
	336205	Dunham, I. et.al.	Minus	30477456-30477311
	336276	Dunham, I. et.al.	Minus	32093320-32093181
10	336433	Dunham, I. et.al.	Minus	34067540-34067425
	336605	Dunham, I. et.al.	Minus	15616509-15616358
	336616	Dunham, I. et.al.	Minus	26021027-26020848
	336679	Dunham, I. et.al.	Minus	2035790-2035681
	337043	Dunham, I. et.al.	Minus	17407330-17407251
	337272	Dunham, I. et.al.	Minus	28241476-28241307
15	337357	Dunham, I. et.al.	Minus	30906179-30906109
	337393	Dunham, I. et.al.	Minus	31471747-31471569
	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337646	Dunham, I. et.al.	Minus	2648689-2648632
	337920	Dunham, I. et.al.	Minus	6051648-6051510
20	338083	Dunham, I. et.al.	Minus	9318438-9318301
	338220	Dunham, I. et.al.	Minus	14166440-14166104
	338752	Dunham, I. et.al.	Minus	26421374-26421135
	338763	Dunham, I. et.al.	Minus	26628148-26628009
	338983	Dunham, I. et.al.	Minus	29908865-29908702
25	339209	Dunham, I. et.al.	Minus	32492953-32492593
	325240	5866848	Minus	32301-32650
	329532	3983505	Plus	42937-43014
	329522	3983507	Minus	35265-35458
30	329519	3983510	Plus	18407-18597
	329511	3983514	Plus	20965-21325
	325326	5866875	Plus	47726-48024
	325303	5866908	Minus	73556-73630
	325369	5866921	Plus	239672-239759
35	325417	5866925	Minus	110635-110745
	325450	5866941	Minus	435379-435552
	325462	5866941	Minus	704103-704202
	325498	5866967	Plus	173372-173930
	325587	6682462	Plus	126724-126967
40	325602	5866994	Plus	79122-79251
	325701	5867028	Minus	72936-73046
	325780	6381953	Plus	63634-63873
	329722	6065785	Minus	112713-112992
	329728	6065785	Minus	207544-207741
	329666	6272129	Plus	98307-98446
45	329815	6624888	Minus	68431-68720
	329841	6672062	Minus	40181-40331
	325824	5867048	Minus	42450-42833
	325866	5867076	Minus	94358-94628
50	325902	5867101	Minus	127729-127842
	325958	5867142	Plus	53437-53550
	326014	5867160	Minus	10358-10447
	329941	6165199	Minus	34319-34411
	330002	6623983	Plus	46097-46158
55	326154	5867170	Minus	7103-7179
	326023	5867245	Plus	171799-171896
	326278	5867269	Plus	75250-75903
	330036	6042048	Plus	117120-117216
	326547	5867307	Minus	623677-623870
60	326495	5867423	Plus	11843-11930
	326507	5867435	Minus	13038-13111
	326505	5867435	Minus	8818-8949
	326506	5867435	Minus	9368-9509
	326530	5867441	Minus	303000-303122
65	326508	6682496	Plus	78904-79112
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326858	6552462	Minus	69337-69670
	326983	5867657	Minus	16023-16581
	327014	5867664	Plus	1017630-1017788

5	326930	6456782	Plus	606950-607705
	326920	6456782	Minus	42425-42519
	327058	6531965	Plus	2384268-2384835
	327061	6531965	Minus	3486389-3486673
	327075	6531965	Plus	4041318-4041431
10	327120	6531970	Minus	6-1088
	330126	6093735	Plus	82458-82623
	327157	5866841	Minus	4408-4746
	327183	5867442	Plus	84317-84531
	327192	5867445	Minus	194652-194764
15	327288	5867481	Plus	48583-48773
	327469	5867772	Plus	145549-145708
	327489	6004459	Minus	57796-58015
	327526	6381882	Minus	97010-97123
	327574	5867818	Plus	68767-69128
20	327685	5867839	Plus	141736-141900
	327752	5867949	Plus	93721-94421
	327819	5867968	Minus	92202-92717
	327796	5867982	Plus	85267-85405
	330260	6671884	Plus	45203-45269
25	330282	6671910	Plus	3982-4114
	328078	5868008	Plus	72807-72865
	328121	5868031	Plus	153782-153850
	328190	5868077	Plus	21082-21165
	328227	5868105	Minus	21082-21242
30	327871	5868131	Minus	88889-89221
	328018	5902482	Minus	542547-543133
	328624	5868246	Minus	120666-120836
	328744	5868290	Plus	138639-138722
	328799	5868316	Minus	80771-80923
35	328291	5868363	Minus	144244-144434
	328329	5868375	Plus	191709-192239
	328369	5868388	Plus	75371-75583
	328385	5868395	Plus	369952-370155
	328397	5868397	Plus	344967-345063
40	328412	5868405	Plus	86427-86519
	328538	5868485	Plus	3814-4243
	328656	6004473	Plus	792616-792729
	328638	6004473	Plus	294618-294903
	328903	5868514	Plus	23625-24468
45	328960	6456775	Plus	38547-38837
	330320	5932415	Minus	54458-54697
	328993	5868536	Plus	49160-50084
	329081	5868602	Plus	93368-93510
	329089	5868614	Plus	25805-26923
50	329109	5868626	Plus	102168-102273
	329192	5868716	Plus	166936-167020
	329218	5868726	Minus	71408-71707
	329224	5868728	Plus	27422-27664
	329246	5868732	Minus	250541-250792
	329415	5868874	Plus	1011438-1011818
	329454	5868887	Plus	51342-51593

TABLE 15: 169 GENES WITH SEQUENCE INFORMATION DEPICTED IN TABLE 16

Table 15 depicts UnigeneID, UnigeneTitle, Primekey, Predicted Cellular Localization, and Exemplar Accession for all of the sequences in Table 16. The information in Table 15 is linked by EosCode to Table 16.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 EosCode: Internal Eos name
 Localization: Predicted cellular localization of gene product

	Pkey	ExAccn	UnigeneID	Unigene Title	EosCode	Localization
	100394	D84276	Hs.66052	CD38 antigen (p45)	PBC1	plasma membrane
	100452	D87742	Hs.241552	KIAA0268 protein	PAB7	not determined
	101249	L33881	Hs.1904	protein kinase C, iota	OAA1	cytoplasmic
20	101485	M24736		selectin E (endothelial adhesion molecule	ACC5	plasma membrane
	101514	M28214	Hs.123072	RAB3B, member RAS oncogene family	PFJ2	cytoplasmic
	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor	LBH9	secreted
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	PDG3	
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	PFJ4	plasma membrane
25	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	LEM9	cytoplasmic
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	LBG2	plasma membrane
	103709	AA037316	Hs.13804	hypothetical protein dJ462O23.2	PDO6	
	104080	AA402971	Hs.57771	kallikrein 11	PBA6	secreted
	104144	AA447439	Hs.183390	hypothetical protein FLJ13590	PDM3	
30	104691	AA011176	Hs.37744	Homo sapiens beta-1 adrenergic receptor	PAV1	plasma membrane
	105370	AA236476	Hs.22791	transmembrane protein with EGF-like and	PDM9	plasma membrane
	106149	AA424881	Hs.256301	hypothetical protein MGC13170	PDO8	
	106579	AA456135	Hs.23023	ESTs	PAA4	plasma membrane
	107102	AA609723	Hs.30652	KIAA1344 protein	PAA3	not determined
35	107217	D51095		DKFZP586E1621 protein	PDG8	
	108153	AA054237	Hs.40808	ESTs	PBF1	plasma membrane
	109014	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	PDG7	
	109112	AA169379	Hs.257924	hypothetical protein FLJ13782	BCU4	not determined
	109890	H04649	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	PDG4	
40	110151	H18836	Hs.31608	hypothetical protein FLJ20041	PAV9	plasma membrane
	112971	T17185	Hs.83883	transmembrane, prostate androgen induced	CHA1	not determined
	113021	T23855	Hs.129836	KIAA1028 protein	PDO3	
	114908	AA236545	Hs.54973	cadherin-like protein VR20	PFJ6	plasma membrane
	114965	AA250737	Hs.72472	ESTs	BCY2	mitochondrial
45	116393	AA599463		hypothetical protein MGC2648	PDV3	secreted
	116416	AA609219	Hs.39982	ESTs	OAB6	
	117698	N41002	Hs.45107	ESTs	PDT9	ER
	117984	N51919	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	PAJ5	not determined
	118985	N94303	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	PDM8	
50	119018	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds		-PAB2 plasma membrane
	119126	R45175	Hs.117183	ESTs	PBF8	
	120992	AA398246	Hs.97594	KIAA1210 protein	PDG5	
	121710	AA419011		prostate androgen-regulated transcript 1	PDV5	
	121913	AA428062		ESTs; protease inhibitor 15 (PI15)	BCU7	vesicular
55	122041	AA431407	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT		PAZ1 not determined
	122593	AA453310	Hs.128749	alpha-methylacyl-CoA racemase	PDO1	
	123209	AA489711	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	PAA2	plasma membrane
	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	PAV4	plasma membrane
	126399	AA128075		transmembrane, prostate androgen induced	PDY4	
60	126645	AH167942	Hs.61635	six transmembrane epithelial antigen of	PAA5	plasma membrane
	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	PDO5	plasma membrane
	127537	AA569531	Hs.162859	ESTs	PAA6	not determined
	128790	AA291725	Hs.105700	secreted frizzled-related protein 4	BCX2	secreted
	129109	AA491295	Hs.108708	calcium/calmodulin-dependent protein kin	PFJ7	
65	129184	W26769	Hs.109201	CGI-86 protein	PAV6	vesicular
	129389	AA621604		spondin 2, extracellular matrix protein	CJA5	not determined

	129404	AA172056	ESTs	PAB4	
	129534	R73640	Hs.11260 hypothetical protein FLJ11264	PAJ3	secreted
	130760	AA128997	Hs.18953 phosphodiesterase 9A	PEE6	nuclear
5	131425	AA219134	Hs.26691 ESTs	PBA7	
	132964	AA031360	ESTs	PAA7	plasma membrane
	132967	AA032221	Hs.61635 six transmembrane epithelial antigen of	PM17	plasma membrane
	133179	U81599	Hs.66731 homeo box B13	PFJ5	nuclear
	133330	U42360	Hs.71119 Putative prostate cancer tumor suppressor	PDM1	plasma membrane
10	133520	X74331	Hs.74519 primase, polypeptide 2A (58kD)	PDM2	
	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133944	AA045870	Hs.7780 Homo sapiens mRNA; cDNA DKFZp564A072 (fr		PAB9 cytoplasmic
	134110	U41060	Hs.79136 LIV-1 protein, estrogen regulated	BCR4	plasma membrane
15	301805	AI800004	Hs.142846 hypothetical protein	PEU4	nuclear
	302005	AI869666	Hs.123119 MAD (mothers against decapentaplegic, Dr	PBJ6	cytoplasmic
	302681	AA508353	Hs.105314 relaxin 1 (H1)	PBH3	secreted
	303506	AA340605	Hs.105887 ESTs, Weakly similar to Homolog of rat Z	PEG4	
	303699	D30891	Hs.19525 hypothetical protein FLJ22794	PBM4	not determined
20	303753	AW503733	Hs.9414 KIAA1498 protein	PBY3	not determined
	308050	AI600004	Hs.31608 hypothetical protein FLJ20041	PEU5	plasma membrane
	310382	AI734009	Hs.127699 KIAA1603 protein	PCQ8	
	310431	AI420227	Hs.149358 ESTs, Weakly similar to A46010 X-linked	PBH1	plasma membrane
	310573	AW292180	Hs.156142 ESTs	PEN3	plasma membrane
	310598	AI338013	Hs.140546 ESTs	PCW3	
25	310816	AI973051	Hs.224965 ESTs	PET5	
	311595	AI682088	Hs.79375 holocarboxylase synthetase (biotin-[prop	PBH8	
	313676	AA861697	Hs.120591 ESTs	PBY2	
	314121	AI732100	Hs.187619 ESTs	PBY1	
30	314691	AW207206	Hs.136319 ESTs	BFF8	not determined
	314785	AI538226	Hs.32976 guanine nucleotide binding protein 4	CBO7	cytoplasmic
	314907	AI672225	Hs.222886 ESTs, Weakly similar to TRHY_HUMAN TRICH		PBM2 not determined
	315051	AW292425	ESTs	PBM9	
	315052	AA876910	Hs.134427 ESTs	PBJ7	plasma membrane
35	316442	AA760894	Hs.153023 ESTs	PBJ9	
	317548	AI654187	Hs.195704 ESTs	PBQ6	
	317669	AW295184	Hs.129142 deoxyribonuclease II beta	PBQ7	
	318524	AW291511	Hs.159066 hypothetical protein FLJ10188	PBJ1	cytoplasmic
	319191	AF071538	prostate epithelium-specific Ets transcr	PEN1	
40	319763	AA460775	Hs.6295 ESTs, Weakly similar to T17248 hypotheti	PEO7	
	320324	AF071202	Hs.139336 ATP-binding cassette, sub-family C (CFTR	PBH5	plasma membrane
	320561	NM_006953	Hs.159330 uropod 3	PEL9	plasma membrane
	320796	AF038966	Hs.31218 secretory carrier membrane protein 1	PBY4	not determined
	321441	AW297633	Hs.118498 Homo sapiens LUCA-15 protein mRNA, splic		PBY8 not determined
	322303	W07459	Hs.157601 ESTs	CBF9	secreted
45	322782	AA056080	Hs.202577 Homo sapiens cDNA FLJ12166 fis, clone MA		PBQ1 not determined
	322818	AW043782	Hs.293616 ESTs	PCQ7	plasma membrane
	323226	AF055019	Hs.21906 Homo sapiens clone 24670 mRNA sequence		PCI2 not determined
	323287	AA639902	Hs.104215 ESTs, Moderately similar to SPCN_HUMAN S	PBJ5	
50	324295	AI146686	Hs.143691 ESTs	PBQ9	not determined
	324430	AA464018	Hs.184598 Homo sapiens cDNA: FLJ23241 fis, clone C		PBY6 not determined
	324603	AW016378	Hs.292934 ESTs	PBM3	
	324617	AA508552	Hs.195839 ESTs, Weakly similar to I38022 hypotheti	PBH4	cytoplasmic
	324626	AI685464	Hs.104215 gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	PCW6	
	324658	AI694767	Hs.129179 Homo sapiens cDNA FLJ13581 fis, clone PL		PBJ4 plasma membrane
55	324718	AI557019	Hs.116467 small nuclear protein PRAC	CBK1	nuclear
	330211			PBJ2	not determined
	330546	U31382	Hs.299867 guanine nucleotide binding protein 4	PEW1	cytoplasmic
	330762	AA449677	Hs.15251 hypothetical protein	PBM1	not determined
60	330790	T48536	Hs.122764 TMPRSS2, transmembrane protease, serine		PEL3 plasma membrane
	330892	AA149579	Hs.91202 ESTs	PBQ4	plasma membrane
	331039	R36671	Hs.14846 Homo sapiens mRNA; cDNA DKFZp564D016 (fr		PCQ1 cytoplasmic
	331490	N32912	Hs.291039 ESTs	PCI4	nuclear
	331889	AA431407	Hs.98802 ESTs, Moderately similar to T14342 NSD1	PBH7	not determined
65	332247	N58172	gb:za21f09.s1 Scores fetal liver spleen	PBQ5	nuclear
	332396	AA340504	gb:hw31a09.x1 NCI_CGAP_Kid11 Homo sapien		PBJ8 not determined
	332697	T94885	transgelin 2	PBQ8	secreted
	332798			PBH2	nuclear
	334447			PBY9	not determined
	338255			PBY7	not determined

	401424			PFG2	mitochondrial
	407122	H20276	Hs.31742	ESTs	PEW7
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	PEZ3
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	PEY1
5	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	PFG1
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog	PEW3
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	PEZ9
	413125	BE244589	Hs.75207	glyoxalase I	PFJ3
	413623	AA825721	Hs.246973	ESTs	OBH6
10	414422	AA147224	Hs.337232	Homeo box A13	PFC6
	415263	AA948033	Hs.130853	ESTs	PEZ5
	417153	X57010	Hs.81343	*collagen, type II, alpha 1 (primary ost	PFJ1
	418601	AA279490	Hs.86368	calmegin	PFA1
	418848	AI820961	Hs.193465	ESTs	PEY4
15	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	OBH2
	419839	U24577	Hs.93304	*phospholipase A2, group VII (platelet-a	PFH9
	421887	AW161450	Hs.109201	CGI-86 protein	PFH2
	422083	NM_001141	Hs.111256	*arachidonate 15-lipoxygenase, second ty	PFH5
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	PFA3
20	425071	NM_013989	Hs.154424	*deiodinase, iodothyronine, type II"	PFH6
	425710	AF030880		solute carrier family, member 4	PFD4
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	PFH1
	428819	AL135623	Hs.193914	KIAA0575 gene product	PFD6
	429900	AA460421	Hs.30875	ESTs	PEZ7
25	429918	AW873986	Hs.119383	ESTs	PEY5
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	PEZ4
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	PFG6
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	PEZ1
	431992	NM_002742	Hs.2891	protein kinase C, mu	PFH4
30	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	PFA2
	432244	AI669973	Hs.200574	ESTs	PEW8
	432437	W07088	Hs.293635	ESTs	PFG3
	432968	AA650114	Hs.325198	ESTs	PEY3
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	PEW5
35	440260	AI972867	Hs.7130	copine IV	PEW6
	440901	AA909358	Hs.128612	ESTs	PFC8
	445424	AB028945		cortactin SH3 domain-binding protein	PEZ6
	446320	AF126245	Hs.14791	*acyl-Coenzyme A dehydrogenase family, m	PFH7
	447210	AF035269		phosphatidylserine-specific phospholipas	PFH8
40	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	PEZ8
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	PEZ2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	PFD2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	PFJ8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	PFG9
45	452039	AI922988		ESTs	PFD8
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	PFG4
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	PFC5
	452946	X95425	Hs.31092	EphA5	PFH3

TABLE 15A shows the accession numbers for those primekeys lacking a unigeneID in Table 15. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Pkey	CAT number	Accession
20	116393	131543_1	AI972402 AI634409 AI523716 AI799749 W44518 AI424438 AI688513 AI971048 AI686324 AW013854 AA588483 AA528111 AI627428 AI582200 AI669296 AI826926 AI620526 AI669958 AI972458 AI924500 AA512903 W44517 AA335363 AW238997 BE300165 BE250665 AA284195 AA523420 W52834 AI471970 AI952824 AW003820 AW0039463 AA669796 AA114966 AI653342 AA115038 AI342150 AI092100 AI968211 W51994 AI804005 AI201420 AI123210 AI738405 AI674964 AI970341 AW027500 AI493316 AI333193 AI139353 AA599463 AI656163 AI804200 AI365321 AI990213 AI657011 AA650025 AI968810 AI341978 AA599839 AW592602 AA644289 AI468578 AI565265 AI565228 BE221535 AW973052
25	101485	18113_1	AA296520 AL021940 M30640 NM_000450 M24736 M61894 AL047443 H39560 AI694691 AA916787 AI214796 AA939085 AI150616 AA412553 AA412545 AI051015 T27654 AA694430
	126399	17331_1	AA089767 AF224278 AA128075 AL035541 AA027926 AI761441 AI972096 AW071693 AI742327 AI377498 AI804815 AI640802 AI885001 AI921394 AA595115 N71820 AI921217 AW007283 AI467828 AI369306 AA917446 AI493698 AA088701 AA126899 AI936228 AW204238 AI039567 AI925027 BE138909 AW452945 AW135998 AA310984 AA027860 AW073519 AI537597 AA953976 AI521341 AW273569 AW050740 AA536113 AA559064 AI474392 AW135709 AA535181 AW572959 AA570597 AI905464 AI677810 AI587642 AW975102 AA424310 AA482527 N64192 AA658276 AW889117 AA486591 AW889172 AI381990 AI381891 AI673419 AI990950 AA487031 AI272934 AI150565 AA229168 AW316722 AI142707 BE222396 AA614168 AA122026 AW338227 AA632457 AI968726 AW369662 AA512956 AA541675 AA451748 AI250993 BE146418 AA122025
30	132964	94346_1	AI362575 AI805082 AW263421 AI432462 AA135870 AA031360 AA031604 AA298475 AA298464
35	129389	21074_1	NM_012445 AB027466 BE407510 BE047605 AA047125 AW084003 AA149494 AA149490 AA292528 AA570505 AA526186 AW006250 AW007762 AI341557 AI799666 AI972710 AI377966 AI962810 AI084783 AI458032 AI190971 AW148913 AA372354 AW970032 AW007426 AA650188 AI123203 AI122890 AI280975 W73595 W73495 AI863238 AA374109 AA603986 AW149089 AW957523 AI307748 AI921067 AI336463 F24537 AI380460 AI367500 AI189309 AI814701 AI766921 AW572106 AA037024 AW072576 AA578293 AI288103 AA235464 AW450642 AA574230 AW294024 AI589229 AI580733 AW512227 AA877009 AI660255 AW188597 AA558228 AI572782 AA658397 AI274828 AI866359 AA864573 AI264439 AA621604 AW515493 AW243333 Z39737 AI567038 AA573997 AA573559 AW236431 AI652870 AI684973 AA034505 AA047126
40	129404	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172055 AW958465 AA172236 AW953397 AA355086
	107217	9836_1	AL060235 AA031750 D81382 AI480231 AI095947 AI560953 BE010721 AI870290 AA374945 AA125792 D51527 D51556 AI685541 D51559 AW117286 AA195741 AI675138 AW593439 AI201885 T30590 AW952100 D51095 AA523664 W70043 AA987586 AI421515 AI205532 AA127069 AI337367 D51595 AI453785 AW075677 AW088359 C14287 C14284
45	121710	19266_1	AF163474 NM_016590 AF163475 AI761105 AI770098 AA410580 AA411616 AI590343 AI739050 AL050198 AI862645 AA419104 AA513809 AA333032 AI816915 AW139625 AA640889 AI311391 AI627693 AW135514 AA419011 AI269149 AI245259 AI970008 AI970017 AW139445 AA569503 AI761072 AI766179 AI759995 AI300776 AI670129 AW150770 AA226501 AA226220
50	121913	291015_1	AI249368 AI742316 AA426082 AA442089 AI864189 BE349478 AI803475 AI584049 BE552085 AI088609 AI264197 AI886144 AI129474 AI307145 BE181300 AW058403 AI696838 AW748958 AA442196 AI216428
	102398	entrez_U42359U42359	
	315051	347217_1	AW292425 BE467167 AI702953 BE550961 BE222309 AI299348 AI693336 AA541708
	324626	336411_1	AI685464 AW971336 AA513587 AA525142
55	319191	16065_1	NM_012391 AF071538 AB031549 AI685592 AI745526 AA662204 AW130657 AA662164 AW971121 AI668916 AA513274 AI991223 AI979170 AW298436 AA639621 AI859010 AW513942 AI687669 AA662521 AA548598 AI345056 AI305374 BE043418 AI432856 AI334840 AI379796 AI492693 AI307915 BE042082 AI307834 AI307858 AI309488 BE042210 AI435670 AI371605 AI862491 AI284563 AI306872 AI255044 AI254601 AI251236 AI473073 AI473042 AI432760 AI435664 AI336826 AI289365 AI369096 AI862274 AI334871 AI349663 AI250405 AI377617 AI309895 AI313017 AI862291 AI311936 AI378718 AI305722 AI306769 AI308888 AI334565 AI962296 AI344230 AI435685 AI344087 AI378696 AI311209 AI435775 AI310611 AI311154 AI432289 AI431561 AI492681 AI432867 AI335288 AI492796 AI432769 AI310299 AI432273 AI379820 AI275319 AI435753 AI609441 AI432767 AI369100 AI311420 AI349974 AI247157 AI334677 AI270910 AI224320 AI305608 AI334489 AI377152 AI350012 AI370086 AI335053 AI306781 AI306750 AI334849 AI334874 AI340380 AI307876 AI305974 AI305972 AI311521 AI334872 AI862509 AI311498 AI335051 AI289684 AI310859 AI311862 AI862483 AI492775 AI307906 AI492708 AI289693 AI340373 AI307910 AI311359 AI435653 AI334865 AI311492 AI492809 AI492690 AI431576 AI862268 AI311879 AI308435 AI492792 AI862512 AI275321 AI431588 AI431564 AI307885 AI307926 AI435692 AI435778 AI310182 AI308694 AI492707 AI492713 AI308560 AI307829 AI343234 AI580598 AW472796 AI340918 AI310243 AI309368 AI307920 AI289665
60			
65			

AI306777 AW086318 AW086292 AW086378 AI310027 AI275293 AI369082 AI340900 AI306749 AI371558 AW086287 BE043803
 AI306793 AI306272 AI287948 AI270917 AI284816 AI336813 AI284546 AI308044 AI275290 AI270872 AI306795 AI289687 AI223570
 AI305303 AI289677 AI287742 AI275284 AI306812 AI336701 AI371554 AI378719 AI344988 AI223631 AI335141 AI343222 AI284568
 AI305357 AI275270 AI345932 AI436549 AI307925 AI311502 AI344238 AI343182 AI308508 AI305988 AI270790 AI379792 AI305647
 AI305410 AI432251 AI436517 AI343227 AI305534 AI340387 AI271043 AI305499 AI271046 AI305962 AI289465 AI305378 AI289725
 AI310848 AI305848 AI289362 AI252964 AI307049 AI310831 AI306993 AI306796 AI224659 AI305969 AI349855 AI306164 AI306948
 AI284676 AI309155 AI343202 AI432785 AI306815 AI369081 AI270885 AI289699 AI435704 AI309647 AI305716 AI311281 AI287927
 AI472995 AI340423 AI270958 AI307069 AI305364 AI270807 AI275306 AI311890 AI275263 AI432750 AI289371 AI432661 AI255113
 AI305709 AI473008 AI311168 AI309711 AI377164 AI271201 AI289560 AI309710 AI306195 AI311201 AI287741 AI271066 AI432876
 AI275281 AI379795 AI472972 AI311967 AI308826 AI305465 AI270792 AI473019 AI305340 AI270922 AI305995 AI305462 AI254144
 AI270969 AI473012 AI305390 AI275278 AI223644 AI289692 AI250318 AI305372 AI289691 AI250521 AI306283 AI306814 AI307933
 AI473160 AI432903 AI223720 AI254979 AI334862 AI306926 AI289541 AI432248 AI435722 AI435698 AI432859 AI310683 AI473175
 AI335144 AI289467 AI436489 AI306928 AI473033 AI305763 AI307868 AI307882 AI348959 AI435736 AI432857 AI432896 AI435735
 AI432283 AI473086 AI432863 AI473081 AI432825 AI307840 AI473164 AI432885 AI473166 AI472982 AI437534 AI473060 AI473171
 AI432279 AI432882 AI334670 AI436512 AI432827 AI432852 AI473051 AI473077 AI435697 AI271509 AI492781 AI472983 AI473018
 AI432897 AI473043 AI432871 AI436536 AI473157 AI349715 AI432777 AI473016 AI473158 AI340369 AI307941 AI432773 AI377146
 AI492791 AI270950 AI305342 AI284604 AI308269 AI284811 AI270811 AI289347 AI334869 AI334852 AI311759 AI250382 AI309520
 AI289550 AI305721 AI340870 AI270901 AI308575 AI307904 AI340715 AI270941 AI309808 AI246867 AI473014 AI307039 AI289360
 AI473069 AI492786 AI344013 AI305876 AI436510 AI340742 AI473028 AI307891 BE041871 BE041268 BE042340 BE041946
 BE041783 AI306173 AI201948 AI926972 AI275769
 338255 CH22_6856FG_LINK_EM:AC00
 330211 c_5_p2
 332798 CH22_14FG_6_5_LINK_C4G1.G
 334447 CH22_1746FG_387_7_LINK_EM
 332247 372969_1
 332396 20265_1
 AA669097 AA513815 AA026798 AA676526 AA704429 AA704269 AW118292 AA579216 N58172
 AW579842 BE156562 BE156489 BE081033 AK001559 BE149402 M85387 AW367811 AW367798 R17370 AI908947
 AA362932 R58449 H18732 AA371231 AW962899 AA713530 AW892946 R53463 H11063 AW068542 Z40761 BE176212 BE176155
 W23952 W92188 AW374883 AA303497 AW954769 AA036808 BE168063 AW382073 AW382085 AL041475 H80748 AI078161
 BE463983 AI805213 AI761264 W94885 N94502 AI623772 AI419532 AI810302 AI634190 AW002516 AW150777 AI352312 AI367474
 AW204807 AI675502 AI337026 AW134715 BE328451 AI123157 AI560020 AI300745 AI608631 AI248873 AA742484 AW051635
 H18646 AI245045 AA507111 AI640510 AI925594 AA115747 AA143035 AA151106
 X51405 NM_001873 T11322 AL118886 BE328175 AW136009 BE467445 AW470313 AA774852 BE504139 AW501046 AA082792
 AW389231 AA370044 R36841 AA371457 C04813 R25791 R25556 AW895854 AW903819 AW895671 AW895677 BE159723
 AW895664 AW895597 AW895595 AW895665 AW888518 AI903724 F06081 F08503 AL119462 AW895730 AW888516 R26511
 R26489 AA334126 AA327626 N85713 AW895998 AA223622 F05468 AA370749 W05590 M78202 AA371073 AW498607 R15017
 T16991 AA001282 AA001138 AA551566 AA330159 AI922855 AA383512 AA029603 D82246 D82171 T94933 H56545 AA348060
 AA176888 R98764 AW451817 AA385766 AA452818 AI690057 AA988822 BE549928 AA150901 W57992 AW899925 C05281
 AA932042 AA370980 AW962877 W04741 AA369982 AW385948 AA922466 N75882 AI422070 AI361256 AI680224 D57122 T94885
 R53266 R46713 T19071 AW796277 AA325333 F04719 F02334 AA358146 AA826597 AA358304 AW028099 AL119570 D57290
 D58273 D57796 N48555 AI361959 AA329457 D57225 AW024046 AA992606 AW022118 AW021538 AA935845 H89870 H56546
 AW961219 AA453239 AW837541 N45521 BE218029 AA318877 AA327740 AW961809 T92139 D53216 D52365 D53363 D53312
 D53116 AI547267 AA679935 AW026552 AW026418 AW190507 AI927710 AW244108 D50948 AW054991 AW021063 AW022511
 AA493436 AI365636 BE464751 AW149384 AA102442 AW771368 AI818251 AI126368 D51049 AI421542 AI559467 AW079779
 AW021048 AW023969 AW044214 AI458264 AA027274 AI620254 AW028917 BE219511 AA326242 N67561 AI971273 AA878328
 D57131 AA770662 AI309299 AI796767 AA613338 W58076 AI566287 AI445573 AI880260 AA001919 AW339259 AI492610 AI492611
 R97692 AI301425 AA722603 D58361 AI350323 AA973926 AI431263 AA516126 AA865467 AI925177 N39443 AA001943 AI299371
 AI082412 AA665090 AA583433 H89871 AA977231 AI382219 AI056096 AI270446 N67524 N22103 AW614224 AA744054 AW243622
 AI613188 AI929173 AI350243 AI362138 AA744004 AA176661 D56787 AI955625 AI393109 AI094769 AI479728 AI423107 AI955617
 AI034036 AI582196 AW264534 AI418961 AA570761 AI343538 AA650341 AA992503 AA770004 AL039966 AI862675 AW190335
 AA610274 AW418627 BE467472 D56786 T26749 AI217610 AI359556 T23523 AL040189 AA846222 AA651636 D51280 AI888996
 AI521167 AI340177 AW612815 AI625285 AA621607 AA177059 AA229768 AA829788 AI749682 AW190631 N75299 AA230089
 AI915632 BE089542 AA890020 AA528397 AA995390 BE503860 AA570812 AW339396 AI197986 AI203725 AI282379 AA670375
 AA461513 F01728 AW243599 C00856 N75567 R95995 AA150932 R95961 AA648060 AA933800 AA927073 AA101126 AA864190
 T93566 BE167472
 AF030880 NM_000441 AC002467 AA385554 H23053 AW891838 AI139968 AA653057 AI695233
 AA527941 AI810608 AI620190 AA635266
 AB028945 T77648 F13328 AL157605 Z46212 AA304736 F11855 T66098 T30174 AW954164 AW176301 AW748243 AA456428
 AI369958 AA938565 AW959613 Z42008 AA994779 AI683909 F11019 F10926 AI769597 AI752550 T65015 AI884314 AA643954
 Z41838 AW020147 AI038822 AW571822 AA299781 AA894928 AF131790 BE005411 AI902476 AW082695 AA464384 R42750
 AW902301 AA464273 R05837 Z38294 H41098 AI134507 M86079
 AF035269 AF035268 NM_015900 T96213 U37591 AA156832 AA299371 AI084325 H95977 AI765967 BE221465 AA156726 AI969563
 AW024539 AI436791 AI949451 AA843093 AI452756 AA824232 AI306667 T96131 AW207447 AW243556 AW957032 AI084332
 H95978 U30998
 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370
 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526
 T61415 AA331486
 AI922988 H05475 AA021608 AW169947 AA913750 Z41614 AW800012

TABLE 15B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
334447	Dunham, I. et.al.	Plus	14308764-14308824
332798	Dunham, I. et.al.	Minus	232147-231974
338255	Dunham, I. et.al.	Minus	15242294-15242231
330211	6013592	Plus	59158-59215
401424	8176894	Plus	24223-24428

TABLE 11 AND SEQUENCE LISTING

SEQ ID NO:1 BCU4 DNA SEQUENCE

5 Nucleic Acid Accession #: NM_024915
Coding sequence: 13-1890 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 ATTGGATCAA ACATGTCACA AGAGTCGGAC AATAATAAAA GACTAGTGGC CTTAGTGGCC 60
ATGCCCAGTG ACCCTCCATT CAATACCCGA AGAGCCTACA CCAGTGAGGA TGAAGCCTGG 120
AAGTCATACT TGGAGAATCC CCTGACAGCA GCCACCAAGG CCATGATGAT CATTAATGGT 180
GATGAGGACA GTGCTGTGCG CCTCGGCTG CTCTATGACT ACTACAAGGT TCCTCGAGAC 240
AAGAGGCTGC TGTCTGTAA GCAAAGCAAGT GACAGCCAAG AAGACCAGGA GAAAAGAAAC 300
TGCCTTGGCA CCAGTGAAGC CCAGAGTAAT TTGAGTGGAG GAGAAAACCG AGTGCAAGTC 360
15 CTAAAGACTG TTCCAGTGA CCTTCCCTA AATCAAGATC ACCTGGAGAA TTCCAAGCGG 420
GAACAGTACA GCATCAGCTT CCCCAGAGAG TCTGCCATCA TCCCGGTGTC GGGAAATCAG 480
GTGGTGAAAG CTGAAGATT CACACCAGTT TTCTAGGCCC CACCTGTGCA CTATCCCCGG 540
GGAGATGGGG AAGAGCAACG AGTGGTTATC TTGAAACAGA CTCAGTATGA CGTGGCCTCG 600
CTGGCCACCC ACAGCGCCTA TCTCAAAGAC GACCAGCGCA GCATCCCGGA CAGCACATAC 660
20 AGCGAGAGCT TCAAGGACGC AGCCACAGAG AAATTCGGA GTGCTTCAGT TGGGGCTGAG 720
GAGTACATGT ATGATCAGAC ATCAAGTGGC ACATTTCAGT ACACCCTGGA AGCCACCAAA 780
TCTCTCCGTC AGAAGCAGGG GGAGGGCCCC ATGACCTACC TCAACAAAGG ACAGTTCTAT 840
GCCATAACAC TCAGCGAGAC CGGAGACAAC AAATGCTTCC GACACCCCAT CAGCAAAGTC 900
AGGAGTGTGG TGATGGTGGT CTTCAAGTGA GACAAAAACA GAGATGAACA GCTCAAATAC 960
25 TGGAATACTT GGCCTCTCG GCAGCATAAC GCGAAGCAGA GGGTCTTGA CATTGCCGAT 1020
TACAAGGAGA CTCTTAATAC GATTGGAAC ATTGAAGAGA TTGCATATAA TGCTGTTTCC 1080
TTTACTGGG ACGTGAATGA AGAGGCGAAG ATTTTCATCA CCGTGAATTG CTGAGCACA 1140
GATTCTCTCT CCAAAAAGG GGTGAAAGGA CTTCCTTTGA TGATTGAGT TGACACATAC 1200
AGTTATAACA ATCTAGACAA TAAACCCATT CATAGAGCTT ATTGCCAGAT CAAGGTCTTC 1260
30 TGTGACAAAG GAGCAGAAAG AAAAAATCCGA GATGAAGAGC AGAAGCAGAA CAGGAAGAAC 1320
GGGAAAGGCC AGGCCTCCCA AACTCAATGC AACAGCTCCT CTGATGGGAA GTTGGCTGCC 1380
ATACCTTTAC AGAAGAAGAG TGACATCACC TACTTCAAAA CCATGCCTGA TCTCCACTCA 1440
CAGCCAGTTC TCTTCATACC TGATGTTTAC TTGCAAAC TGCAGAGGAC CGGACAGGTG 1500
TATTACAACA CGGATGATGA ACGAGAAGGT GGCAGTGTCC TTGTTAAACG GATGTTCCGG 1560
35 CCCATGGAAG AGGAGTTTGG TCCGGTGCCT TCAAAGCAGA TGAAAGAAGA AGGGACAAAG 1620
CGAGTGCTCT TGTACGTGAG GAAGGAGACT GACGATGTGT TCGATGCATT GATGTTGAAG 1680
TCTCCCAAGC TGATGGGCTT GATGGAAGCG ATATCTGAGA AATATGGGCT GCCCGTGGAG 1740
AAGATAGCAA AGCTTTACAA GAAAAGCAAA AAAGGCATCT TGGTGAACAT GGATGACAAC 1800
ATCATCGAGC ACTAGTATCA CGAGGACACC TTCTCTCTCA ACATGGAGAG CATGGTGGAG 1860
40 GGCTTCAAGG TCACGCTCAT GGAATCTAG CCTTGGGTTT GGCATCCGCT TTGGCTGGAG 1920
CTCTCAGTGC GTTCTCTCCT GAGAGAGACA GAAGCCCCAG CCCCAGAAC TGGAGACCCA 1980
TCTCCCCAT CTACACAATC CTGTTACAAG ACCGTGCTGG GAGTGGGGC AAGGGACAGG 2040
CCCCACAGTC GGTGTGCTTG GCCCATCCAC TGGCACCTAC CACGGAGCCG AAGCCTGAGC 2100
CCCTCAGGAA GGTGCCTTAG GCCTGTGGA TTCTTATTTA TTGCCACCT TTTCTGGAG 2160
45 CCCAGGTCCA GCGCCGCCAG GACTCTGCAG GTCAGTCTCA GCTCCAGATG AGACCGTCCA 2220
GGGTTCCTCC TTCAAGAGAA ACACTCATCC CGAACAGCCT AAAAAATTCC CATCCCTTCT 2280
TTCTCACCCC TCCATCTCTA TATCTCCGA GTGGCTGGAC AAAATGAGCT ACGTCTGGGT 2340
GCAAGTAGTA TAGGTGGGGC AAGAGGTGGA TGCCCACTTT CTGGTCAGAC ACCTTTAGGT 2400
TGCTCTGGGG AAGGCTGTCT TGCTAAATAC CTCCAGGGTT CCCAGCAAGT GGCCACCAGG 2460
50 CCTGTACAG GAAGACATTC AGTCACCGTG TAATTAGTAA CACAGAAAGT CTGCTGTCT 2520
GCATTGTACA TAGTGTATAT AATATTGTA TAATATATT TACCTGTGGT ATGTGGGCAT 2580
GTTTACTGCC ACTGGCCTAG AGGAGACACA GACCTGGAGA CCGTTTAAAT GGGGGTTTTT 2640
GCCTCTGTGC CTGTTCAAGA GACTTGCAGG GCTAGGTAGA GGGCCTTTGG GATGTTAAGG 2700
TGACTGCAGC TGATGCCAAG ATGGACTCTG CAATGGGCAT ACCTGGGGGC TCGTTCCTG 2760
55 TCCCAGAGG AAGCCCCCTC TCCTTCTCCA TGGGCATGAC TCTCTTCA GGGCCACCAG 2820
TTTATCTCAC AATGATGTGT TTGCTCTGAC TTTCCTTTG CGTGTCTCG TGGGAAAGGT 2880
CATTCTGTCT GAGACCCAG CTCTTCTCC AGCTTTGGCT GCGGGCATGG CCTGAGCTTT 2940
CTGGAGAGCC TCTGCAGGGG GTTGGCATC AGGGCCCTGT GGCTGGGTCT GCTGCAGAGC 3000
60 TCCTTGGCTA TCAGGAGAAT CTTGGACACT GTACTGTGCC TCCCAGTTA CAAACACGCC 3060
CTTCATCTCA AGTGGCCCTT TAAAAGCCCT GCTGCCATGT GAGAGCTGTG AACAGCTCAG 3120
CTCTGAGTCG GCAGACTGGG GCTTCTCTCT GGGCCACCAG ATGGAAGGGG GGTATTGTTT 3180
GCCTCACTCC TGGATGTCTG GTTTAAGGA AGTGAGTGAG AAAGAATGTG CCAAGATACC 3240
TGGCTCTGT GAAACACGCC TCAGGAGGGA AACTGGGAGA GAGAAGCTGT GGTCTCTCTG 3300
TACATGCCCT GGGAGCTGGA AGAGAAAAAC ACTCCCTAA ACAATCGAA AATGATGAAC 3360
65 CATCATGGGC CACTGTTCTC TTTGAGGGGA CAGGTTTAGG GGTTTGGCTT CGCCCTTGTG 3420
GGCTGAAGCA CTAGCTTTT GTTAGCTAGA CACATCTGCG ACCCAAAGGT TCTCTACAAA 3480
GGCCAGATT TGTTTGTAAG GCATTTGAC TCTTACCTGG AGGCCCGCTC TCTAAGGGCT 3540
TCTTCGCTC CCACCTCAT TGTCCCTGAG ATGCAGAGCA GGATGGAGGG TCTGCTTCTA 3600
GCTCAGCTGT TTCTCTTGA GGTGCGGAG GAATTGAAT GAATGGGACA GAGGGCAGGT 3660
70 GCTGTGGCCA AGAAGATCTC CGAGCAGCAG TGACGGGGCA CCTTGTCTGT TGTCTCTGG 3720
GCATGTTAAC CCTTCTGTGG GGCCAAAGGT TTGCATCGTG GATCCAGCTG TGCTCCAGTC 3780
TGTCCCTCC TCTTCCACTC TGACTGCCAC GCCCGGACC AGCAGCTTGG GGACCTTCCA 3840
GGGTACTAAT GGGGCTCTGT TCTGAGATGG ACAAATTCAG TGTGGAAT ACATGTTGTA 3900
CTATGCACTT CCGATGCTCC TAGGTTAGG AATAGTTTCA AACATGATTG GCAGACATAA 3960
75 CAACGCCAAA TACTCGGACT GGGGCATAGG ACTCCAGAGT AGGAAAAAGA CAAAAGATT 4020
GGCAGCTCT CACAGGCAAC CTACCCCTCT CTCTCCAGCC TCTTATGAA ACTGTTTGT 4080
TGCCAGTCTT GCCTAAGGC AGAAGATGAA TTGAAGATGC TGTGATGTT TCCTAAGTCC 4140
TTGAGCAATC ATGGTGGTGA CAATTGCCAC AAGGGATATG AGGCCAGTGC CACCAGAGGG 4200

TGGTGCCAAG TGCCACATCC CTTCGGATCC ATTCCTCTCT GTATCCTCGG AGCACCCAG 4260
 TTTGCCTTTG ATGTGTCCGC TGTGTATGTT AGCTGAACCT TGATGAGCAA AATTTCTGA 4320
 GCGAAACACT CCAAAGAGAT AGGAAAACCT GCCGCCTCTT CTTTTTGTG CCTAATCAA 4380
 ACTCAAATAA GCTTAAAAAA AATCCATGGA AGATCATGGA CATGTGAAAT GAGCATTTTT 4440
 5 TTTCTTTCTT TTTTTTTTTT TTTTAAAC AAAGTCTGAA CTGAACAGAA CAAGACTTTT 4500
 TCCTCATACA TCTCCAAATT GTTTAAACTT ACTTTATGAG TGTITGTTA GAAGTTCGGA 4560
 CCAACAGAAA AATGCAGTCA GATGTCATCT TGGAAATTGGT TTCTAAAAGA GTAAGGCATG 4620
 TCCCTGCCCA GAAACTTAGG AAGCATGAAA TAAATCAAAT GTTTATTTC CTCTTATTT 4680
 10 AAAATCATGC TAATGCAACA GAAATAGAGG GTTTGTGCA AATGCTATGA ACGGCCCTTT 4740
 CTAAAGACA AGCAAGGGAG ATTGATATAT GTACAATTG CTCTCATGTT TTT

SEQ ID NO:2 BCU4 Protein sequence:

Protein Accession #: NP_079191.1

1 11 21 31 41 51
 MSQESDNNKR LVALVPMPSD PPFNTRRAYT SEDEAWKSYL ENPLTAATKA MMIINGDEDS 60
 AAALGLLYDY YKVRPRDKRL SVSKASDSQE DQEKRNCLGT SEAQSNLSGG ENRVQVLKTV 120
 20 PVNLSLNQDH LENSKEQYS ISPESSAII PVSGITVVKA EDTFPVFMAP PVHYPRGDGE 180
 EQRVVFIEQT QYDVPSLATH SAYLKDDQRS IPDSTYSESF KDAATEKFRS ASVGAEYMY 240
 DQTSSGTFQY TLEATKSLRQ KQEGPMTYL NKGQFYAITL SETGDNKCFR HPISKVRSV 300
 MVVFSDEKKNR DEQLKYWKYW HSRQHTAKQR VLDIADYKES FNTIGNIEEL AYNVSVFTWD 360
 VNEEAKIFT VNCLSDFSS QKGVKGLPLM IQIDTYSYNN RSNKPIHRY CQIKVFCDKG 420
 25 AERKIRDEEQ KQNRKNGKGQ ASQTQCNSSS DGKLAAILQ KKSDFYFKT MPDLHSQPV 480
 FIPDVHFANL QRTGQVYYNT DDEREGGSVL VKRMFRPMEE EFGVPVSKQM KEEGTRKRV 540
 YVRKETDDVF DALMLKSFTV MGLMEASEK YGLPVEKIAK LYKSKKGIL VNMDNIEH 600
 YSNEDTFILN MESMVEGFKV TLMEI

SEQ ID NO:3 BCU7 DNA SEQUENCE VARIANT 1:

Nucleic Acid Accession #: AA428062

Coding sequence: 1-777 (entire sequence represents open reading frame)

1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCCTGTTCT CCCTTCTCTG TGAAGCAAGT 60
 ACCGTCTGTC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATTT CACTGATATT 120
 40 GAAGCAGCTC TGAAGCACAC ATTAGATTCA GCGGATATCC CCAAGCCAG GCGGAAGCGC 180
 TACATTTCCG AGAATGACAT GATCGCCATT CTGTGATTAT ATAATCAAGT TCGGGGCAAA 240
 GTGTTCCAC CGGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 GCAGAGGCTT GGGCGGCTAC TTGCATTGGG GACCATGGAC CTCTTACTT ACTGAGATTT 360
 45 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATTCTCCA GTTGGTCAAG 420
 CCATGTTATG ATGAAGTGAA AGATTATGCT TTTCATATC CCCAGGATTG CAACCCGAGA 480
 TGTCCATGCA GATGTTTGG TCCCATGTGC ACACATTATA CGCAGATGGT TTGGGCCACT 540
 TCCAATCGGA TAGGATGCGC AATTCAATCT TGCCAAAACA TGAATGTTG GGGATCTGTG 600
 TGGCGACGTG CAGTTTACTT GGTATGCAAC TATGCCCCAA AGGGCAATTG GATTGGAGAA 660
 50 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTTGTCCTC CAAGTTATGG GGGATCTTGT 720
 ACTGACAATC TGTGTTTTC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA

SEQ ID NO:4 BCU7 DNA SEQUENCE VARIANT 2:

Nucleic Acid Accession #: AA428062

Coding sequence: 1-777 (entire sequence represents open reading frame)

1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCCTGTTCT CCCTTCTCTG TGAAGCAAGT 60
 ACCGTCTGTC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATTT CACTGATATT 120
 60 GAAGCAGCTC TGAAGCACAC ATTAGATTCA GCGGATATCC CCAAGCCAG GCGGAAGCGC 180
 TACATTTCCG AGAATGACAT GATCGCCATT CTGTGATTAT ATAATCAAGT TCGGGGCAAA 240
 GTGTTCCAC CGGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 65 GCAGAGGCTT GGGCGGCTAC TTGCATTGGG GACCATGGAC CTCTTACTT ACTGAGATTT 360
 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATTCTCCA GTTGGTCAAG 420
 CCATGTTATG ATGAAGTGAA AGATTATGCT TTTCATATC CCCAGGATTG CAACCCGAGA 480
 TGTCCATGCA GATGTTTGG TCCCATGTGC ACACATTATA CGCAGATGGT TTGGGCCACT 540
 70 TCCAATCGGA TAGGATGCGC AATTCAATCT TGCCAAAACA TGAATGTTG GGGATCTGTG 600
 TGGCGACGTG CAGTTTACTT GGTATGCAAC TATGCCCCAA AGGGCAATTG GATTGGAGAA 660
 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTTGTCCTC CAAGTTATGG GGGATCTTGT 720
 ACTGACAATC TGTGTTTTC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA

SEQ ID NO:5 BCU7 Protein sequence Variant 1:

Protein Accession #: none

1 11 21 31 41 51
 MIAISAVSSA LLFSLLCERS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIPKARRKR 60

YISQNDMIAI LDYHNQVRGK VFPPAANMEY MVWDENLAKS AEAWAATCIW DHGPSYLLRF 120
 LGQNLISVRTG RYRSILQLVK FWYDEVKDYA FYPQDCNPR CPMRCFGPMC THYTMVWAT 180
 SNRIGCAIHA CQNMNVWGSV WRRAVYLVCN YAPKGNWIGE APYKVGVPSC SCPPSYGGSC 240
 TDNLCPFPGVT SNLYWFK

SEQ ID NO:6 BCU7 Protein sequence Variant 2:

Protein Accession #: none

1 11 21 31 41 51
 | | | | |
 MIAISAVSSA LLFSLLEAS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIPKARRKR 60
 YISQNDMIAI LDYHNQVRGK VFPPAANMEY MVWDENLAKS AEAWAATCIW DHGPSYLLRF 120
 LGQNLISVRTG RYRSILQLVK FWYDEVKDYA FYPQDCNPR CPMRCFGPMC THYTMVWAT 180
 SNRIGCAIHT CQNMNVWGSV WRRAVYLVCN YAPKGNWIGE APYKVGVPSC SCPPSYGGSC 240
 TDNLCPFPGVT SNLYWFK

SEQ ID NO:7 BCX2 DNA SEQUENCE

Nucleic Acid Accession #: NM_003014

Coding sequence: 238-1278 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGCGGGTTCG CGCCCCGAAG GCTGAGAGCT GGCCTGCTC GTGCCCTGTG TGCCAGACGG 60
 CGGAGCTCCG CGGCCGGACC CCGCGGCCCC GCITTTGCTG CGACTGGAGT TTGGGGGAAG 120
 AAATCTCCT CGCCTCCAGA AGATTCTTC CTCGGCGAAG GGACAGCGAA AGATGAGGT 180
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGC GGGTCTGCAG CGCAGAGAGG CAGTGCCATG 240
 TTCCTTCCA TCTAGTGGC GCTGTGCTG TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300
 GCGCCTGCG AGGCGGTGCG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCACGCG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCTTGGG GTTCTGTCAC GACCTATCA AGCCGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGACGACTG CGAGCCCCCT ATGAAGATGT ACAACACAG CTGGCCCGAA 600
 AGCCTGGCCT GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCATTTC GCCTGAAGCC 660
 ATCGTCACGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAAGGC CTCITGATGT TGACTGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGTAAG 780
 AAGGTGAAGC CAACITTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTATGCC 840
 AAAATAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCTCTTCA ACCATCCCT CGAAGTCAAG TCCGCTCAT TACAAATTCT 960
 TCTTGCCAGT TCACACACAT CCTGCCCAT CAAGATGTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140
 AAGAAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAAAGGG AAGCCTCCT 1200
 GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGCCCA GAAGAGAACA 1260
 AACCCGAAAA GAGTGTGAGC TAACTAGTTT CCAAAGCGGA GACTTCGAC TTCCTTACAG 1320
 GATGAGGCTG GGCATTGCTT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAACA 1380
 ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTTCTTAAGG CTATGCTTCA 1440
 GTTTTCTTT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500
 GAGTTAAAGC TGGTGAAAAA GGCTTATGCG ATTGCATICA GAGTAACCTG TGTGCATACT 1560
 CTAGAAGAGT AGGGAATAA ATGCTTGTTA CAATTCGACC TAATATGTGC ATTGTAAAAAT 1620
 AAATGCCATA TTCAACAAA AACACGTAAT TTTTATACAG TATGTTTAT TACCTTTTGA 1680
 TATCTGTGTG TGCAATGTTA GTGATGTTT AAAATGTGAT GAAAAATAAA TGTTTTAAAG 1740
 AAGGAACAGT AGTGGAAATG ATGTTAAAAA ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800
 TTTTGTGAT GAAAGGGGAT TTTTGAATAA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860
 TGTGTTTTT ACCAATGAC TTCAGTTTCT GTTTTATGCT AGAACTTAA AACAAAAAT 1920
 AATAATAAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTC CTGTTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTT TTGTCAACAC CCTCTAAGC AGCACCAGAA 2040
 ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTGGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACTT CCGAGGACAT CCACCCTGAG 2160
 AATAATTGGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTCTTCAT 2220
 TTAATATTTT TCTTTGCCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 AAAGTTGAGT TCCACCTCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAGAACT TATTTCAGC ATTTATCAA CAAATTCAT AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACAATT TTATTGGCCT TTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATICAA TAAATGCACA ACGCCCAAAG GAAATAAAT CCTATCTAAT CTAATCTTCC 2520
 ACTACACAGA GGTAATCACT ATTAGTATT TTGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACITATAA AATGATTGGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCCTT TGCTTGGCCC TTTATTGAGA TAAGTTTCC TGTCAAGAAA GCAGAAACCA 2700
 TCTATTTCCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGGTGTTT TCTTACTGA CAATACTGAA TAAACATCTC ACCGGAATTC

SEQ ID NO:8 BCX2 Protein sequence:

Protein Accession #: NP_003005.1

1 11 21 31 41 51
 | | | | |
 MFLSILVALC LWLHLALGV GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60

YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPCKSV CQRARDCEP LMKMYNHSWP 120
ESLACDELFP YDRGVCSPE AIVTDLPELV KWIDITPDMM VQERPLDVDC KRLSPDRCKC 180
KKVKPILATY LSKNYSYVIH AKIKAVQMSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN 240
SSCQCPLHP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRIVQD 300
KKKTAGRTSR SNPPKPKGKP PAPKPASPCK NIKTRSAQKR TNPKRK

SEQ ID NO:9 CBK1 DNA SEQUENCE

Nucleic Acid Accession #: NM_032391

Coding sequence: 129-302 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
15 | | | | |
GTCCTTCCTC TCCTAGCCTA AGCGGTGCAA ACAGAGCGCC ACTGGGAGGC TGAAACCTTT 60
AGGCCGATGC TTGCTTGCAA GGTCAGGCAA GCTGGATCTT GGTCCTCCAC TTTCAGAGA 120
GAACAGCGAT GTTGTGCGCC CATTCTCAG ATCAAGGACC GGCCCATCTT ACTACCTCCA 180
AGAGTGCTTT TCTCTCTAAT AAGAAAACAT CTACTTTGAA ACATCTACTG GGCGAGACCA 240
GGAGTGATGG CTCAGCCTGT AATCTTGGAA TTTCGGGAGG CCGAGGCAGG AAGATTCTTT 300
20 GAGCACAGGA GTTCCAGACC AGCCTGGGCA ATGTAGCAAG ACGCTGTCTC TATTATATACA 360
ATAAAATTTT TTTAAAAAAG G

SEQ ID NO:10 CBK1 Protein sequence:

Protein Accession #: NP_115767

1 11 21 31 41 51
30 | | | | |
MLCAHFSQDQ PAHLTTSKSA FLSNKKSTL KHLLEGTRSD GSACNSGISG GRGRKIP

SEQ ID NO:11 CHA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_020182

Coding sequence: 96-854 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
40 | | | | |
TCCTTGGGGT CGGGTGAAG CGCCTGGGGG TCGTGGCCA TGATCCCGA GCTGCTGGAG 60
AACTGAAGGC GGACAGCTCT CTGCGAAACC AGGCAATGGC GGAGCTGGAG TTTGTTCAGA 120
TCATCATCAT CTGTGTGGTGA ATGATGGTGA TGGTGGTGGT GATCAGCTGC CTGCTAGACC 180
ACTACAAGCT GTCGTGACGG TCCTTCATCA GCCGGCACAG CCAGGGGCGG AGGAGAGAAG 240
ATGCCCTGTC CTCAGAAGGA TGCCCTGTGGC CTTCCGAGAG CACAGTGTCA GGCAACGGAA 300
45 TCCAGAGGCC GCAGGTCTAC GCCCGCCTC GGGCCACCGA CCGCTGGCC GTGCCGCCCT 360
TCGCCAGCG GGAGCGCTTC CACCGCTTCC AGCCACCTA TCCGTACCTG CAGCACGAGA 420
TCGACCTGCC ACCCACCATC TCGCTGTCTAG ACGGGGAGGA GCCCCACCC TACCAGGGCC 480
CCTGCACCTT CCAGCTTCGG GACCCGAGC AGCAGCTGGA ACTGAACCGG GAGTCGGTGC 540
GCGCACCCCT AAACAGAAC ATCTTCGACA GTGACCTGAT GGAATAGTCC AGGCTGGGCG 600
50 GCCCTGCCCT CCCAGCAGT AACTCGGGCA TCAGCGCCAC GTGCTACGGC AGCGCGGGCC 660
GCATGGAGGG GCCCGCGCCC ACCTACAGCG AGGTCATCGG CCACTACCCG GGGTCTCTCT 720
TCCAGCACCA GCAGAGCAGT GGGCCGCCCT CCTTGCTGGA GGGGACCCGG CTCCACCACA 780
CACACATCCG GCCCTTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT AAACAGAAAG 840
GACACCTCT CTAGGGTCCC CAGGGGGGCC GGGCTGGGGC TCGTAGGTG AAAAGGCAGA 900
55 ACACCTCCCG CTTCTTAGAA GAGGAGTGAG AGGAAGCGG GGGGCGCAGC AACGCATCGT 960
GTGGCCCTCC CCTCCACCT CCTGTGTAT AAATATTAC ATGTGATGTC TGGTCTGAAT 1020
GCACAAGCTA AGAGAGCTTG CAAAAAAGAA AAGAAAAAAG AAAAAAAGAA ACCACGTTTC 1080
TTTGTGAGC TGTGCTCTGA AGGCAAAAGA AAAAAAATTT CTACAGTAAA AAAAAAAGAA 1140
60 A

SEQ ID NO:12 CHA1 Protein sequence:

Protein Accession #: NP_064567

1 11 21 31 41 51
65 | | | | |
MALEFVQII IIVVMMVMV VVITCLLSHY KLSARSFISR HSQGRRREDA LSSEGCLWPS 60
ESTVSGNGIP EPQVYAPPRP TDLRAVPFFA QRERFHRFPQ TYPYLQHEID LPPTISLSDG 120
70 EEPFPYQGPC TLQLRDFEQQ LELNRESVRA PENRTIFDSD LMDSARLGGP CPPSSNSGIS 180
ATCYGSGGRM EGFPPTYSEV IGHYFGSSFQ HQSSGPPSL LEGTRLHHTH IAPLESAAIW 240
SKEKDRQKGH PL

SEQ ID NO:13 CJA5 DNA SEQUENCE

Nucleic Acid Accession #: NM_012445

Coding sequence: 276-1271 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
80 | | | | |

5 GCACGAGGGA AGAGGGTGAT CCGACCCGGG GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA 60
 GCGGCAGCCC CCGCCCGCCC CGCAGCCCTT TCTCCTCCTT TCTCCACAGT CCTATCTGCC 120
 TCTCGCTGGA GGCACAGCCG TGCAGCATCG AAGACAGGAG GAACCTGGAGC CTCATTGGCC 180
 GGCCTGGGGC GCGGCTCCGC TGCTCCTGCC GGGTGATGGA AAACCCAGC CCGCCGCGCG 240
 CCCTGGGCAA GGCCTCTGCG GCTCTCCTCC TGGCCACTCT CGGCGCCGCC GGCACGCTC 300
 TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCCCAGCCAA ATACAGCATC ACCTTCACGG 420
 GCAAGTGGAG CCAGACGGCC TTCCCAAGC AGTACCCCT GTTCCGCCCC CTTGCGCAGT 480
 GGTTCTTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCAGT 540
 10 ACGTCAGTAA CCGGCTCGCG GACTTTGCGG AGCGCGGCGA GGCTTGGGCG CTGATGAAGG 600
 AGATCGAGGC GCGGGGGGAG GCGCTGCAGA GCGTGCACGC GGTGTTTTCG GCGCCGCGCG 660
 TCCCCAGCGG CACCGGGCAG ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
 TCTCGTTTGT GGTGCGCATC GTGCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
 15 ACCTGTGCGA CCGGACCGT TGGCGGGAAC AGCGCGCGCT GGACCTGTAC CCCTACGAGG 840
 CCGGGACCGA CAGCGGCTTC ACCTTCTCCT CCCCACACTC CGCCACCATC CCGCAGGACA 900
 CCGTGACCGA GATPACGTCC TCTCTCCTCA GCCACCCGGC CAACTCCTTC TACTACCCGC 960
 GGCTGAAGGC CCGCTCTCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCA 1020
 GGGCCCTTCAT CCGTCCCGCC CCAGTCTGCG CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
 20 CTTAGTTTCC AGAAACGCGG CTGGACTGCG AGGTCTCCCT GTGGTCTGTC TGGGGACTGT 1140
 GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC TCGCTACGTC CCGGTCCAGC 1200
 CGGCCAACAA CCGGAGCCCG TGCCCCGAGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA 1260
 ACTGCGCTCTA AGACAGAGC CCGCAGCCCG CTGGGGCCCC CGGAGCCATG GGTGTGCGG 1320
 GGCTCTCTGT CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTCG CGCTGTCTCT 1380
 25 GACCGCGGTG AGCGCGCGCC GACCATCTCT GCACTGAAGG GCCCTCTGGT GCGCCGACAG 1440
 GGCTATGGGA AACAGCCTCC TCCCTTCCCA ACCTTGCTTC TTAGGGGCCG CCGTGTCCCG 1500
 TCTGCTCTCA GCGTCTCTCT CCTGCAGGAT AAAGTCATCC CCAAGGCTCC AGCTACTCTA 1560
 AATTATGGTG TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCTAT CGTCCAGGGG 1620
 CCTGCTCCCG ACCTGCTTGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
 30 CTCTCCCGAG GCGCGCATCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GCGCGGTTTC 1740
 GGAAGCGCTA GTGTTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
 TGCTCAC

35 SEQ ID NO:14 CJA5 Protein sequence;
 Protein Accession #: NP_038577

1 11 21 31 41 51
 40 MEMPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60
 PLFRPPAQWS SLGLAAHSSD YSMWRKNQYV SNGLRDFABR GEAWALMKEI EAAGEALQSV 120
 HAVFSAPAVP SGTGSAEL EVQRHSLVS FVVRIVPSPD WFGVDSLDEL CDGDRWREQA 180
 ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYPRRL KALPPIARVT 240
 45 LVRLRQSPRA FIPPAFVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRIGTKS 300
 RTRYVRVQPA NNGSPCPELE EEAECVPDNC V

SEQ ID NO:15 LBH9 DNA SEQUENCE

50 Nucleic Acid Accession #: NM_002391
 Coding sequence: 26-457 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 55 CCGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCTCT 60
 CGCCCTGCTG CCGCTCACTT CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
 CCGGGGAGC GAGTGGCGTG AGTGGGCTTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
 CGGCGTGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAGGGT 240
 GCCCTGCAAC TGAAGAAGG AGTTTGAGC GCACTGCAAG TACAAGTTTG AGAACTGGGG 300
 60 TGGCTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360
 CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGAAGTACAG CCAAGCCTGG ATGCCAAGGA 480
 GCGCCCTGGT TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAAGTGC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCTT TGTCCCTCTC 600
 65 ACTCCCCAGC CCCACCCCTA AGTGCCCAA GTGGGGAGGG ACAAGGATT CTGGGAAGCT 660
 TGAGCCCTCC CCAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTCTCTCC CCACATTTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCTCC CAATAAAGC TCTCTCTTTT 780
 TAATAT

70 SEQ ID NO:16 LBH9 Protein sequence;
 Protein Accession #: NP_002382

1 11 21 31 41 51
 75 MQHRGFLLLT LLALLALISA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DGVGFREGT 60
 CGAQTQRIIC RVPCNWKKEF GADCKYKPFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
 RVTKECTPKT KAKAKAKKGK GKD

SEQ ID NO:17 LEM9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005244

Coding sequence: 1-1617 (underlined sequences correspond to start and stop codons)

5
10
15
20
25
30
35

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGTAGAAC TAGTGATCTC ACCCAGCCTC ACTGTAAACA GCGATTGTCT GGATAAACTG 60
AAGTTTAACC GTGCTGACGC TGCTGTGTGG ACTCTGAGTG ACAGACAAGG CATCACCAAA 120
TCGGCCCCCC TGAGAGTGTC CCAGCTCTTC TCCAGATCTT GCCCACGTGT CCTCCCCCGC 180
CAGCCTTCCA CAGCCATGGC AGCCTACGGC CAGACGCAGT ACAGTGCGGG GATCCAGCAG 240
GCTACCCCTT ATACAGCTTA CCCACCTCCA GCACAAGCCT ATGGAATCCC TTCTACAGC 300
ATCAAGACAG AAGACAGCTT GAACCAATTC CCTGGCCAGA GTGGATTCTT CAGCTATGGC 360
TCCAGCTTCA GCACCTTCAC CACTGGACAG AGCCCATACA CCTACCAGAT GCACGGCACA 420
ACAGGGTTCT ATCAAGGAGG AATGGAAGTG GGCAACGCAG CCGGTTTCGG GAGTGTGCAC 480
CAGGACTATC CTCTCTACCC CGGCTTCCCC CAGAGCCAGT ACCCCAGTA TTACGGCTCA 540
TCCTACAACC CTCCCTACGT CCCGGCCAGC AGCATCTGCC CTTCGCCCTT CTCCACGTCC 600
ACCTACGTCC TCCAGGAGGC ATCTCACAAAC GTCCCAACCC AGAGTTCGGA GTCACTTGCT 660
GGTGAATACA ACACACACAA TGGACCTTCC ACACCAGCGA AAGAGGGAGA CACAGACAGG 720
CCGCACCGGG CTCCGACGGG GAAGCTCCGA GGCCGGTCTA AGAGGAGCAG TGACCCGTCC 780
CCGGCAGGGG ACAATGAGAT TGAGCGTGTG TTCTGTGTGG ACTTGGATGA GACAATAATT 840
ATTTTCACT CTCTTACTAC GGGGACATTT GCATCCAGAT ACGGGAAGGA CACCACGACG 900
TCCGTGCGCA TTGGCCTTAT GATGGAAGAG ATGATCTTCA ACCTTGCAGA TACACATCTG 960
TTCTTCAATG ACCTGAGAGG TTGTGACCAG ATCCACGTGT ATGACGTCTC ATCAGATGAC 1020
AATGGCCAAG ATTTAAGCAC ATACAACCTT TCCGCTGACG GCTTCCACAG TTCGCCCCA 1080
GGAGCCCAACC TGTGCTTGGG CTCTGGCGTG CACGCGCGCG TGGACTGGAT GAGGAAGCTG 1140
GCCTTCCGCT ACCGCGCGGT GAAGGAGATG TACAATACCT ACAAGAACAA CGTTGGTGGG 1200
TTGATAGGCA CTCCCAAAAG GGAGACCTGG CTACAGCTCC GAGCTGAGCT GGAAGCTCTC 1260
ACAGACCTCT GGCCTGACCA CTCCCTGAAG GCACTAAACC TCATCAACTC CCGGCCCAAC 1320
TGTGTCAATG TGCTGGTAC CACCACCTCA CTAATTCCTG CCTGGCCAA AGTCTGTCTA 1380
TATGGCTGGG GGTCTGTGTT TCCTATTGAG AACATCTACA GTGCAACCAA GACAGGGAAG 1440
GAGAGCTGCT TCGAGAGGAT AATGCAGAGA TTCGGCAGAA AAGCTGTCTA CGTGGTGATC 1500
GGTGTATGTT TGAAGAGGA GCAAGGAGCG AAAAAGCACA ACATGCCTTT CTGGCGGATA 1560
TCCTGCCACG CAGACCTGGA GGCAGTGAG CACGCCCTGG AACTGGAGTA TTTATAG

```

SEQ ID NO:18 LEM9 Protein sequence:

Protein Accession #: NP_005235

40
45
50

```

1      11      21      31      41      51
|      |      |      |      |      |
MVELVISPSL TVNSDCLDKL KFNRAAAVW TISDRQGITE SAPLRVSQLF SRSCPRLVLR 60
QPSTMAAYG QTQYSAGIQQ ATPYTAYPPP AQAYGIPSYI IKTEDSLNHS PQQSGFLSYG 120
SSFSTSPITQ SPYTYQMHTG TGFYQGGNGL GNAAGFGSVH QDYPSYGFPP QSQYFPQYYS 180
SYNPPYVPAF SICPSPLSTS TYVLQEASHN VFNQSSSLA GEYNTNHPGS TPAKEGDTDR 240
PHRASDGKLR GRSKRSSDPS PAGDNEIERV FVWDLDETII IFHSLLTGTF ASRYGKDTPT 300
SVRIGLMMEI MIFNLADTHL FFDNLEDCDQ IHVDVSSDD NGQDLSTYNF SADGFHSSAP 360
GANLCLGSGV HGGVDWMRKL AFYRRVKEM YNTYKNNVGG LGTTPKRETW LQRLAELEAL 420
TDLWLTHSLK ALNLINSREN CVNVLVTTTQ LIPALAKVLL YGLGSVPFIE NIYSATKTGK 480
ESCFERIMQR FGRKAVYVVI GDGVEEBQGA KHNMPFWRI SCHADLEALR HALELEYL

```

SEQ ID NO:19 OAA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002740

Coding sequence: 178-1968 (underlined sequences correspond to start and stop codons)

55
60
65
70
75
80

```

1      11      21      31      41      51
|      |      |      |      |      |
CCGCGGTTCG GGCTGCTCCG GCGAGGCGAC CCTTGGGTCT GCGCTGCGGG CGAGGTGGGC 60
AGGTAGGTGG GCGGACGGCC GCGGTTCTCC GGCAAGCGCA GGCGGCGGAG TCCCCACGG 120
CGCCCCAAGC GCCCCCCGCA CCCCCGGCCT CCAGCGTTGA GGCGGGGGAG TGAGGAGATG 180
CCGACCCAGA GGGACAGCAG CACCATGTCC CACACGTCG CAGGCGGCGG CAGCGGGGAC 240
CATTCCCACC AGGTCCCGGT GAAAGCCTAC TACGCGGGG ATATCATGAT AACACATTTT 300
GAACCTTCCA TCTCTTTGA GGGCCTTTGC AATGAGGTC GAGACATGTG TTCTTTTGAC 360
AACGAACAGC TCTTCAACCA GAAATGGATA GATGAGGAAG GAGACCCGTG TACAGTATCA 420
TCTCAGTTGG AGTTAGAAGA AGCCTTAGA CTTTATGAGC TAAACAAGGA TTCTGAATC 480
TTGATTTCATG TGTTCCTCTG TGTACCAGAA CGTCTGGGA TGCCCTGTTC AGGAGAAGAT 540
AAATCCATCT ACCGTAGAGG TGCAACGCCG TGGAGAAAAG TTTATTGTGC CAATGGCCAC 600
ACTTTCCACG CCAAGCGTTT CAACAGGCGT GCTCACTGTG CCATCTGCAC AGACCGAATA 660
TGGGGACTTG GACGCCAAGG ATATAAGTGC ATCAACTGCA AACTTTGGT TCATAAGAAG 720
TGCCATAAAC TCGTCACAAT TGAATGTGGG CGGCATTCTT TGCCACAGGA ACCAGTGATG 780
CCCATGGATC AGTCATCCAT GCATTCTGAC CATGCACAGA CAGTAATTC ATATAATCCT 840
TCAAGTCATG AGAGTTTGA TCAAGTTGGT GAAGAAAAAG AGGCAATGAA CACCAGGGAA 900
AGTGGCAAAG CTTCTACGAG TCTAGGCTCT CAGGATTTTG ATTTGCTCCG GGTAATAGGA 960
AGAGGAAGTT ATGCCAAAGT ACTGTTGGTT CGATTAAAAA AACACAGATC TATTATATGA 1020
ATGAAAGTTG TGAAAAAAGA CTTTGTTAAT GATGATGAGG ATATTGATTG GGTACAGACA 1080
GAGAAGCATG TGTTTGAGCA GGCATCCAAT CATCCTTTC TTGTTGGGCT GCATTCTTGC 1140
TTTCACAGAG AAAGCAGATT GTTCTTTGTT ATAGAGTATG TAAATGGAGG AGACCTAATG 1200
TTTCATATGC AGCGACAAAG AAAACTTCCT GAAGAACATG CCAATTTTA CTCTCAGAA 1260

```


5 ATCAGTCTAG CATTAATAA TCTTCATGAG CGAGGGATAA TTTATAGAGA TTTGAAACTG 1320
 GACAATGTAT TACTGGACTC TGAAGGCCAC ATTAACTCA CTGACTACGG CATGTGTAAG 1380
 GAAGGATTAC GGCCAGGAGA TACAACCAGC ACTTTCCTGTG GTACTCCTAA TTACATTGCT 1440
 CCTGAAATTT TAAGAGGAGA AGATTATGGT TTCAGTGTG ACTGGTGGGC TCTTGGAGTG 1500
 CTCTATGTTG AGATGATGGC AGGAAGGTCT CCATTGATA TTGTTGGGAG CTCCGATAAC 1560
 CCTGACCAGA ACACAGAGGA TTATCTCTTC CAAGTTATTT TGGAAAACA AATTCGCATA 1620
 CCACGTTCTC TGTCTGTAAA AGCTGCAAGT GTTCTGAAGA GTTTTCTTAA TAAGGACCC 1680
 AAGGAACGAT TGGGTGTGCA TCCTCAAACA GGATTGCTG ATATTACAGG ACACCCGTT 1740
 10 TTCCGAAATG TTGATTGGGA TATGATGGAG CAAAACAGG TGGTACCTCC CTTTAAACCA 1800
 AATATTTCTG GGAATTTGG TTTGGACAAC TTTGATTCTC AGTTTACTAA TGAACCTGTC 1860
 CAGCTCACTC CAGATGACGA TGACATTGTG AGGAAGATTG ATCAGTCTGA ATTTGAAGGT 1920
 TTTGAGTATA TCAATCTCTT TTTGATGTCT GCAGAAGAT GTGTCTGATC CTCATTTTTC 1980
 AACCATGTAT TCTACTCATG TTGCCATTTA ATGCATGGAT AAACCTGCTG CAAGCCTGGA 2040
 15 TACAATTAAC CATTTTATAT TTGCCACCTA CAAAAAACA CCAATATCT TCTCTGTAG 2100
 ACTATATGAA TCAATTATTA CATCTGTTTT ACTATGAAAA AAAAATTAAT ACTACTAGCT 2160
 TCCAGACAAT CATGTCAAAA TTAGTTGAA CTGGTTTTC AGTTTTTAAA AGGCCTACAG 2220
 ATAGTAATG AAGTTACCTT TTTGTTTAA AAAAAAAGA G

20 SEQ ID NO:20 QAA1 Protein sequence:
 Protein Accession #: NP_002731

1 11 21 31 41 51
 25 MSHTVAGGGS GDHSQVRVK AYYRGDIMIT HFEPSISFEG LCNEVRDMCS FDNEQLFTMK 60
 WIDEEGDECT VSSQLELEEA FRLYELNKDS ELLIHVPCV PERPGMPCPG EDKSIYRGA 120
 RRWRKLYCAN GHTPQAKRFN RRAHCAICTD RIWGLGRQGY KCINCKLLVH KKCHKLVITIE 180
 CGRHSLPQEP VMFMQSSSMH SDHAQTVIPY NPSSHESLDQ VGEKEAMNT RESGKASSSL 240
 30 GLQDFDLRLV IGRGSYAKVL LVRLKKTDR IYAMKVVKEL VNDDEDIDWV QTEKHVFQEA 300
 SNHPFLVGLH SCFQTESRLF FVIEVYNGGD LMFHMOROK LPEEHARFYS ABISLALNYL 360
 HERGIYRDL KLDNVLLDSE GHKLFDVGM CKGLRFGDT TSTFCSTFNY IAPBLLRGED 420
 YGFVSDWVAL GVLMPEMMAG RSPFDIVGSS DNPQNTEDY LFQVILEKQI RIPRSLSVKA 480
 ASVLKSLFNK DPKERLQCHP QTGFADIQGH PFRNVWDWM MEQKQVVPFP KFNISGEFGL 540
 35 DNFDSEQTNE PQVLTPDDDD IVRKIDQSEF EGFEYINPLL MSAEECV

SEQ ID NO:21 OBH2 DNA SEQUENCE

40 Nucleic Acid Accession #: L05628
 Coding sequence: 197-4792 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 45 CCAGGCGGCGG TTTGCGGCCCC GGCCTCGGCT CCTGCGCGG CCGCGCGCGC CGCGCGCGCC 60
 GCCGCGCGCGG CGCGCGCGCG CGGTAGCGCC AGCAGCGCGG CCGGATCACC CGCGCGCGCG 120
 TGCCCGCGCGG CGCCCGCGCG AGCAACCGGG CCGGATCACC CGCGCGCGCG TGCCCGCGCG 180
 CGCCCGCGCGG ACCGCGATGG CGCTCCGGGG CTCTCGCAGC GCGGATGGCT CCGACCGGCT 240
 CTGGGACTGG AATGTCACGT GGAATACCAG CAACCCGAC TTTACCAAGT GCTTTCAGAA 300
 CACGGTCTCT GTGTGGGTGC CTGTGTTTAA CCTCTGGGCC TGTGTTCCCT TCTACTTCCT 360
 50 CTATCTCTCC CGACATGACC GAGGCTACAT TCAGATGACA CCTCTCAACA AAACCAAAAC 420
 TGCCTTGGGA TTTTTCGTGT GGAATCGTCTG CTGGGCGAGC CTCTCTTACT CTTTCTGGGA 480
 AAGAAGTCGG GGCATATTCC TGGCCCCAGT GTTCTTGCTC AGCCCAACTC TCTTGGGCAT 540
 CACCACGCTG CTTGCTACCT TTTTAATTCA GCTGGAGAGG AGGAAGGGAG TTCAGTCTTC 600
 AGGGATCATG CTCACCTTCT GGCTGGTAGC CCTAGTGTGT GCCCTAGCCA TCCTGAGATC 660
 55 CAAAATTATG ACAGCCTTAA AAGAGGATGC CCAGGTGGAC CTGTTTCGTG ACATCACTTT 720
 CTACGTCTAC TTTTCCCTCT TACTCATTCA GCTCGTCTTG TCCTGTCTCT CAGATCGCTC 780
 ACCCCTGTTT TCGGAAACCA TCCACGACCC TAATCCCTGC CCAGAGTCCA GCGCTTCCCT 840
 CCTGTCTGAG ATCACCTTCT GGTGGATCAC AGGGTTGATT GTCCGGGGCT ACCGCCAGCC 900
 60 CCTGGAGGGC AGTGACCTCT GTTCTTTAAA CAAGGAGGAC ACGTCGGAAC AAGTCGTGCC 960
 TGTTTTGGTA AAGAACTGGA AGAAGGAATG CGCCAAGACT AGGAAGCAGC CGGTGAAGGT 1020
 TGTGTACTCC TCCAAGGATC CTGCCAGCC GAAAGAGAGT TCCAAGTGG ATGCCAATGA 1080
 GGAGGTGGAG GCTTTGATCG TCAAGTCCCG ACAGAAGGAG TGGAAACCCCT CTCTGTTTAA 1140
 GGTGTTATAC AAGACCTTTG GGCCTTACTT CCTCATGAGC TTCTTCTTCA AGGCCATCCA 1200
 CGACCTGATG ATGTTTTCGG GGCCTGAGAT CTAAAGTTG CTCATCAAGT TCGTGAATGA 1260
 65 CACGAAGGCC CCAGACTGGC AGGGCTACTT CTACACCGTG CTGCTGTTTG TCACTGCTCT 1320
 CCTGCAGACC CTCGTGCTGC ACCAGTACTT CCACATCTGC TTCGTCAAGT GCATGAGGAT 1380
 CAAGACCGCT GTCATTTGGG CTGTCTATCG GAAGGCCCTG GTGATCACC AATCAGCCAG 1440
 AAAATCTCTC ACGGTCGGGG AGATGTCAA CCTCATGTCT GTGGACGCTC AGAGGTTCAT 1500
 70 GGACTTGGCC ACGTACATTA ACATGATCTG GTCAGCCCCC CTGCAAGTCA TCCTTGCTCT 1560
 CTACCTCTCT TGGCTGAATC TGGGCCCTTC CGTCTGCGCT GGAGTGGCGG TGATGGTCTC 1620
 CATGTTGCCC GTCAATGCTG TGATGGCGAT GAAGACCAAG ACGTATCAGG TGGCCACAT 1680
 GAAGAGCAAA GACAATCGGA TCAAGCTGAT GAACGAAAT TCAATAGGGA TCAAGTGTCT 1740
 AAAGCTTTAT GCTTGGGAGC TGGCATTCAA GGACAAGGTG CTGGCCATCA GGCAGGAGGA 1800
 GCTGAAGGTG CTGAAGAAGT CTGCTTACCT GTCAGCCGTG GGCACCTTCA CTTGGGTCTG 1860
 75 CACGCCCTTT CTGTTGGGCT TGTGCACATT TGCCGTCTAC GTGACCATG ACGAGAACA 1920
 CATCTGCTCC GCCCAGACAG CCTTCGTGTC TTTGGGCTTG TCAACATCC TCCGTTTCC 1980
 CCTGAACATT CTCCCATATG TCATCAGCAG CATCGTGCAG GCGAGTGTCT CCCTCAACG 2040
 CCTGAGACTT TTTCTCTCCC ATGAGGAGCT GGAACCTGAC AGCATCGAGC GACGGCCTGT 2100
 80 CAAAGACGGC GGGGGCAGCA ACAGCATCAC CGTGAGGAAT GCCACATTA CTTGGGCCAG 2160
 GAGCGACCTT CCCACATGTA ATGGCATCAC CTCTCCATC CCCGAAGGTG CTTTGGTGGC 2220

	CGTGGTGGGC	CAGGTGGGCT	GC GGAAAGTC	GTCCCTGCTC	TCAGCCCTCT	TGGCTGAGAT	2280
	GGACAAAGTG	GAGGGGCACG	TGGCTATCAA	GGGCTCCGTG	GCCTATGTGC	CACAGCAGGC	2340
	CTGGATTACG	AATGATTCTC	TCCGAGAAAA	CATCCCTTTT	GGATGTCAGC	TGGAGGAACC	2400
5	ATATTACAGG	TCCGTGATAC	AGGCCGTGTC	CCTCCTCCCA	GACCTGGAAA	TCCTGCCCCAG	2460
	TGGGGATCGG	ACAGAGATTG	GCGAGAAGGG	CGTGAACCTG	TCTGGGGGCC	AGAAGCAGCG	2520
	CGTGAGCCTG	GCCCCGGGCG	TGTACTCCAA	CGCTGACATT	TACCTCTTGC	ATGATCCCCCT	2580
	CTCAGCAGTG	GATGCCCATG	TGGGAAAACA	CATCTTTGAA	AATGTGATTG	GCCCCAAGGG	2640
	GATGCTGAAG	AACAAGACGC	GGATCTTGGT	CACGCACAGC	ATGAGCTACT	TGCCGCAGGT	2700
	GGACGTCATC	ATCGTCATGA	GTGGCGGCAA	GATCTCTGAG	ATGGGCTCCT	ACCAGGAGCT	2760
10	GCTGGCTCGA	GACGGCGCCT	TCGCTGAGTT	CCTGCGTACC	TATGCCAGCA	CAGAGCAGGA	2820
	GCAGGATGCA	GAGGAGAACG	GGGTCACGGG	CGTCAGCGGT	CCAGGGGAAG	AAGCAAAGCA	2880
	AATGGAGAAT	GGCATGCTGG	TGACGGACAG	TGCAGGGGAG	CAACTGCAGA	GACAGCTCAG	2940
	CAGCTCCTCC	TCCTATAGTG	GGGACATCAG	CAGGCACCAC	AACAGCACCG	CAGAACTGCA	3000
15	GAAAGCTGAG	GCCAAGAAGG	AGGAGACCTG	GAAGCTGATG	GAGGCTGACA	AGGCGCAGAC	3060
	AGGGCAGGTC	AAGCTTTCCG	TGTACTGGGA	CTACATGAAG	GCCATCGGAC	TCTTCACTCT	3120
	CTTCTCCAGC	ATCTTCCCTT	TCATGTGTAA	CCATGTGTCC	GCGCTGGCTT	CCAACATATT	3180
	GCTCAGCCTC	TGGACTGATG	ACCCCATCGT	CAACGGGACT	CAGGAGCACA	CGAAAGTCCG	3240
	GCTGAGGCTC	TATGGAGCCC	TGGGCATTTC	ACAAGGGATC	GCCGTGTTTG	GCTACTCCAT	3300
20	GGCCGTGTCC	ATCGGGGGGA	TCCTTGGCTTC	CCGCTGTCTG	CACGTGGACC	TGCTGCACAG	3360
	CATCTGCGG	TCACCCATGA	GCTTCTTTGA	GCGGACCCCC	AGTGGGAACC	TGCTGAACCG	3420
	CTTCTCCAAG	GAGCTGGACA	CAGTGGACTC	CATGATCCCG	GAGGTGATCA	AGATGTTTAT	3480
	GGGCTCCCTG	TTCAACGTCA	TTGGTGCTTG	CATCGTTATC	CTGCTGGCCA	CGOCCATCGC	3540
	CGCCATCATC	ATCCCGCCCC	TTGGCCTCAT	CTACTTCTTC	GTCCAGAGGT	TCTACGTGGC	3600
25	TTCTCTCCCG	CAGCTGAAGC	GCCTCGAGTC	GGTCAGCCGC	TCCCGGCTCT	ATTCCCATTT	3660
	CAACGAGACC	TTGCTGGGGG	TCAGCGTCAT	TCGAGCCTTC	GAGGAGCAGG	AGCGCTTCAT	3720
	CCACCAGAGT	GACCTGAAGG	TGGACGAGAA	CCAGAAGGCC	TATPACCCCA	GCACTCGTGG	3780
	CAACAGGTGG	CTGGCCGTGC	GGCTGGAGTG	TGTGGGCAAC	TGCATCGTTC	TGTTTGCTGC	3840
	CCTGTTTGGC	GTGATCTCCA	GGCACAGCCT	CAGTGTCTGC	TTGGTGGGCC	TCTCAGTGTG	3900
30	TTACTCATGT	CAGCTACCCA	CGTACTTGAA	CTGGCTGGTT	CGGATGTGAT	CTGAAATGGA	3960
	AACCAACATC	GTGGCCGTGG	AGAGGCTCAA	GGAGTATTCA	GAGACTGAGA	AGGAGGCGCC	4020
	CTGGCAAAAT	CAGGAGACAG	CTCCGCCAG	CAGCTGGCCC	CAGGTGGGCC	GAGTGAATTG	4080
	CCGGAACATC	TGCCCTCGCT	ACCAGAGGGA	CCTGGACTTC	GTCTCAGGCG	ACATCAATGT	4140
	CACGATCAAT	GGGGGAGAAA	AGGTGCGCAT	CGTGGGGCGG	ACGGGAGCTG	GGAAGTCGTC	4200
35	CCTGACCCCT	GGCTTATTTT	GGATCAACGA	GTCTGCCGAA	GGAGAGATCA	TCATCGATGG	4260
	CATCAACATC	GCCAAAGATC	GGCTGCACGA	CCTCCGCTTC	AAGATCACCA	TCATCCCCCA	4320
	GGACCCCTGT	TTGTTTTCGG	GTTCCTCCCG	AATGAACCTG	GACCCATTCA	GCCAGTACTC	4380
	GGATGAAGAA	GTCTGGACGT	CCCTGGAGCT	GGCCACCTGG	AAGGACTTCG	TGTGAGCCCT	4440
	TCCTGACCAAG	CTAGACCATG	AATGTGCAGA	AGCGGGGGAG	AACTCAGTGT	TCGGGCGAGC	4500
40	CCAGCTTGTG	TGCCCTAGCC	GGGCCCTGCT	GAGGAAGACG	AAGATCCTTG	TGTTGGATGA	4560
	GGCCACCGCA	GCGCTGGACC	TGGAAACGGA	CGACCTCATC	CAGTCCACCA	TCCGGACACA	4620
	GTTCGAGGAC	TGCACCGTCC	TCACCATGCG	CCACCGGCTC	AACACCATCA	TGGACTACAC	4680
	AAGGGTGATC	GTCTTGGACA	AAGGAGAAAT	CCAGGAGTAC	GGCGCCCCAT	CGGACCTCCT	4740
	GCAGCAGAGA	GGCTTTTCTT	ACAGCATGGC	CAAAGACGCC	GGCTTGGTGT	GAGCCCCAGA	4800
45	GCTGGCATAT	CTGCTCAGAA	CTGCAGGGCC	TATATGCCAG	CGCCACAGGA	GGAGTCAGTA	4860
	CCCTTGATTA	ACCAAGCCTC	CCACACTGAA	ACCAAAACAT	AAAACACAAA	CCCAGACAAAC	4920
	CAAAACATAT	TCAAAGCAGC	AGCCACCGCC	ATCCGGTCCC	CTGCCTGGAA	CTGGCTGTGA	4980
	AGACCCAGGA	GAGACAGAGA	TGCGAACCAAC	C			

50 SEQ ID NO:22 QBH2 Protein sequence:
Protein Accession #: AAB46616

	1	11	21	31	41	51	
55	MALRGFCSAD	GSDPLWDWNV	TWNTSNPDFT	KCFQNTVLVW	VPCFYLWACF	FFYFLYLSRH	60
	DRGYIQMTPL	NKTKTALGFL	LWIVCWADLF	YSFWERSRGI	FLAPVFLVSP	TLLGITTLA	120
	TFLIQLERRK	GVQSSGIMLT	FWLVALVCAL	AILRSKIMTA	LKEDAQVDLF	RDITFYVYFS	180
	LLLIQLVLSC	PSDRSPLFSE	TIHDPNCPCE	SSASFLSRIT	FWWITGLIVR	GYRQPLEGSD	240
60	LWSLNKEDTS	EQVVPVLVKN	WKKECAKTRK	QPVKVYVSSK	DPAQPKESSK	VDANEVEEAL	300
	IVKSPQKEWN	PSLFKVLKYT	FGPYFLMSFF	FKAIHDLMMF	SGPQILKLLI	KFVNDTKAPD	360
	WQGYFYTVLL	FVTACLQTLV	LHQYFHICFV	SGMRIKTAIV	GAVYRKALVI	TNSARKSSTV	420
	GEIVNLSMDV	AQRFMDLATY	INMWSAPLQ	VILALYLLWL	NLGFSLVLAGV	AVMVLWVFN	480
	AVMAMTKTKY	QVAHMKSKDN	RIKLMNEILN	GIVKVLKYAW	ELAFKDKVLA	IRQEBELKVLK	540
65	KSAYLSAVGT	FTWVCTPFVL	ALCTFAVYVT	IDENNILDAQ	TAFVSLALFN	ILRFPLNILP	600
	NVSSIVQAS	VSLKRLRIFL	SHEELEPDSI	ERRPVKGGG	TNSITVRNAT	FTWARSPPPT	660
	LNGITFSIPE	GALVAVVGOV	GCGKSSLLSA	LLAEMDKVEG	HVALKGSVAY	VPQQAWIQND	720
	SLRENILFGC	QLEEFYVRSV	IQACALLPDL	EILPSGDRTE	IGEKGVNLSG	GQKQVSLAR	780
	AVYSNADIYL	FDDPLSAVDA	HVGKHIFENV	IGPKGMLKNK	TRILVTHSMS	YLPQVDVIV	840
70	MSGGKISEMG	SYQELLARDG	AFABFLRTYA	STEQEQDAEE	NGVTGVSGPG	KEAKQMENG	900
	LVTDSAGKQL	QRQFSSSSSY	SGDISRHNS	TAELOKAEAK	KEETWKLMEA	DKAQTQGVKL	960
	SVYWDVMKAI	GLFISFLSIF	LFMCNHVSAL	ASNYWLSLWT	DDPIVNGTQE	HTKVRLSVYG	1020
	ALGISQGIIV	FGYSMAVSIG	GILASRCLHV	DLHSLILRSP	MSFFERTFSG	NLVNRFPSKEL	1080
	DTVDSMIPV	IKMFMSLFPN	VIGACIVILL	ATPIAAITIP	PLGLIYFFVQ	RFYVASSRQL	1140
75	KRLSVSRSP	VYSHFNTELL	GVSIVIRAFEE	QERFIHQSDL	KVDENQKAYY	PSIVANRWLA	1200
	VRLECVNCI	VLFAALFAVI	SRHSLSAGLV	GLSVSYSLQV	TTYLNWLVRM	SSEMETNIVA	1260
	VERLKEYSET	EKEAPWQIQE	TAPPSSWPQV	GRVEFRNYCL	RYRELDLDFV	RHINVTINGG	1320
	EKVGIVGRGT	AGKSSLLTGL	FRINESAEGE	IIDIGNIAK	IGLHDLRFKI	TIIPQDFVLF	1380
	SGSLRMLDP	FSQYSDEEIV	TSLELAHLKD	FVSALPDKLD	HECAEGGENL	SVGQRQLVCL	1440
80	ARALLRKTKI	LWLDEATAAV	DLETDDLQIS	TIRTQPEDCT	VLTHAHLRNT	IMDYTRIVIVL	1500
	DKGEIQEYGA	PSDLLQQRGL	FYSMAKDAGL	V			

SEQ ID NO:23 PAA2 DNA SEQUENCE

5		Nucleic Acid Accession #: NM_013309	
		Coding sequence: 1-1290 (underlined sequences correspond to start and stop codons)	
		1 11 21 31 41 51	
10		ATGGCCGGCT CTGGCGCGTG GAAGCGCCTC AAATCTATGC TAAGGAAGGA TGATGCGCCG	60
		CTGTTTPTAA ATGACACCAG CGCCTTTGAC TTCTCGGATG AGGCGGGGGA CGAGGGGCTT	120
		TCTCGGTTCA ACAAACTTCG AGTTGTGGTG GCCGATGACG GTTCCGAAGC CCCGGAAGG	180
15		CCTGTTAACG GGGCGCACCC GACCCCTCCAG GCCGACGATG ATTCTTACT GGACCAAGAC	240
		TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCTGTGACAA CTGCAGCAAA	300
		CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTGC TGCCGTTCTG	360
20		TACTTGCTTT TCATGATTGG AGAAGTTGTA GGTGGATACA TTGCAAAATAG CCTAGCAATC	420
		ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT	480
		TTGTGGCTAT CATCAAATC ACCAACCAAA AGATTCACTT TTGGATTTC TCGCTTAGAG	540
25		GTTTGTGTCAG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT	600
		GAAGCTGTGC AAAGAACTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC	660
		ACCGCAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGGT TTCTGTGTA CCAGTCTGGT	720
30		CACCGTCACT CCGATTCCCA CTCCCTGCCT TCAAATTCCT CTACCAAGAG TTCTGGGTGT	780
		GAACGTAACC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTTGTACA TGCTTTGGGA	840
		GATTTGGTAC AGAGTGTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA	900
35		TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA	960
		TTTCGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTTTGAAT	1020
		GTAGACTATA TCAAGAAGC CTTGATGAAA ATAGAAGATG TATATTCACT CGAAGATTTA	1080
		AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT	1140
		GGAAAGTTCAT CTAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTATAT ATTGAACACA	1200
		TTTGGCATGT ATAGATGTAC TATTCACTT CAGAGTTACA GGCAAGAAAT GGACAGAACT	1260
		TGTGCAAAAT GTCAGAGTTC TAGTCCCTGA	

SEQ ID NO:24 PAA2 Protein sequence:

35		Protein Accession #: NP_037441	
		1 11 21 31 41 51	
40		MAGSGAWKRL KSMRLKDDAP LFLNDTSAPD FSDEAGDEGL SRFNKLRVVV ADDGSEAPER	60
		PVNGAHPFLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCSK QREILKQRKV KARLTIAAVL	120
		YLLFMIGELV GGYIANSALAI MTDALHMLTD LSAILLTLLA LWLSSKSPTK RFTFGFHRLE	180
45		VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDINLI TAAVGVAVNV IMGFLLNQSG	240
		HRHSHSHSLP SNSPTRSGSGC ERNHGQDSLA VRAAFVHALG DLVQSVGVLI AAYIIRFKPE	300
		YKIADPICTY VFSLVAFVFT FRIIWDTVVI ILEGVPSHLN VDYIKEALMK IEDVYSVEDL	360
		NIWSLTSGKS TAIWHIQLIP GSSSKWEVQ SKANHLLNT FGMRYCTIQL QSYRQEVDR	420
		CANQSSSP	

SEQ ID NO:25 PAA3 DNA SEQUENCE

50		Nucleic Acid Accession #: AB037765	
		Coding sequence: 375-2798 (underlined sequences correspond to start and stop codons)	
		1 11 21 31 41 51	
55		GCCGAGTCGG TGGCGGCTGC AGGCTGGGAG GGAGAAGTGC TACGCCCTTG CAGGTTGGCG	60
		AAGTGGTTCC AGGCTACCCG GCTAGTCTGG CACGGCCCGG TCTTCGCCTT CCTCTCCCGT	120
		CGCGTGGCGG CGGGAACCTG TGGCCGCGCG GCCTCGGGAA CGGCCCAGGT CCCGCCCGC	180
60		AGGTCCCGGG CAGATAACAT AGATCATCAG TAGAAAACTT CTTGAAGTTG TTCAAGAAAA	240
		ATTTGAAAGT AGCAAAATAG AAAATAAAGA ATTAACAGCA GATACAGAGG ACAGCATGGA	300
		AGTGTGTCTT TAGGAAACAG AACACAGCAG TGAAAAAACA GACAAAATCC GCTCAGATAC	360
65		AACTGCAGCT GATAATGTTT TCCGGCTTCA ATGTCTTTAG AGTTGGGATC TCTTTTGTC	420
		TAATGTGCAT TTTTACATG CCAACAGTAA ACTCTTTACC AGAACTGAGT CCTCAGAAAT	480
		ATTTTAGTAC ATTTCAACCA GGTCTTGAAG AACTGAATGA GGCTGTAGA CCTCTGCAGG	540
70		ACTATGGAAT TTCAGTTGCC AAGGTTAAT GTGTCAAGA AGAAATATCA AGATACTGTG	600
		GAAAAGAAAA GGATTGTATG AAAGCATATT TATTCAGGG CAACATATFG CTCAGAGAT	660
		TCCCTACTGA CACCTTGTTT GATGTGAATG CCATTGTGCG CCATGTTCTC TTTGCTCTTC	720
75		TTTPTAGTGA AGTGAATAT ATTACCAACC TGGAAAGACT TCAGAACATA GAAAATGCTC	780
		TGAAAGGAAA AGCAATATAT ATATCTCAT ATGTAAGAGC CATTTGAATA CCAGAGCACA	840
		GAGCAGTCAT GGAAGCCGGT TTTGTGTATG GGACTACATA CCAATTTGTC TTAACACAG	900
80		AAATTGCCCT TTTGGAAAGT ATTTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT	960
		TTTATTTGTA ACTAGTCTTG GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAGC	1020
		CATTGACTAC ACTGAACATT CACCTGTTTA TTAAGACRAAT GAAAGCACCT CTGTGACTG	1080
		AAGTTGCTGA AGATCTCTAA CRAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACCACTGG	1140
		TTTTTATTTT TAGCCAACAG GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTGT	1200
		CTTGGCGTCT TCTGGGAAAA GCAGGAGTTC TACTCTTTGT AAGGGACTCT TTGGAAGTGA	1260
		ACATTTCTCA AGATGCTAAT GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCAGTGGAAAT	1320
		TTTTTGTATT ACATGATGTT GATTTAATAA TATCTCATGT GGAATAATAT ATGCACATG	1380
		AGGAATATCA AGAAGATGAA GACAAATGACA TGGAAGGTCC AGATATAGAT GTTCAGGATG	1440
		ATGAAGTGGC AGAAACTGTT TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACCTACAG	1500

5	TGGAACCTAAC	AGAAGAAACA	TTTAAATGCAA	CAGTGTATGGC	TTCTGACAGC	ATAGTACTCT	1560
	TCTATGCTGG	TTGGCAAGCA	GTATCCATGG	CATTTTTCGA	ATCCTATATT	GATGTGGCAG	1620
	TTAAACTGAA	AGGCACATCT	ACTATGCTTC	TTACTAGAAT	AAACTGTGCA	GATGTGCTCG	1680
	ATGTATGTAC	TAAGCAAAAT	GTTACTGAAT	TTCTATCAT	AAAGATGTAC	AAGAAAGGCG	1740
	AGAACCCAGT	ATCTTATGCT	GGAAATGTTAG	GAACCAAGA	TCTCCTAAAA	TTTATCCAGC	1800
	TCAACAGGAT	TTTATATCCA	GTGAATATAA	CATCGATCCA	AGAAGCAGAA	GAATATTTAA	1860
	GTGGGGAAAT	ATATAAAGAC	CTCATCTTGT	ATTCTAGTGT	GTCAATATTG	GGACTATTTA	1920
	GTCCAACCAT	GAAGAACAGCA	AAAGAAGATT	TTAGTGAAGC	AGGAACTAC	CTAAAAGGAT	1980
	ATGTTATCAC	TGGAATTTAT	TCTGAAGAAG	ATGTTTTCGT	ACTGTCAACC	AAATATGCTG	2040
10	CAAGTCTTCC	AGCCCTGCTG	CTTGCCAGAC	ACACAGAAGG	CAAAATAGAG	AGCATCCCAC	2100
	TAGCTAGCAC	ACATGTCACAA	GACATAGTTC	AAATAATAAC	AGATGCACCTA	CTGGAAATGT	2160
	TTCCGGAAT	CAGCTGTGAA	AATCTTCCCA	GTTATTTTCAG	ACTTCAGAAA	CCATTATTTGA	2220
	TTTTGTTCAG	TGATGGCAGT	GTAATCTCT	AATATAAAAA	AGCAATATTG	ACACTGGTAA	2280
15	AGCAGAAATA	CTTGGATTCA	TTTACTCCAT	GCTGGTTAAA	TCTAAAGAAT	ACTCCAGTGG	2340
	GGAGAGGAAT	CTTGCGGGCA	TATTTTGATC	CTCTGCCCTCC	CCTTCCTCTT	CTTGTTTTGG	2400
	TGAATCTGCA	TTTCTAGTGG	CAAGTATTTG	CATTTCCTTC	AGACCAGGCT	ATAATTGAAG	2460
	AAAACCTTGT	ATTGTGGCTG	AAGAAATTAG	AAGCAGGACT	AGAAAATCAT	ATCACAATTT	2520
	TACCTGCTCA	AGAAATGGAA	CCTCCTCTTC	CAGCTTATGA	TTTCTAAGT	ATGATAGATG	2580
20	CCGCAACATC	TCAACGTGGC	ACTAGGAAAG	TTCCCAAGTG	TATGAAAGAA	ACAGATGTGC	2640
	AGGAGAATGA	TAAGGAACAA	CATGAAGATA	AATCGGCAGT	CAGAAAGAA	CCGATTGAAA	2700
	CTCTAGCAAT	AAAGCATTTG	AATAGAAGTA	ATTGGTTTAA	AGAAGCAGAA	AAATCATTTA	2760
	GACGTGATAA	AGAGTTAGGA	TGCTCAAAAG	TGAACCTAAT	TTATAGGGCT	GTGGTTTCCA	2820
	AAATTTTTTT	GGCATGATAG	ACTTAATTTA	TTTCCTTAAA	GAATAATATT	AAATCATTTT	2880
25	AAGTTTGAG	ACTAGTGCCA	TCCAATAGAA	TTATAATATA	AGTCACATAT	TTTATTTAAA	2940
	ATTTTCTAGT	AACATACATTA	AACAAAGTAA	AAGTGAGCAG	GGCAAAATAA	TTTTGATATT	3000
	ACTTTTCACC	CAGTAGTATA	CCCAAAATAG	CGAAATATAG	AAATTATTAA	TGAGATATTT	3060
	TACATCCTTT	TTTGTACCAA	GTCTTCTAAA	TGCAGTACAT	ATTTTATACT	TACTGCATT	3120
	CTTACTCCG	AGTAGCCATA	TTTCAAGTGT	TCATTGGCCAC	ATGTGGCCTG	TGACTACTGT	3180
30	ATTGAGCAGT	TCAGCTACTAG	ACAAAACTA	GCATAATTAA	CTTAGTTCTA	GCCATGATTT	3240
	CTATTGGAT	TAAATTTAAA	CTCTAATCAC	AGTTAACTCC	ACAGTGCATT	CATGCAGCTG	3300
	ACAGTTATAT	TTGTTTATTT	GGAGTCATGA	TATTAAATC	AGCGTTTGTG	AACCTCAGGG	3360
	GATATTTAGC	AATTTGTCGG	AGACATTTTT	GATGTCAATGA	CTAGGGCAGT	TATTTGACATT	3420
	TAGTGAGTAG	AGGCCATGGA	TCCTGCTAAA	TAACTGTCAT	TGGACAGCGC	CCCACAACAA	3480
35	AGAATTTATC	TGCCCGAAAT	GGTAGTCGTG	CCAAGGCTGA	GTAACCTTGT	GTTAAAAGTA	3540
	ACCTGTGGCA	GACTAGGTTT	CCAGAATTTT	CTGGTTCTGC	TCACGTATCA	TGTTTGAAAA	3600
	AATTTTGGCT	ATTAAAGATA	TGTATTAGAT	GGTCTTATCC	TGATTATTAC	CTGGATACAA	3660
	CTTGATCTTT	TCTAATATT	TCAGAAAGTG	ATGGGATAAC	CCTAGAAGAG	GACTCAGAAAT	3720
	GATATTTATA	TTTAAAGTGA	GTCTTAAAC	CTCCTCTTAT	TTCTACAAGT	TATATGGCTA	3780
40	AATTTACAGT	TGAACAGGGA	TTTCACTATC	TGCAATCTCC	TCATGGAAAG	AGAGGCTCCC	3840
	TCATCTGAAG	CGTCTCTGAA	ATCTACCCCT	GCAAGCTTCA	GACAAATCAG	TTGATCTCCC	3900
	TGAGGCACAC	GGGCTCATTC	TGTGAGGGAG	GGAAAGATTA	GCCAAAGAGT	TAAATTTTCA	3960
	TCCAAATCAC	TTAGCTGTGA	GACTGATCTG	TTTGTAGCAG	TTGTTTGTCT	CATTTTGTCT	4020
	CTGTGCAATT	TTTGAGACAT	TTGTTGAGAA	TATTTCTATT	GGTGTCTTAC	TGTATTTTTC	4080
45	TTTTTAATAT	CTACTTGATA	TCTTGTCTTT	TAAATTTTCT	TCACATATGG	TTTGCCTGAT	4140
	ACAACCTGAT	TTTATTAAGT	AAATTTAAGG	AATCTAACAG	CTAAACTTCA	GTAAGTGCAT	4200
	MTATTTCTCT	ATAACATAGA	CCCGTTGCTA	CTCTCAGCAC	CCTCTCCTCA	ATTTTPTTTC	4260
	CTGTAGCATG	TGATGCTCTA	TTTAACTCAT	TTTCAATTGC	TTTTATTFTT	AAATAGGGAA	4320
	CAATGAGAGT	GAATCTTAAA	TATAGGTTGT	AGTAATATAA	CATCATTAGC	CTAATTTATTA	4380
50	GAAAATGCTA	ATTAAAGTACC	AGCACATAGA	AACATGAAAT	TGCTTAGTCA	TTGTACCTTT	4440
	GTGAGCAATT	TTGACAGTCA	TTAATGTTTG	TCATAAATTT	AAATAAAGTG	TCTGGGTTTC	4500
	AGAATACCTT	CAAAAAAATA	AAAAAA				

SEQ ID NO:26 PAA3 Protein sequence:

Protein Accession #: BAA92582

55	1	11	21	31	41	51	
	MFSGFNVRV	GISFVIMCIF	YMPVNSLPE	LSPQKYFSTL	QPGLEELNEA	VRPLQDYGIS	60
60	VAKVNCVKEE	ISRYCKEKED	LMKAYLFKGN	ILLREFPTDT	LFQVNAIVAH	VLFFALFSEV	120
	KYITNLEDLQ	NIENALKGKA	NIIFSIVRAI	GIPEHRAVME	AGFVYGTYYQ	FVLTTETIALL	180
	ESIGSEDEVEY	AHLFFPHCKL	VLDLTQQCRR	TLMEQPLFTL	NIHLFIKTMK	APLLTEVAED	240
	PQQVSTVHLQ	LGLPLVFVIVS	QQAITYEADRR	TAENVAWRL	GKAGVLLLLR	DSLEVNIPQD	300
	ANVVFKEAEE	GVPVEFLVLH	DVDLIISHVE	NMHIIEEIQE	DEDNDMEGPD	IDVQDDEVAE	360
65	TVFRDRKRKL	PLELTVELTE	ETFNATVMAS	DSIVLFYAGW	QAVSMAFLQS	YIDVAVKLKG	420
	TSTMLLTRIN	CADWSDVCTK	QNVTEFPITK	MYKKGENPVS	YAGMLGTDKL	LKFIQLNRIS	480
	YFVNITSIQE	ABEYLSGELY	KDLILYSSVS	VLGLFSPTMK	TAKEDFSEAG	NYLKGIVITG	540
	IYSEEDVLLL	STKYAASLPA	LLLARHTECK	IESIPLASTH	AQDIVQIITD	ALLEMPREIT	600
	VENLPSYFRL	QKPLLLFLSD	GTVPNPQYKA	ILTLVKQKYL	DSFTPCWLNL	KNFPVGRGIL	660
70	RAYFDLPLPL	PLLVLVNLSH	GGQVFAFPSD	QAIIEENLVL	WLKLEAGLE	NHITILPAQE	720
	WKFPPLPAYDE	LSMIDAATSQ	RGTRKVPKCM	KETDVQENDK	EQHEDKSAVR	KEPIETLRIK	780
	HWNRSNWFKE	BEKSFRRDKK	LGCSKVN				

SEQ ID NO:27 PAA5 DNA SEQUENCE

Nucleic Acid Accession #: NM_012449

Coding sequence: 66-1085 (underlined sequences correspond to start and stop codons)

75	1	11	21	31	41	51	
	CCGAGACTCA	CGGTCAAGCT	AAGGCGAAGA	GTGGGTGGCT	GAAGCCATAC	TATTTTATAG	60
80	AATTAAATGA	AAGCAGAAAA	GACATCACAA	ACCAAGAAGA	ACTTTGGAAA	ATGAAGCCCTA	120

5 GGAGAAATTT AGAAGAAGAC GATTATTTTC ATAAGGACAC GGGAGAGACC AGCATGCCTAA 180
 AAAGACCTGT GCTTTTGGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACTTCA GCACACACAG GAACCTCTTC CACAGTGGCA CTGCGCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTCTTTTACA CTCTTCTGAG GGAAGTAATT CACCTTTAG 360
 CAACCTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
 CAATGGTTC CATCACTCTC TTGGCATTGG TTACCTGCC AGGTGTGATA GCAGCAATTG 480
 TCCAACTTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTCG TGTACTGCAT GCAATTTATA 600
 10 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
 AGGTCCAACA AAATAAAGAA GATGCCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
 ATGTGTCTCT GGGAAATTGT GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTCTACTA TATTCAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCCTGGAAT AAGTGGATAG 900
 ATATAAACA ATTTGTATGG TATACACCTC CAACCTTTAT GATAGCTGTT TTCCTTCCAA 960
 15 TTGTGTCTCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGTACTCTA 1020
 AGATTAGACA TGGTTGGGAA GACGTACCAA AAATTAACAA AACTGAGATA TGTTCCCACT 1080
 TGTAGAATTA CTGTTTACAC ACATTTTGTG TCAATATTGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

20 **SEQ ID NO:28 PAA5 Protein sequence**
 Protein Accession #: NP_036581

25 1 11 21 31 41 51
 MESRKDITNQ EELWKMMPRR NLEEDDYLRK DTGETSMLKR FVLLHLHQTA HADEFDPCPSE 60
 LQHTQELFPQ WHPPIKIAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120
 VSTLLALVY LFGVIAAIVQ LHNQTKYKPF PHWLDKMWLT RKQFGLLSFF FAVLHAIYSL 180
 SYPMRRSYRY KLNINWAYQV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 30 VSDSLWREF HYQSKLGLV SLLLTIALH IFANWKWIDI KQFVWYTPPT FMLAVFLPIV 300
 VLIFKSILFL PCLRKKILKI RHGWEDVTIK NKTEICSQL

SEQ ID NO:29 PAA7 DNA SEQUENCE
 Nucleic Acid Accession #: NM_030774
 Coding sequence: 1-963 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 ATGAGTTCCT GCAACTTCAC ACATGCCACC TTGTGCTTGA TTGGTATCCC AGGATTAGAG 60
 AAAGCCCAT TCTGGGTGG CTTCCCTCTC CTTTCCATGT ATGTAGTGGC AATGTTTGA 120
 40 AACTGCATCG TGGTCTTCAT CGTAAGGACG GAACGCAGCC TGCAAGCTCC GATGTACCTC 180
 TTCTCTGCA TGCTTGCAGC CATGTACCTG GCCTTATCCA CATCCACCAT GCCTAAGATC 240
 CTGCGCTTT TCTGGTTTGA TTCCCGAGAG APTAGCTTTG AGGCCTGTCT TACCCAGATG 300
 TTCTTTATTC ATGCCCTCTC AGCCATTGAA TCCACCATCC TGCTGGCCAT GGCCTTTGAC 360
 CGTTATGTGG CCACTCTGCC CCCACTGCGC CATGCTGCAG TGCTCAACAA TACAGTAACA 420
 45 GCCCAGATG GCATCGTGGC TGTGGTCCGC GGATCCCTCT TTTTTCCTCC ACTGCCCTG 480
 CTGATCAAGC GGCTGGCCCT CTGCCACTCC AATGTCTCTC CGCACTCCTA TTGTGTCCAC 540
 CAGGATGTAA TGAAGTTGGC CTATGCAGAC ACTTTGCCCA ATGTGGTATA TGGTCTTACT 600
 GCCATTCCTG TGGTCAAGGG CGTGGACGTA ATGTCTCATC CTTTGTCTTA TTTTCTGATA 660
 ATACGAACCG TTCTGCAACT GCCTTCCAAG TCAGAGCGGG CCAAGGCCTT TGGAACTCTG 720
 50 GTGTCAACA TTGTGTGGT ACTCGCTTC TATGTGCCAC TTATTTGGCT CTCAGTGGTA 780
 CACCGCTTTG GAAACAGCCT TCATCCCAT TGTGCTGTG TCATGGGTGA CATCTACCTG 840
 CTGCTGCCCT CTGTCACTAA TCCCATCATC TATGGTGCCA AAACCAAAAC GATCAGAACA 900
 CGGGTCTGCG CTATGTTCAA GATCAGCTGT GACAAGGACT TGCAAGCTGT GGGAGGCAAG 960
 TGACCCCTAA CACTACACTT CTCTTATCT TTATTGGCTT GATAACATA ATTATTCTA 1020
 55 ACATCAAGCT ATTTCCAGTT GCCCATAAGC ACATCAGTAC TTTTCTCTGT CTGGAATAGT 1080
 AAACATAAGT ATGTGATATC TACCTAAAGG ACTATTATGT GGAATAATAC ATACTAATGA 1140
 AGTATTACAT GATTATAAGA CTACAATAAA ACCAAACATG CTTATAACAT TAAGAAAAAC 1200
 AATAAAGATA CATGATTGAA ACCAAGTTGA AAAATAGCAT ATGCCCTTGA GGAAATGTGC 1260
 60 TCAAAATAC TATGATTATG TGTGTCCCT ACTTCTCTC TCTTTTCTCT TTTCTTTTCT 1320
 TTTATTATGG TTAGCTGTCA CATACAACCT TTTTCTTCTT TGAGATGGGG TCTGCTCTG 1380
 TCACCAAGCT GAGATGTCAGT GCGCGCATCT CGGCTCACTG CAACCTCCAC ATCCCATGTT 1440
 GAAGTAATTC TTCTGCCTCA GCCTCCCGAG TAGCTGGGAC TAGAGGAACG TGCCACCATG 1500
 65 ACTGGCTAAT TTTCTGTATT TTTAGTAGA GACAGAGTTT CACCATGTTG GCCAGGATGG 1560
 TCTCGATCTC CTGACCTTGT GATCCACCCG CCTCAGCCTC CCAAGTGTGT GGGATTACAG 1620
 GTGTGAACCA CTGTGCCCGG CCTGTGTACA ACTTTTAAAG TAGGGAATAT GATAGCTTCG 1680
 CATGGTGGTG TGCACCTATA GCCCCCACTG CCTGGAAAGC TGAGGTGGGA GAATCGCTTG 1740
 AGTCCAGGAG TTTGAGGTTA CAGTGATCCA CGATCGTACC ACTCACTCTC AGCCTGGGCA 1800
 ACAGAGCAAG ACCCTGTCTC AAAGCATAAA ATGGAATAAC ATATCAAAATG AAACAGGGAA 1860
 70 AATGAAGCTG ACAATTTATG GAAGCCAGGG CTGTCTACAG TCTCTACTGT TATTATGCAT 1920
 TACCTGGGAA TTTATATAAG CCCTTAATAA TARTGCCAAT GAACATCTCA TGTGTGCTCA 1980
 CAATGTTCTG GCAGTATPAT AAGTGCTTCA CAGGTTTTAT GTGTCTCTCG TAACCTTTATG 2040
 GAGTAGGTAC CATTTGTGTC TCTTTATPAT AAGTGAGAGA AATGAAGTTT ATATTATCAA 2100
 GGGGACTAAA GTCACACGGC TTGTGGGCAC TGTGCCAAGA TTTAAAAATTA AATTTGATGG 2160
 75 TTGAATACAG TTACTTTAAT ACCATGTTAT ATTGCTTCTT GTGTAAATC TGCCATTAT 2220
 TTCTCAGCT GTACAAATCC TCTGTTTCT CTCTGTTACA CACTAAATC AATGGCTTTG 2280
 TACTTGTGAT GAGAGATAAC CTTGCCCTAG TTGTGGGCAA CACATGCAGA ATAATCTCTG 2340
 TTTACAGCTG CCTTCTGTGA TCTTATTGCT TGCTTTTCTC CAGATTACAG GAGAATGTTG 2400
 TTGTCTATTT GTCTCTTACA TCTCTTGAT CATGTCTTCA TTTTAAATG TGCTCTGTAC 2460
 80 CTGTCAAAAA TTTTGAATGT ACACCAATG CTATTGTCTG AACTTGAGTA TAAGATAAAA 2520
 TAAATTTTAA TTTTAAATTT T

SEQ ID NO:30 PAA7 PROTEIN SEQUENCE

Protein Accession #: NP_110401

5 1 11 21 31 41 51
 | | | | | |
 MSSCNFTHAT FVLIGIPGLE KAHFWVGFPL LSMYVVAMFG NCIVVFIVRT ERSLSHAPMYL 60
 FLCMLAIDL ALSTSTMFKI LALFWFDSRE ISFEACLQOM FFIHALSAIE STILLAMAFD 120
 RYVAICHLR HAAVLNNTVT AQIGIVAVVR GSLFFFLPL LIKRLAFCHS NVLSHSYCVH 180
 10 QDVMKLAYAD TLFNVVYGLT AILLVMGVDV MFISLSYFLI IRTVLQLPSK SERAKAFGTC 240
 VSHIGVVLAF YVPLIGLSV HRFGNSLHPI VRVVMGDIYL LPPVINPII YGAKTKQIRT 300
 RVLAMFKISC DKDLQAVGGK

SEQ ID NO:31 PAV6 DNA SEQUENCE

Nucleic Acid Accession #: XM_050837

Coding sequence: 1-1020 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | | |
 20 ATGAAGTGGG AGCTGCTGCT GTGGCTGCTG GTGCTGTGCG CGCTGCTCCT GCTCTTGGTG 60
 CAGCTGCTGC GCTTCTCTGAG GGCTGACGGC GACCTGACGC TACTATGGGC CGAGTGGCAG 120
 GGACGACGCC CAGAATGGGA GCTGACTGAT ATGGTGGTGT GGGTGACTGG AGCCTCGAGT 180
 GGAATTGGTG AGGAGCTGGC TTACCACTTG TCTAAACTAG GAGTTTCTCT TGTGCTGTCA 240
 25 GCCAGAAAG TGCATGAGCT GGAAAGGGTG AAAAGAGAT GCCTAGAGAA TGGCAATTTA 300
 AAAGAAAAG ATATACTTGT TTTGCCCTTT GACCTGACCG ACCTGCTTC CCATGAAGCG 360
 GCTACCAAG CTGTCTCTCA GGAGTTTGGT AGAATCGACA TTCTGGTCAA CAATGGTGGA 420
 ATGTCCTCAGC GTTCTCTGTG CATGGATACC AGCTTGGATG TCTACAGAAA GCTAATAGAG 480
 CTTAACTACT TAGGGACGGT GTCTTTGACA AAATGTGTTT TGCTTCACAT GATCGAGAGG 540
 AAGCAAGGAA AGATTGTTAC TGTGAATAGC ATCCTGGGTA TCATATCTGT ACCTCTTTCC 600
 30 ATTGGATACT GTGCTAGCAA GCATGCTCTC CGGGTTTTT TTAATGGCCT TCGAACAGAA 660
 CTTGCCACAT ACCCAGGTAT AATAGTTTCT AACATTTGCC CAGGACCTGT GCAATCAAAT 720
 ATTTGTGAGA ATTCCTTAGC TGGAGAAATC ACAAGACTA TAGGCAATAA TGGAGACCAG 780
 TCCACAGA TACCAACAGC TCGTTGTGTG CGGCTGATGT TAATCAGCAT GGCCCAATGAT 840
 35 TTGAAGAAG TTGTGATCTC AGAACAACCT TTCTTGTAG TAACATATTT GTGGCAATAC 900
 ATGCCAACCT GGGCTGTGTG GATAACCAAC AAGATGGGGA AGAAAGGAT TGAGAACTTT 960
 AAGATGGTG TAGATGCAGA CTCTCTTAT TTTAAATCT TTAAGACAAA ACATGACTGA

SEQ ID NO:32 PAV6 Protein sequence

Protein Accession #: XP_050837

1 11 21 31 41 51
 | | | | | |
 40 MNWELLLWLL VLCALLLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MUVVWVTGASS 60
 GIGEELEYQL SKLGVSLVLS ARRVEHLERV KRCLENGNL KEKDILVLP DLTDTGSHEA 120
 45 ATKAVLQEFQ RIDILVNNGG MSQRLCMDT SLDVYRKLE LNYLGTVSLT KCVLFPHMIR 180
 KQKLIIVFNS ILGILSVPLS IGYCASKHAL RGFFNGLRTE LATYPLIIV NICPGFVQSN 240
 IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISQEP FLVLYLWQY 300
 MPTWAWWIIN KMGKKRIENF KSGVDADSSY FKFKTKHD

SEQ ID NO:33 PBA6 DNA SEQUENCE

Nucleic Acid Accession #: NM_006853

Coding sequence: 26-874 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | | |
 55 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
 ATCGGGGAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTGTAG GGGGAGAGAC 180
 60 CAGGATCATC AAGGGGTTCC AGTGCAAGCC TCACTCCAG CCTTGGCAGG CAGCCTGTGT 240
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300
 AGCCCACTGC CTCAGACCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCAGAAAGGA 360
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCACCCCG GCTTCAACAA 420
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
 65 CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTGCCTC ATTTCCGCTT GGGGCGACAC GTCCAGCCCC CAGTTACGCC TGCTTCACAC 600
 CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAAGC CCTACCCCGG 660
 CAACATCACA GACACATGG TGTGTGCCAG CGTGACGAA GGGGGCAAGG ACTCCTGCCA 720
 GGGTGACTCC GGGGGCCTC TGGTCTGTAA CAGTCTCTT CAAGGCATTA TCTCCTGGGG 780
 70 CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAATATGAT 840
 GGACTGTGAT CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
 ACCCTCCATT TCACCTTGGT GTTTGGTTCC TGTTCACCTT GTTAATAAGA AACCTTAAGC 960
 CAAGACCCTC TACGAACATT CTTTGGGCTC CTTGGACTAC AGGAGATGCT GTCACTTAAT 1020
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCGCTCTT GAAATATTGT 1080
 75 GACTCTGGGA ATGACAACAC CTGGTTTGT CTCTGTGTA TCCCCAGCCC CAAAGACAGC 1140
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

SEQ ID NO:34 PBA6 PROTEIN SEQUENCE

Protein Accession #: NP_006844

1 11 21 31 41 51
 5 MRILQLILLA LATGLVGGET RIIRKGFCEKP HSQFWQAALF EKTRLLCGAT LIAPRWLLTA 60
 AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRRND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIIE HQKCENAYPG 180
 NITDTMVCAS VQEGGKDSQC GDSGGPLVCN QSLQGIISWG QDFCAITRKP GVTYTKVCKYV 240
 DWIQETMKNN

10 SEQ ID NO:35 PBC1 DNA SEQUENCE

Nucleic Acid Accession #: NM_001775

Coding sequence: 70-972 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 CTAAAGCTCT CTGTGCTGCT AGCCTCCTGC CGGCCTCATC TTGCCCCAGC CAACCCCGCC 60
 TGGAGCCCTA TGGCCAACTG CGAGTTCAGC CCGGTGTCCG GGGACAAACC CTGCTGCCGG 120
 CTCTCTAGGA GAGCCCAACT CTGTCTTGCC GTCAGTATCC TGGTCTGAT CCTCGTCGTG 180
 20 GTGCTCGCGG TGGTCGTCCC GAGGTGGCGC CAGACGTGGA CGGTGCCGGG CACCACCAAG 240
 CGCTTTCCCG AGACCGTCTT GGCCTGATGC GTCAAGTACA CTGAAATTC TCTTGAGATG 300
 AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAGG GTGCATTAT TTCAAAACAT 360
 CCTTGCAACA TTACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
 CCTTGCACA AGATTCTTCT TTGGAGCAGA ATAAAAGATC TGCCCATCA GTTCACACAG 480
 25 GTCCAGCGGG ACATGTTTAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540
 ACATGGTGTG GTGAATTCAC CACTTCCAAA ATAACTATC AATCTTGGCC AGACTGGAGA 600
 AAGGACTGCA GCAACAACCC TGTTCAGTA TTCTGGAAAA CGGTTTCCCG CAGGTTTGCA 660
 GAAGCTGCCT GTGATGTGGT CCATGTGATG CTCAATGGAT CCGCAGTAA AATCTTTGAC 720
 AAAAACAGCA CTTTGGGGAG TGTGGAAGTC CATAATTGCT AACAGAGAA GGTTCAGACA 780
 CTAGAGCCCT GGGTGATACA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840
 30 ACCATAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAAT 900
 ATCTACAGAC CTGACAAGTT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGACAC 960
 TCTGAGATCT GAGCCAGTCG CTGTGGTGTG TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020
 CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGGA GGGTCTCCCA 1080
 CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCCAA AGTCTTAAAA TAACCTATAT 1140
 35 CATCAGATA CCTTTATGT GATCTATCAA TAGTCAAGAA AAATTATTCT ATAAGATTAG 1200
 AATGAAATT GTATGTTAAG TTACTTCCTT TAG

SEQ ID NO:36 PBC1 Protein sequence

Protein Accession #: NP_001766

1 11 21 31 41 51
 40 MANCEFSEVS GDKPCCLRSR RAQLCLGVSI LVLILVVVLA VVVRWRQTV SGPSTTKRFP 60
 ETULARCVMK TEIHPMRHV DQSVWDAFK GAFISKHPN ITEEDYQPLM KLGTQVPCN 120
 45 KILLWSRIKD LAHQFTQVQR DMFTLEDLL GYLADDLTWC GFNPSTKINY QSCPDRKDC 180
 SNNPVSVFWK TVSRFFAEAA CDVVHVMNLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTELA 240
 VWIHGGREDS RDLQDQPTIK ELESLISKRN IQFSCKNIYR BDKFLQCVKN PEDSSCTSEI

50 SEQ ID NO:37 PBH1 DNA SEQUENCE

Nucleic Acid Accession #: XM_017718

Coding sequence: 1-3315 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 55 ATGTCTTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC 60
 ACCCGGACCC TGTACTCCAG CGCGTCTCGG AGCACAGACT TGTCTTACAG TGAAAGCGAC 120
 TTGGTGAATT TTATTCAAAG AAATTTTAAG AAACGAGAAT GTGCTTCTTT TACCAAAGAT 180
 60 TCCAAGGCCA CGGAGAATGT GTGCAAGTGT GGCTATGCC AGAGCCAGCA CATGGAAGGC 240
 ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
 GACGCCCTTG GGGATATTCA GTTTGAGACA CTGGGGAAGA AAGGGAAGTA TATACGTCGT 360
 TCTTGCGACA CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGARA 420
 ACACCCAACC TGGTCATTTC TGTGACCGGG GCGGCCAAGA ACTTCGCCCT GAAGCCGCGC 480
 ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATCGCGCAGT CCAAAGGTGC TTGGATTCTC 540
 65 ACGGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGCTGAG AGATAACACC 600
 ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGGCATGGTC 660
 TCCAACCGGG ACACCCCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTC AGCCAGTAC 720
 CTTATGGATG ACTTCACAAG AGATCCACTG TATATCCTGG ACAACAACCA CACACATTG 780
 CTGCTCGTGG ACAATGCTGT TCAATGGACAT CCCACTGTGC AAGCAAAGCT CCGGAATCAG 840
 70 CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
 ATTGTGTGTT TTGCCCAAGG AGGTGGAAAA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
 AAAAATAAAA TTCTTGTGTG GTTGGTGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
 AGCCTGTGTG AGGTGGAGGA TGCCCTGACA TCTTCTGCCG TCAAGGAGAA GCTGGTGCCT 1080
 TTTTACCCCT GCACGGTGTG CCGGCTGCCT GAGGAGGAGA CTGAGAGTTG GATCAATAGG 1140
 75 CTCAGAGAAA TTCTCGAATG TTCTCACCTA TTAACAGTTA TTAAGTGA AGAAGCTGGG 1200
 GATGAAATTG TGAGCAATGC CATCTCCTAC GCTCTATACA AAGCCTTCAG CACCAGTGAG 1260
 CAAGACAGAG ATAAGTGGAA TGGGAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAC 1320
 TTAGCCAAATG ATGAGATTTT CACCAATGAC CGCCGATGGG AGTCTGCTGA CCTTCAAGAA 1380
 80 GTCATGTTTA CGGCTCTCAT AAAGGACAGA CCAAGTTTTC TCCGCTCTTT TCTGGAGAA 1440
 GGCTTGAAAC TACGGAAGTT TCTCACCAT GATGTCTCTA CTGAACCTT CTCCAACCAC 1500
 TTCAGCACGC TTGTGTACCG GAATCTGCAG ATGCGCAAGA ATTCTATATA TGATGCCCTC 1560

	CTCACGTTTG	TCTGGAAACT	GGTTGCGAAC	TTCCGAAGAG	GCTTCCGGAA	GGAAGACAGA	1620
	AATGGCCGGG	ACGAGATGGA	CATAGAAGTC	CACGACGTGT	CTCCTATTAC	TCGGCACCCC	1680
	CTGCAAGCTC	TCTTCATCTG	GGCCATTCTT	CAGAATAAGA	AGGAACCTCT	CAAAGTCATT	1740
5	TGGGAGCAGA	CCAGGGGCTG	CACTCTGGCA	GCCCTGGGAG	CCAGCAAGCT	TCTGAAGACT	1800
	CTGGCCAAAG	TGAAGAACGA	CATCAATGCT	GCTGGGGAGT	CCGAGGAGCT	GGCTAATGAG	1860
	TACGAGACCC	GGGCTGTGTA	GCTGTTCAC	GAGTGTAC	GCAGCGATGA	AGACTTGGCA	1920
	GAACAGCTGC	TGGTCTATTC	CTGTGAAGCT	TGGGGTGGAA	GCAACTGTCT	GGAGCTGGCG	1980
	GTGGAGGCCA	CAGACAGACA	TTTCATCGCC	CAGCCTGGGG	TCCAGAATTT	TCTTCTAAG	2040
10	CAATGGTATG	GAGAGATTTC	CCGAGACACC	AAGAACTGGA	AGATTATCCT	GTGTCTGTTT	2100
	ATTATACCCT	TGGTGGGCTG	TGGCTTTGTA	TCATTTAGGA	AGAAACCTGT	CGACAAGCAC	2160
	AAGAAGCTGC	TTTGGTACTA	TGTGGCGTTC	TTACCTCCC	CCTTCGTGGT	CTTCTCCTGG	2220
	AATGTGGTCT	TCTACATCGC	CTTCTCCTG	CTGTTTGCTT	ACGTGCTGCT	CATGGATTTC	2280
	CATTGCGTGC	CACACCCCCC	CGAGCTGGTC	CTGTACTCGC	TGGTCTTTGT	CCTCTTCTGT	2340
15	GATGAAGTGA	GACAGTGGTA	CGTAAATGGG	GTGAATATT	TTACTGACCT	GTGGAATGTG	2400
	ATGAGACCGC	TGGGCTTTT	TTACTTCATA	GCAGGAATTG	TATTTCCGGT	CCACTCTTCT	2460
	AATAAAGCT	CTTTGTATTC	TGGACGAGTC	ATTTCTGTG	TGGACTACAT	TATTTTCACT	2520
	CTAAGATTGA	TCCACATTTT	TACTGTAAGC	AGAACTTAG	GACCAAGAT	TATATGCTG	2580
	CAGAGGATGC	TGATCGATGT	GTTCTTCTTC	CTGTTCTCTT	TGCGGTGTG	GATGGTGGCC	2640
20	TTTGGCGTGG	CCAGGCAAGG	GATCCTTAGG	CAGAATGAGC	AGCGCTGGAG	GTGGATATTTC	2700
	CGTTCCGTCA	TCTACGAGCC	CTACCTGGCC	ATGTTCCGGC	AGGTGCCAG	TGACGTGGAT	2760
	GGTACCACT	ATGACTTTTC	CCACTGCACC	TTCACTGGGA	ATGAGTCCAA	GCCACTGTGT	2820
	GTGGAGTGG	ATGAGCACAA	CCTGCCCGG	TTCCCCGAGT	GGATCACCAT	CCCCCTGGTG	2880
	TGCATCTACA	TGTTATCCAC	CAACATCCTG	CTGCTCAACC	TGCTGTGCG	CATGTTTGGC	2940
25	TACACGGTGG	GCACCGTCCA	GGAGAACAA	GACCAGTCT	GGAAGTTCCA	GAGGTACTTC	3000
	CTGGTGCAGG	AGTACTGACG	CCGCTTCAAT	ATCCCCCTTC	CCTTCATCGT	CTTCGCTTAC	3060
	TTCTACATGG	TGGTGAAGAA	GTGCTTCAAG	TGTTGCTGCA	AGGAGAAAAA	CATGGAGTCT	3120
	TCTGTCTGCT	GTTTCAAAAA	TGAAGACAAT	GAGACTCTGG	CATGGGAGGG	TGTCATGAAG	3180
	GAAAACTACC	TTGTCAAGAT	CAACACAAAA	GCCACGACA	CCTCAGAGGA	AATGAGGCAT	3240
30	CGATTTAGAC	AACGTGATAC	AAAGCTTAAT	GATCTCAAGG	GTCCTTCGAA	AGAGATTGCT	3300
	AATAAATCA	AATGA					

SEQ ID NO:38 PBH1 Protein sequence
Protein Accession #: XP_017718

35	1	11	21	31	41	51	
	MSFRAARLSM	RNRNRDLDLS	TRTLYSSASR	STDLSYSESD	LVNFIQANFK	KRECVFFTKD	60
	SKATENVCCK	GVAQSQHMEG	TQINQSEKWN	YKKHTKEFFT	DAFGDIQFET	LGKKGYIRL	120
40	SCDTDABILY	ELLTQHWHLK	TPNLVISVTG	GAKNFALKPR	MRKIFSRLIY	IAQSKGAWIL	180
	TGGTHYGLMK	YIGEVVRENT	ISRSSEENIV	AIGIAWGMV	SNRDLIRNC	DAEGYFLAQY	240
	LMDDFTRDPL	YILDNNHTHL	LLVDNGCHGH	PTVEAKLRNQ	LEKYISERTI	QDSNYGKIP	300
	IVCFAGGGGK	ETLKAINTSI	KNKIPCVVVE	GSQIADVIA	SLVEVEDALT	SSAVKEKLV	360
	FLPRTVSRLP	EEETESWIKW	LKEILECSHL	LTVIKMEEAG	DEIVSNALSY	ALYKAFSTSE	420
45	QDKDNWNGQL	KLLLEWNLQD	LANDEIFTND	RRWESADLQE	VMTALIKDR	PKFVRLPLEN	480
	GLNLRLKPLTH	DVLTFLFSNH	FSTLVYRNLO	IAKNSYNDAL	LTFVWKLVAN	FRGFRKEDR	540
	NGRDEMDEL	HDVSPITRHP	LQALFIWAIL	QNKKELSKVI	WEQTRGCTLA	ALGASKLLKT	600
	LAKVKNDINA	AGESEBELANE	YETRAVELFT	ECYSSDEDLA	EQLLVYSCEA	WGGSNCLBLA	660
	VEATDOHFIA	QGVONFLSK	QWYGEISRDT	KNWKIILCLF	IIPLVGCGFV	SFRKKPVVDKH	720
50	KKLLWYIVAF	FTSPFVVFVS	NVVFYIAFLL	LFAYVLLMDE	HSVPHPELV	LYSLVFLVLC	780
	DEVROQWVNG	VNYFTDLWNV	MDTLGLFYFI	AGIVFRLHSS	NKSSLYSGRV	IFCLDYIIFT	840
	LRLHIHPTVS	RNLGPKIIML	QRMLIDVFFF	LFLFAVWVMA	FGVARQGILR	QNEQRWRWIF	900
	RSVIYEPLA	MFGQVPSDND	GTTYDFAHCT	FTGNESKPLC	VELDEHNLPR	FEWITITPLV	960
55	CIYMLSTNLL	LVNLLVAMFG	YTVGTVOENN	DQVWKFQRYF	LVQEYCSRLN	IFFPFIIVFAY	1020
	FYMVVKCKPK	CCCKEKNMES	SVCCFKNEDN	ETLAWEGVMK	ENYLVKINTK	ANDTSEMRH	1080
	RFRQLDTKLN	DLKGLLKEIA	NKIK				

SEQ ID NO:39 PBH3 DNA SEQUENCE

Nucleic Acid Accession #: XM_011804
Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

60	1	11	21	31	41	51	-
	ATGCCTCGCC	TGTTCTTGTT	CCACCTGCTA	GAATTCTGTT	TACTACTGAA	CCAATTTCCT	60
	AGAGCAGTCG	CGGCCAAATG	GAAGACGAT	GTTATTAAAT	TATGCGGCCG	CGAATTAGTT	120
65	CGGCGCCAGA	TGTCCTTTTG	CGGCATGAGC	ACCTGGAGCA	AAAGGTCTCT	GAGCCAGGAA	180
	GATGCTCTCT	AGACACCTAG	ACCAGTGGCA	GAAATGTGAC	CATCTTTCAT	CAACAAAGAT	240
	ACAGAACTA	TAAATATCAT	GTGGGAATTC	ATGCTAAT	TGCCACCGGA	GCTGAAGGCA	300
	GCCCTATCTG	AGAGGCAACC	ATCATTACCA	GAGCTACAGC	AGTATGTACC	TGCATPAAAG	360
70	GATTCCAATC	TTAGCTTTGA	AGAATTTAAG	AAACTTATTC	GCAATAGGCA	AAGTGAAGCC	420
	CGAGACAGCA	ATCCTTCAGA	ATTAAATAC	TTAGGCTTGG	ATACTCATTC	TCAAAAAAG	480
	AGACGACCT	ACGTGGCACT	GTTTGAGAAA	TGTTGCCTAA	TTGGTTGTAC	CARAAGGTCT	540
	CTTGCTAAAT	ATTGCTGA					

SEQ ID NO:40 PBH3 PROTEIN SEQUENCE

Protein Accession #: NP_008842

75	1	11	21	31	41	51	
	MPRLFLPHLL	EPCLLLNQFS	RAVAAKWKDD	VIKLCGRLELV	RAQIAICGMS	TWSKRSLSQE	60

DAPQTPRPVA EIVPSFINKD TETIIIMLEF IANLPPELKA ALSERQPSLP ELQYVPALK 120
 DSNLSPFEFK KLIRNRQSEA ADSNPSELKY LGLDTHSQKK RRPYVALFEK CCLIGCTKRS 180
 LAKYC

5

SEQ ID NO:41 PBH5 DNA SEQUENCE

Nucleic Acid Accession #: NM_005845

Coding sequence: 1-3978 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 ATGCTGCCCG TGTACCAGGA GGTGAAGCCC AACCOCCTGC AGGACGCGAA CCTCTGCTCA 60
 CGCGTGTTCCT TCTGGTGGCT CAATCCCTTG TTAAAAATTG GCCATAAACG GAGATTAGAG 120
 GAAGATGATA TGTATTTCAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG 180
 CAAGGGTTCT GGGATAAAGA AGTTTAAAGA GCTGAGAATG ACGCACAGAA GCCTTCTTTA 240
 ACAAGAGCAA TCATAAAGTG TTACTGGAAA TCTTATTTAG TTTTGGGAAT TTTTACGTTA 300
 ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTGGG GAAAAATTAT TAATATTTTT 360
 GAAAAATTATG ATCCCATGGA TTCTGTGGCT TTGAACACAG CGTACGCCCTA TGCCACGGTG 420
 CTGACTTTTT GCACGCTCAT TTTCGGCTATA CTGCATCACT TATATTTTFA TCACGTTTCAG 480
 TGTGCTGGGA TGAGGTTACG AGTAGCCATG TGCCATATGA TTATTCGGAA GGCACCTTCGT 540
 CTTAGTAACA TGGCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT CTTGTCCAAT 600
 GATGTGAACA AGTTTGTATCA GGTGACAGTG TTCTTACACT TCCTGTGGGC AGGACCACTG 660
 CAGGCGATCG CAGTACATGC CCTACTCTGG ATGGAGATAG GAATATCGTG CCTGTGCTGG 720
 ATGGCAGTTC TAATCATTTCT CTTGCCCTTG CAAAGCTGTT TTGGGAAATT GTTCTCATCA 780
 CTGAGGAGTA AAACCTGCAAC TTTCACGGAT GCCAGGATCA GGACCATGAA TGAAGTTATA 840
 ACTGGTATTA GGAATAATAA AATGTACGCC TGGGAAAAGT CATTTTCAAA TCTTATTTACC 900
 AATTTGAGAA AGAAGGAGAT TTCCAAGATT CTGAGAAGTT CCTGCCTCAG GGGGATGAAT 960
 TTGGCTTCGT TTTTCAGTGC AAGCAAAATC ATCGTGTITT TGACCTTCAC CACCTACGTG 1020
 CTCCTCGGCA GTGTGATCAC AGCCAGCCGC GTGTTCGTGG CAGTGACGCT GTATGGGGCT 1080
 GTGCGGCTGA CGGTTACCCCT CTTCTTCCCT TCAGCCATTG AGAGGGTGTG AGAGGCAATC 1140
 GTCAGCATCC GAAGAATCCA GACCTTTTGT CTACTTGATG AGATATCACA CGCCAACCGT 1200
 CAGCTGCCGT CAGATGGTAA AAGATGGTG CATGTGCAGG ATTTTACTGC TTTTGGGGAT 1260
 AAGGCATCAG AGACCCCAAC TCTACAAGGC CTTTCCCTTA CTGTACAGCC TGGCGAATG 1320
 TTAGCTGTGG TCGGCCCCGT GGGAGCAGGG AAGTCATCAC TGTTAAGTGC CGTGTCTGGG 1380
 GAATGGGCCC CAAGTACGGG GCTGCTCAGC GTGCATGGAA GAATTCGCTA TGTGTCTCAG 1440
 CAGCCCTGGG TGTTCCTCGG AACTCTGAGG AGTAATATTT TATTTGGGAA GAAATACGAA 1500
 AAGGAACGAT ATGAAAAAGT CATAAAGGCT TGTGCTCTGA AAAAGGATTT ACAGCTGTGT 1560
 GAGGATGGTG ATCTGACTGT GATAGGAGAT CGGGGAACCA CGCTGAGTGG AGGGCAGAAA 1620
 GCACGGGTAA ACCTTTCAGG AGCAGTGTAT CAAGATGCTG ACATCTATCT CCTGGACGAT 1680
 CCTCTCAGTG CAGTAGATGC GGAAGTTAGC AGACACTTGT TCGAACTGTG TATTTGTCAA 1740
 ATTTTGCATG AGAAGATCAC AATTTTAGTG ACTCATCAGT TGCAGTACCT CAAAGCTGCA 1800
 AGTCAGATTC TGATATTGAA AGATGGTAAA ATGGTGCAAG AGGGGACTTA CACTGAGTTC 1860
 CTAAATCTCG GTATAGATTT TGGCTCCCTT TTAAGAAGG ATAATGAGGA AAGTGAACAA 1920
 CCTCCAGTTC CAGGAATCC CACACTAAGG AATCGTACCT TCTCAGATC TCGGTTTGG 1980
 TCTCAACAA CTCTAGACC CTCCTTGAAA GATGGTGCTC TGGAGAGCCA AGATACAGAG 2040
 AATGTCCAG TTACACTATC AGAGGAGAAC CGTCTGAAG GAAAAGTTGG TTTTCAGGCC 2100
 TATAAGAAAT ACTTCAGAGC TGGTGCTCAC TGGATTGTCT TCATTTTCTT TATTTCTCTA 2160
 AACACTGCAG CTCAGGTTGC CTATGTGCTT CAAGATGGGT GCCTTTCATA CTGGGCAAAC 2220
 AAACAAAGTA TGCTAAATGT CACTGTAAAT GGAGGAGGAA ATGTAACCGA GAAGCTAGAT 2280
 CTTAAGTGT ACTTAGGAAT TTATTCAGGT TTAAGTGTAG CTACCGTTCT TTTTGGCATA 2340
 GCAAGATCTC TATTTGTATT CTACGTCTCT GTTAAGTCTT CACAAACTTT GCACAACAAA 2400
 ATGTTTGAAT CAATTCTGAA AGCTCCGGTA TATTTCTTTG ATAGAAATCC AATAGGAAGA 2460
 ATTTTAAATC GTTTCCTCAA AGACATTTGA CACTTGGATG ATTTGCTGCC GCTGACGTTT 2520
 TTAGATTTCA TCCAGACTGT GCTACAAGTG GTTGGTGTGG TCTCTGTGGC TGTGGCCGTG 2580
 ATTCCTTGA TCGCAATACC CTTGGTCCCT CTGTGAATCA TTTTCATTTT TCTTCGGCGA 2640
 TATTTTGGG AAACGTTCAAG AGATGTGAAG CGCCTGGAAT CTACAACCTG GAGTCCAGTG 2700
 TTTTCCCACT GTTCATCTCT TCTCCAGGGG CTCTGGACCA TCCGGGCATA CAAAGCAGAA 2760
 GAGAGGTGTC AGGAAGTGT TTATGTCACAC CAGGATTTAC ATTCAGAGGC TTGGTTCTTG 2820
 TTTTGTGACAA CGTCCCGCTG GTTCGCCGTC CGTCTGGATG CCATCTGTGC CATGTTTGTG 2880
 ATCATCGTTG CCTTTGGGTC CCTGATTCTG GCACAAAACCT TGGATGCCGG GCAGGTTGGT 2940
 TTGGCACTGT CCTATGCCCT CACGCTCATG GGGATGTTTC AGTGTGTGT TCGACAAAGT 3000
 GCTGAAGTTG AGAATATGAT GATCTCAGTA GAAAGGGTCA TTGAATACAC AGACCTTGAA 3060
 AAAGAAGCAC CTTGGGAATA TCAGAAACGC CCACCACAG CTTGGCCCCA TGAAGGAGTG 3120
 ATAATCTTTG ACRATGTGAA CTTATGTATC AGTCCAGGTG GGCCCTCTGGT ACTGAAGCAT 3180
 CTGACAGCAC TCATTAAATC ACAAGAAAAG GTTGGCATTG TGGGAAGAAC CGGAGCTGGA 3240
 AAAAGTTCCC TCATCTCAGC CCTTTTTAGA TTGTGAGAAC CCGAAGGTAA AATTTGGATT 3300
 GATAAGATCT TGACAACTGA AATTGGACTT CACGATTTAA GGAAGAAAAT GTCAATCATA 3360
 CCTCAGGAAC CTGTTTGTGT CACTGGAACA ATGAGGAAA ACCTGGATCC CTTTAATGAG 3420
 CACACGGATG AGGAAGCTGT GAATGCCCTA CAAGAGGTAC AACTTAAAGA AACCATTGAA 3480
 GATCTTCTCTG GTAAATATGGA TACTGAATTA GCAGAAATCAG GATCCAAATT TAGTGTGGA 3540
 CAAAGACAACT TGGTGTGCCCT TGCCAGGGCA ATTTCTCAGGA AAAATCAGAT ATTGATTATT 3600
 GATGAAGCCA CGGCAAAATG GGATCCAAGA ACTGATGAGT TAATACAAA AAAAATCCGG 3660
 GAGAAATTTG CCCACTGCAC CGTGCTAACC ATTTGCACACA GATTGAACAC CATTTATGAC 3720
 AGCGACAAGA TAAATGGTTTT AGATTCAGGA AGACTGAAAG AATATGATGA CCGCTATGTT 3780
 TTGCTGCAAA ATAAGAGAG CCTATTTTAC AAGATGGTGC AACAACTGGG CAAGGCAGAA 3840
 GCCGCTGCCCT TCACCTGAAC AGCAAAACAG GTATACTTCA AAAGAAATTA TCCACATATT 3900
 GGTACACACTG ACCACATGGT TACAAACACT TCCATATGAC AGCCCTCGAC CTTAATATT 3960
 TTCGAGACAG CACTGTGA

SEQ ID NO:42 PBH5 PROTEIN SEQUENCE

Protein Accession #: NP_005836

1	11	21	31	41	51	
1	11	21	31	41	51	
MLFVYQEVKP	NPLQDANLCS	RVFFWNLNPL	FKIGHKRRLE	EDDMYSVLPE	DRSQHLGEEL	60
QGFWDKEVLR	AENDAKPESL	TRAIKCYWK	SYLVLGIFTL	IEESAKVIQP	IFLGKIINYF	120
ENYDPMDSVA	LNTAYAYATV	LTFTCLILAI	LHLYFYHVQ	CAGMLRLVAM	CHMIYRKALR	180
LSNMAMGKTT	TGQIVNLLSN	DVNKFDQVTV	FIHFLWAGPL	QAIATVALLW	MEIGISCLAG	240
MAVLIILLPL	QSCFGKLFSS	LRSKTATFTD	ARIRTMNEVI	TGIRIIKMYA	WEKSFSNLIT	300
NLRKKEISKI	LRSSCLRGMN	LASFFSASKI	IVFVTFTTVV	LLGSVITASR	VFVAVTLYGA	360
VRLTVTLFFP	SAIERVSEAI	VSIRRIQTFL	LLDEISQRNR	QLPSDGKKMV	HVQDFTAFWD	420
KASRTPTLQG	LSFTVRPGEI	LAVVGFPVGAG	KSSLLSAVLG	ELAPSHGLVS	VHGRIAYVSQ	480
QFWVFSGTLR	SNILFGKKYE	KERYEKVIKA	CALKKDLQLL	EDGDLTVIGD	RGTTLGGGQK	540
ARVNLRARAV	QDADIYLLDD	PLSAVDAEVS	RHLFELCICQ	ILHEKITILV	THQLQYLKAA	600
SQILILKDGK	MVQGTYTEF	LKSGIDFGSL	LKKDNEESEQ	PFVPGTPTLR	NRTFSESSVW	660
SQGSRSRLK	DGALESQDTE	NVPVTLSEEN	RSEKVGFGQA	YKNYFRAGAH	WIVFIFLILL	720
NTAAQVAYVL	QDWLSYWAN	KQSMNLNVTVN	GGGNVTEKLD	LNWYLGIIYS	LTIVATVLFGI	780
ARSLLVFYVL	VNSSQTLHNN	MFESILKAFV	LPFDRNPIGR	ILNRFSKDIG	HLDDLPLTF	840
LDFTIQTLLQV	QGVVSVAVAV	IPWIALPLVP	LGIIIFILRR	YFLETSRDVK	RLESTTRSPV	900
FSHLSSSLQG	LWTIRAYKAE	BRCELFDAH	ODLHSEAWFL	FLTTSRWFAV	RDLAICAMFV	960
IIVAFGLSIL	AKTLDAGQVQ	LALSYALTLM	GMFQWCVRQS	AEVNMMISV	ERVIEYTDLE	1020
KEAPWEYQKR	PPPAWPEHGV	IIFDNVNFMY	SPGGPLVLKH	LTALIKSQEK	VGIVGRTGAG	1080
KSSLISALFR	LSEPEGKIWI	DKILTTEIGL	HDLRKKMSII	PQEPVLFTGT	MRKNLDPFNE	1140
HTDEELWNAL	QEVQLKBTIE	DLFGKMDTEL	AESGSNFSVG	QRQLVCLARA	ILRNKQILII	1200
DEATANVDPK	TDELIQKKIR	EKFAHCTVLT	IAHRLNTIID	SDKIMVLDSG	RLKEYDEPYV	1260
LLQNKESLFY	KMVQQLGKAE	AAALTETAKQ	VYFKRNYPHI	GHTDHMTNT	SNGQPSTLTI	1320
FETAL						

SEQ ID NO:43 PBQ7 DNA SEQUENCE

Nucleic Acid Accession #: NM_021233

Coding sequence: 34-1119 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
1	11	21	31	41	51	
ATGGGGAAG	TGCTCTGCTG	TGGCATGAAA	TAAATGAAAC	AGAAAATGAT	GGCAAGACTG	60
CTAAGAACAT	CCTTGTGCTT	GCTCTTCCTT	GGCCTCTTTG	GGGTGCTGGG	GGCAGCAACA	120
ATTTTCATCA	GAAATGAGA	AGGGAAGCT	TGGGACTGGT	TTACTTTTTA	TAAGTACCT	180
AAAAGACAAA	ACAAGGAAAG	TGGAGAGACT	GGGTTAGAGT	ACCTGTACCT	AGACTCTACA	240
ACTAGAGCT	GGAGGAAGAG	TGAGCAACTA	ATGAATGACA	CCAAGAGTGT	TTTGGGAAGG	300
ACATTACAAC	AGCTATATGA	AGCATATGCC	TCTAAGAGTA	ACAACACAGC	CTATCTAATA	360
TACAAATGAT	GAGTCCCTAA	ACCTGTGAAT	TACAGTAGAA	AGTATGGACA	CACCAAAGGT	420
TTACTGCTGT	GGAACAGAGT	TCAAGGGTTC	TGGCTGATTC	ATTCCATCCC	TCAGTTTCCT	480
CCAAATCCGG	AAGAAGGCTA	TGATTATCCA	CCCACAGGGA	GACGAAATGG	ACAAAGTGGC	540
ATCTGCATAA	CTTTCAAGTA	CAACCAAGTAT	GAGGCAATAG	ATTCCTCAGT	CTTGGTCTGC	600
AACCCCAAG	TCTATAGCTG	CTCCATCCCA	GCCACCTTTC	ACCAGGAGCT	CAITTCACATG	660
CCCCAGCTGT	GCACCAAGGC	CAGCTCATCA	GAGATTCTCTG	CGAGGCTCCT	CACCACTACT	720
CAGTCGGCCC	AGGGACAAAA	ATTCTCTCCAT	TTTGCAAAAGT	CGGATTCCTT	TCTTGACGAC	780
ATCTTTTCAG	CCTGGATGGC	TCAACGGCTG	AAGACACACT	TGTTAACAGA	AACCTGGCAG	840
CGAAAAGAC	AAGAGCTTCC	TTCAAACTGC	TCCCTTCCTT	ACCATGTCTA	CAATATAAAA	900
GCAATTAAT	TATCACGACA	CTCTTATTTT	AGTCTTATC	AAGATCACGC	CAAGTGGTGT	960
ATTTCCTCAA	AGGGCACCAA	AAATCGCTGG	ACATGTATTG	GAGACCTAAA	TCGGAGTCCA	1020
CACCAAGCCT	TCAGAAAGTG	AGGATTCATT	TGTACCCAGA	ATTGGCAAA	TTACCAAGCA	1080
TTTCAAGGAT	TAGTATTATA	CTATGAAAGC	TGTAAGTAAA	CTTGGTGAAA	GGACACAGGT	

SEQ ID NO:44 PBQ7 Protein sequence

Protein Accession #: NP_067056

1	11	21	31	41	51	
1	11	21	31	41	51	
MMARLLRTSF	ALLFLGLFGV	LGAATISCRN	EEGKAVDWFT	FYKLPKRQNK	ESGETGLEYL	60
YLDSTTRSWR	KSEQLMNDTK	SVLGRTLQQL	YEAYASKSN	TAYLIYNDGV	PKPVNYSRKY	120
GHTKGLLLWN	RVQGFWLHIS	IPQFFPIPEE	GYDYPPTGRR	NGQSGICITF	KYNQYEAIDS	180
QLLVCNENYV	SCSPATFFHQ	ELIHMPLQCT	RASSSEIPGR	LLTLTQSAQG	QKFLHFAKSD	240
SFLDDIFAAW	MAQLKTHLL	TETWQRKQE	LPSNCSLPYH	VYNIKAIKLS	RHSYFSSYQD	300
HAKWCISQKG	TKNRWTCIGD	LNRSPHQAFR	SGGFICTQNW	QIYQAFQGLV	LYYESCK	

SEQ ID NO:45 PCQ8 DNA SEQUENCE

Nucleic Acid Accession #: XM_030453

Coding sequence: 89-1273 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
1	11	21	31	41	51	
CGGIGCCCTG	GGGTGGAATA	TCCCCTACGA	ATTTAACCAG	GCGGACTTTA	ATGCCACTGT	60
GCAATTCATC	CAAAACCACT	TGGATGACAT	GGATGTCAAA	AAGGGTGTCT	CCTGGACCAC	120
CATCCGCTAC	ATGATAGGAG	AGATTCAATA	TGGAGGCAGA	GTCAGTGACG	ACTATGATAA	180
GAGATTGTTC	AACACATTTG	CTAAGGTTTG	GPTCAGTGAA	AATATGTTTG	GACCAGATTT	240
CAGTTTTTAC	CAAGGATACA	ATATTCCAAA	ATGCAGCACA	GTGGATAACT	ATCTTCAGTA	300
TATCCAGAGT	TTCCTCGCTC	ATGACAGCCC	TGAGGTGTTT	GGGCTGCACC	CCAATGCTGA	360

5	CATCACCTAC	CAGAGCAAGC	TGGCCAAGGA	CGTGCTGGAC	ACCATCCTAG	GCATCCNACC	420
	CAAGGACACC	TCTGGTGGAG	GGGATGAGAC	COGGGAGCGC	GTGGTGGCCC	GGCTGGCTGA	480
	TGATATGCTG	GAGAAAGCTGC	CCCCAGACTA	TGTCCTCTTT	GAAGTAAAG	AGAGGCTGCA	540
	GAAGATGGGG	CCATTCACAG	CTATGAACAT	TTTCCTCAGG	CAGGAAATAG	ACAGAAATGCA	600
	AAGGGTACTC	AGCCTTGTCC	GCAGCACCTT	CACCTGAGCTG	AAACTTGCTA	TTGATGGCAC	660
	CATCATCATG	AGCGAAAATC	TGCAAGATGC	ATTGGATTCG	ATGTTTGATG	CTAGAATCCC	720
	TGCTTGGTGG	AAAAAGCCTT	CTTGGGTTTT	TAGTACACTG	GGTTCTTGTT	TTACTGAACT	780
	TATAGAAAGA	AACAGCCAGT	TTACCTCGTG	GGTTTTCAT	GGCCGACCTC	ACTGCTTTTG	840
10	GATGACGGGT	TTTTTTAACC	CCCAGGGATT	TTTAACTGCA	ATGCGACAGG	AAATAACTCG	900
	GGCCAACAAA	GGCTGGGCTC	TGGACAATAT	GGTGCTTTGC	AATGAAGTCA	CCAAATGGAT	960
	GAAGGACGAC	ATTTCCTACCC	CTCCCACAGA	GGGTGTCTAT	GTCTATGGCT	TATATCTTGA	1020
	AGGTGCTGGC	TGGGACAAAG	GGAAACATGA	ACTCATTGAA	TCAAAGCCAA	AAGTGCTCTT	1080
	TGAGTTGATG	CCTGTCATAA	GGATTATGTC	AGAAAACAAT	ACTTTACGAG	ATCCTCGGTT	1140
15	TTACTCCTGT	CCCATCTATA	AGAAGCCAGT	TCGAACGGAC	TTGAACATCA	TTGCCGCTGT	1200
	GGATCTCAGG	ACAGCCCCAGA	CCCCGTAACA	CTGGGTGCTC	CGTGGGGTTG	CCCTTCTGTG	1260
	TGATGTCAAG	TAACTATGTC	GGAGTGTCCC	CACCCAATGC	TTTGGAAAT	GCAAGATCTA	1320
	AATTATTGTA	ACCTTTATTT	CTGTATGACT	GCTGGACAGT	GTATGTTAGG	TCGTTTATGC	1380
	AATTAAATAG	CTGCATAGGT	TTTCCCACT	CCTTAATTGG	ATGCTTATAT	TTTACTTGT	1440
20	TCATCATTAG	TGACCAATGT	CTGAGTTTGT	TGAAAATGTT	ATTTAGTGAT	ATAAAAGTAA	1500
	ATTTACAGCA	TCCTAATGAA	GTGTGGCCCT	CAATCCACA	GTAGTATATT	TTCTTCTTAC	1560
	TTGCTCTCCA	AGACTGACTG	TGATTATAAC	AGCAAAATATA	TTTGCATGTG	GACAAAGATT	1620
	AGATGCAAG	ATAGAAAAT	AAGAACAGAT	GTGATAGCAA	GAATTATAGT	TGGCTTGAAA	1680
	AAATGTGATG	ATCAGGAGAA	AAAATAAAAA	AAGGATAGAA	ATATTAGACG	GTGCGTAGGG	1740
25	ACTTTCTATG	GACTTTTAT	AATTAGGAAA	CATTATCAAA	GGAACCTTTC	ACGTATTTTT	1800
	CTTTAAATTC	TGGTTAGATG	TTATTAATAA	TTCTTCATCT	AACCTACTGA	CTAGAAAAATA	1860
	TAGTCAGTAC	TAAATTAGAA	TTGTGGTTTA	TAACTTTTGG	GTTAGCTCTG	GATCTGTATA	1920
	ACTGCATTTT	TTTGGATAAA	CAGTTTITGG	TAGGTGGATA	CCGGGAGACA	AGTGTGGGTC	1980
	CCCTCTCAGT	GGCTTCATTC	TGTGGACCAG	GATCATTATT	TCATGCTCAT	GATCATGAGA	2040
30	GTTAGGACTG	AGTGGCTCCT	GTGACTCCCA	CCATCTTAGA	TGATACTGTT	TTCTTGTGAG	2100
	TTCTTTCTTT	TGGTGTGGAT	TAGTATATCA	GTTGATTGTT	GTGAATTGTT	GTGAAACAAT	2160
	CATTTCTATT	TGAAAAGCAA	GTAATGAAAA	TGTCAGCATC	ATAGGAATTA	ATAAAATGTT	2220
	TTTACTAAAA	AAAAAATAAA	AAA				

SEQ ID NO:46 PQQ8 Protein sequence

Protein Accession #: BAB15543

35	1	11	21	31	41	51	
	MDVKKGVSWT	TIRYMIGIEIQ	YCGRVTDYD	KRLNLFKAV	WFSENMFGPD	FSFYQYINIP	60
40	KCSTVDNYLQ	YIQSLPAYDS	PEVFGHLPNA	DITYQSKLAK	DVLDTILGIQ	PKDTSGGGDE	120
	TREAVVARLA	DDMLEKLPPD	YVPFVKERL	QKMGPFQPMN	IFLRQEDIRM	QRVLSLVRST	180
	LTELKLAIDG	TIIMSENLOD	ALDCMFDAIR	PAWKKASWV	FSTLGFWFTB	LIERNISOFTS	240
	WVFNGRPHCF	WMTGFNFPGQ	PLTAMRQBIT	RANKGWALDN	MVLCNEVTKW	MKDDISTPPT	300
45	EGVYVYGLYL	EGAGWDKRNH	KLIESKPKVL	FELMEVIRIY	AENNTLRDPR	FYSCPIYKKP	360
	VRTDLNLYAA	VDLRTAQIPE	HWVLRGVALL	CDVK			

SEQ ID NO:47 PDG5 DNA SEQUENCE

Nucleic Acid Accession #: AB033036

Coding sequence: 68-3349 (underlined sequences correspond to start and stop codons)

50	1	11	21	31	41	51	
	GGAGCAGCCT	ACAACCTCAC	AACCAGAAAC	CACCTACCCCT	CAGGGGTTCG	TTTCAGATAA	60
	AGATGACATG	GAAGAGAGAA	ATGCTGGCAT	AGATTTCCGA	TCCAGAAAG	CATCAGCAGC	120
55	ACAGCCCAT	CCTGAAAACA	TGGACAATTC	CATGGTTAGT	GATCCACAAC	CATACCATGA	180
	AGATGCAGCT	TCTGGAGCTG	AGAAGACAGA	AGCCAGAGCT	TCTCTCTCAC	TGATGGTGA	240
	AAGCCTTTCT	ACAACCCCAAG	AGGAGGCCAT	TCTCTCAGTA	GCAGCAGAGG	CTCAGGTGTT	300
	TATGAATCCT	TCTCATATCC	AGTTAGAAGA	TCAAGAAGCT	TTTCACTTTG	ATTTACAAAA	360
60	GGCCCAATCC	AAAATGGAGT	CAGCCCAAGG	TGTTCAAAC	ATCTGCAAG	AAAAGCCTTC	420
	TGGAATGTT	CACCAGACCT	TTACAGCAAG	TGTTTGGGT	ATGACAAGTA	CTACAGCCAA	480
	AGGAGATGTT	TATGCCAAGA	CTCTGCCTCC	CAGAAGCCTT	TTTCACTCCT	CAAGGAAGCC	540
	TGATGCTGAA	GAAGTCTCCT	CAGATTCAGA	GAATATTCTT	GAGGAGGGGG	ATGGTTCTGA	600
	AGAATCTGGT	CATGGTCACT	CTTCCCAAGT	CTTGGGGGAG	TTTGAAGATG	AACAAGAAGT	660
65	CTTCTCAGAA	TCAAAAAGTT	TTGTTGAGGA	CTTGAGCAGC	TCTGAGGAGG	AGCTGGACCT	720
	CAGATGCCTC	TCCCAGGCTT	TAGAGGAGCC	TGAAGATGCA	GAAGTCTTCA	CAGAATCAAG	780
	CAGTTATGTT	GAAAAGTACA	ACACTTCTGA	TGATTGCAGC	AGCTCAGAGG	AAGACCTGCC	840
	TCTCAGACAC	CCTGCTCAGG	CCTTGGGAAA	GCCCAAAAC	CAACAAGAAG	TCTCTCTGCG	900
	TTCAAAATAT	ACTCCTGAAG	AGCAGAATGA	TTTTATGCG	CAGCTGCCTT	CCAGATGCC	960
70	TTCTCAGCCC	ATTATGAATC	CTACTGTTCA	GCAACAAGTC	CCCACCAAGT	CAGTGGGCAC	1020
	TTCTATAAAA	CAGAGCGAAT	CCGTGGAGCC	AATCCCTCCA	AGACACCTTT	TCCAGCCATG	1080
	GGTGAACCTT	AAAGTGGAGC	AAGAAATTTT	CTCATCTCCA	AAGAGCATGG	CTGTTGAAGA	1140
	GAGCATTTCT	ATGAAGCCTC	TGCTCTCTAA	ACTTCTTTGC	CAGCCCTTGA	TGAATCCTAA	1200
	AGTTCAACAA	AACATGTTCT	CAGGTTTCTA	GGACATTGCT	GTTGAGAGAG	TCATTTCTGT	1260
75	GGAGCCACTA	CTCCCCAGAT	ATTCTCCTCA	GTCCTTGACA	GATCCTCAAA	TCCGGCAAA	1320
	CTCAGAAAGC	ACAGCTGTTG	AGGAAGGCAC	TTATGTGGAA	CCGCTGCCTC	CCAGATGCCT	1380
	TTCCAGCCCC	TGGGAGAGGC	CTAAGTTCTT	GGACTCAATG	AGTACTTCTG	CAGAATGGAG	1440
	CAGTCTCTGT	GCACCAACAC	CTTCCAAATA	CACCTCCCGG	CCATGGGTGA	CCCCTAAATT	1500
	TGAGGAAGCT	TATCAACTCT	CTGCACATCC	AGAAAGCACT	ACTGTTGAAG	AGGACATTTT	1560
80	TAAGGAGCAG	TGCTTCCCA	GACATCTTTC	CCAGTTGACT	GTGGGAAATA	AAGTCCAGCA	1620
	ACTGCTCCCA	AATTTGAGAC	GGGCTGCTAT	TGAGGCAGAC	ATTTCTGGGA	GTCCATTGCC	1680

TCCCCAATAT GCTACCCAGT TCTTAAAGAG GTCATAAGTT CAGGAAATGA CCTCAGCACT 1740
 AGAGAAAATG GCTGTGAAGT GCACCTCTAA CAAATCACCG ATTCACAGGC GTCCGACCCA 1800
 GTCATTCGTG AAATTTATGG CACAGCAAAAT CTTTTCAGAG AGCTCTGCTC TTAAGAGGGG 1860
 CAGTGATGTG GCACCTCTGC CTCCCAATCT TCCTTCCAAA TCTTTATCAA AGCCTGAAGT 1920
 CAAGCACCAA GTTTTCTCAG ATTCAGGGAG TGCTAATCCT AAGGGAGGCA TTCTTCCAAA 1980
 GATGCTACCT ATGAAGCACC CTTTACAGTC CTTGGGGAGG CCTGAAGACC CACAGAAAAGT 2040
 TTTCTCTTAT TCAGAGAGAG CTCTGGGAA GTGCAGCAGT TTTAAAGAGC AGCTGTCTCC 2100
 CAGGCAGCTT TCCAGGCCCT TGAGGAAACC TGAGTATGAG CAAAAAGTCT CCCCTGTTTC 2160
 TGCCAGTTCT CTTAAAGAGT GGAGGAATTC TAAAAAGCAG CTGCCTCCCA AACATTCTTC 2220
 CCAAGCCCTA GATAGGTCTA AATTCCAGCC ACAGATGTCA TCAAGGGGCC CAGTGAATGT 2280
 ACCTGTAAAG CAGAGCAGCG GTGAGAAGCA CCTGCCITCA AGTAGTCTCT TCCAGCAACA 2340
 GGTTCATTC AATTCTGTGA ATGCTGCTGC TAGGCGATCT GTTTTGTAGA GCAATTCATGA 2400
 CAATGAGTTC CTAGGAAGAG ATGAAGCTTT TGCAATCAAA ACCAAGAAAT TCAGCCAAGG 2460
 TTCCAAAAGC CCCATAAAGA GCATTCACAG CCTTGCTACC AAACCTGGGA AGTTCAACCA 2520
 TGCTCTCTGC AGCCTAACAT CCACTTCTGG GGGCATTTAC TCTAAGAAAG AAGATCTTGA 2580
 GAGTGGTGAT GGTAATAATA ACCAGCATGC AAACCTATCC AATCAGGATG ATGTTGAAAA 2640
 GCTTTTGTGA GTTCGACTGA AAAGAGCCCC TCCCTCGCAG AAGTATAAGA GTGAGAAAAC 2700
 AGATAACTTC ACCCAGCTTG CTTTCACTGC CTCGGGCCCA ATTTCACTCT CTGTAGGCAG 2760
 GGGACATAAA ATCAGAAGCA CTTCCAGGG GCTCCTGGAT GCTGCAGGGA ACCTCACCAA 2820
 AATATCTTAC GTTCGAGATA AGCAACAGAG CAGGCCCAAA TCTGAAAGCA TGGCCAAGAA 2880
 GCAACCTGCT TGCAAGACCC CAGGAAAGCC TGCTGGTCAA CAGTCAGATT ATGCTGTCTC 2940
 AGAGCCGGTT TGGATAACTA TGGCAAGCA GAAGCAGAAG AGTTTCAAG CCCACATTTT 3000
 TGTGAAGAG CTGAAGACTA AGAGCAATGC TGGAGCCGAT GCTGAGACTA AGGAGCCTAA 3060
 ATATGAGGGA GCTGGCTCTG CAAATGAAAA CCAACCTAAA AAGATGTCTA CTTCAGTGT 3120
 CCATAAACAG GAGAAGACAG CACAGATGAA GCCACCTAAG CCTACAAAAT CAGTTGGATT 3180
 TGAAGCTCAG AGCAGTCTGC AAGTTCTTGC CATGGAAGAA GAAACCAAC GATCTTCAAC 3240
 TCTCCAGCC AGTTTCCAGA ACCCAGTTGA GCCAATTTAG CTTGCTCTGT TCTCACTGGC 3300
 CAGGAAGAAA GCCAAGCAT GGAGCCACAT GGCAGAAATC ACGCAATAAA GAGCTCTTGT 3360
 GTGGAGCATC AGCATTTATTT TATTTTAGTT TTTTCTTTT TTTTCTTTT GAGACAGAGT 3420
 CTCGCTCTGT TACCCAGATT GGAGTGCACT GCGCGCATCT CCGCTCACTG CAAGCTCCGC 3480
 CTCGCGGTTT CACGCCACTC TCCCGCCTCA GTCTCCGAC TAGTGGGAC TACAGGCGCC 3540
 CGCCATCAGC CCGGCTTAAT TTTGTTTTCG TATTTTGTAGT AGAGACGGGG TTTCACCATG 3600
 TTGGCCAGGA TGGTCTTGAT CTCTTGACCT CGTGATCCGC CCGCCTCAGC CTCCCAAAAG 3660
 CTGGGATTAC AGCGCTGAGC CACCGCGCCC GGCACAGCAT CAGCGTTTAA AATGATAATT 3720
 GCTAATAGCT GTATTAAATC TATGTAGTGA TCTTTTFACT GTGACCACT GTATTAGCA 3780
 AATAGAGTAT TAGCAAACT AAGAATTTAT TAAGCAAAAT AAGAATTTAT TAAGCAAAAT 3840
 AGCCTTAGAA ATGCAAAATTA AAACATAATT ATTTGAATGA AATAAATGCC ATGATGCTT 3900
 AACCTTCCAC GTATTCACCT CAGCAGCCCA GAAACCCAGC ATTTCTCTTA TTAATACTAT 3960
 CGAAAACATT TGCACCTGCT TAAAATTGCA AATCTTTTAA CTTTGGACAA TGTGCTTTAT 4020
 AAGGGAGAAA GCAAAAACAT TTTGTTGGAG CAACTAGAAA ATTTGCTATT CCCTCAACCA 4080
 AATAAAGTAA TTTCTAATGA AACATTCAGA TGAATTTGAC TAAAGATTGG CTTTATAGTT 4140
 TTATGAGCCT AGATAGATGC CGCAATTATT TCGTTGTTGC TCTAAGCTTT GCAAGGGATC 4200
 CTAAAAGAGG CGGTGGAAGT GAAAATTCTG GGTCTCCAAG AAAATTCTGT CACAGCCAGT 4260
 TCTCCAAATC TACACTACCC CCTTGAAACA TCTTCCCTGT GTCCCTGGGG GCCCTGATG 4320
 CTTTCTCTCT GGTGATAGT AACATGCAGA GCACCTTACAC AAGCTCCCT CTTTGACAT 4380
 ACCCCACGTC GACCTGTAC AGGCTTGGCT GTAGCGAGCA CCTCCCTATG ACGCAGAAATG 4440
 CTTCTTGGGA ATATCTTAC TCTCTGGAG GGTAGTCCA TCAATGTTTT GCTTCTTGTG 4500
 CCAATACATC TGTGACCCCT TCTGATCGCA CAGAAATCAC TGCCATACAC ATATATCTCTG 4560
 TTAAGCACTA AAGACCCCTA TGAATTTAGA GTTCTACAGA TGCCAAAAGC TGTACTTTCC 4620
 ATCAGGCAGA TGGCAAGCTT ACTGCTTGA TGCACATCTG GAGCCACTGG AGCTCCTTCC 4680
 TCTCTGGTTC CAGCATTAAG GTGGAGAAT CCAATGTAGT TCTTGTCTCT TCCCTCAGC 4740
 TGTCTTTGCT TACAGAGGTT TTAGCCCAAA GCAAGAGTGC AATCCCAAAG CCACAGAGAA 4800
 ATGAATTTTC CGCTACCTGG AAGCTTTAAG TGAGTAAATC AGCTTTTCCC CTCTCATTCC 4860
 TAGAGGCACA CACCTCAAAA GTTACTAGGC TGGAGAGACC CTACCTTCCA GTGACCCACT 4920
 CATCCCCAG CCACGGAGAA GAGGGAAGAC CAAAAGGGA GAGTGAGAAA GAGGATGAGA 4980
 GGGATGGTCA GCTGTGAGGG GAGGGGGCAA GTGGCCAGC AAATGTTGAT GCCTCCCTTC 5040
 CCATCTTGA ACACGCTCT TTTCTTTTGT AGCACAGCCT CCATTAATAA CTCCTCGGCT 5100
 GAGGATGAAG ATGTAGGCAC CTTTACCCCT AGAGCCAGTT CCTTAATTGG CTGGCTTTCT 5160
 GAGATGCAGA CACCCCTAGA ATCTCATCTA GGTTCACAG AAGTTAGTTA AATCTTCTCT 5220
 TCTCTGTCTT TCTCTTCAAT CCATCCCCCA AACCCACCAA ACATAAGGG AGAGCTCCCT 5280
 TTGGATGTCT GGGCAGTAAA CCTAGCTCAT TTTTCTAGGA GACCAGAAAG TGACTTCTGA 5340
 GTAGTTATCA CTGTGCTGCT CTCTGTTACA CTGTGCTGCT TGTCTTAAAC AGAAATGCAG 5400
 GCCTGGACAT CTGACTGTGC CTTTATATTC TGAGTGGGGT GCTGCCCAT GCACAAAAAT 5460
 CCAGAGAGGT AGTGAGGTGT CAGAGCTAAA CACTTGGTGC TGGGTTTGT TGAATGCTGT 5520
 ATAAATGTAC ACAGTACAA TACATGCTAA ATTTTGCAAT TTCTCTATAT AACATCTATT 5580
 TTTCTGTATA CTGTGCTCTT GCCATTTTGA TAATGCTATT TTGATTGAGT GAATTTTATT 5640
 TCTTTTGTAT TCCCATAGTG AACAATATAT TAAGGTAGAT GCCCTTTATC TGGGTACTCC 5700
 TGGTAGATTA GCTGTACAC CTCCCTTCCC TTTTTCACAG TGAACCTGTA TTCAGTTATT 5760
 GTCACTCTGA GAATCTCCA ATAACAATTT CTTTTCACCA GTTAACAACA CAGCTGTATT 5820
 ACCTCCCTTC CTTTTCCTCA CAGTGAACCT GTATTCAGCT ATCTCTACTC TGAGAACTCT 5880
 CCAATAACAA TTTCTTTTCC ACAGTTAACA ACAAGTTCT GTTTTAAAT GAAGAGATTA 5940
 AGTTCTTTT AAATGCCTAA AGGCATATTC TGACAATTT TCTACTTCTT TAACTTTATT 6000
 GATTTAAGAT ATATGCAAG CAAATAAATT CAATAAGCC T

SEQ ID NO: 48 PDG5 Protein sequence
 Protein Accession #: BAA86524

1 11 21 31 41 51
 EQPTTSQPET TTFQGLLSDK DDMGRRNAGI DFGSRKASAA QIPENMDNS MVSDPQFYHE 60

5	DAASGAEKTE	ARASLSLMVE	SLSTTQEEAI	LSVAAEAQVF	MNPSHIQLED	QEAFFSFDLQK	120
	AQSKMESAQD	VQTIQCKEKP	GNVHQTTTAS	VLGMTSTTAK	GDVYAKTLPP	RSLFQSSRRK	180
	DABEVSSDSE	NIPEEGDGSE	ELAHGHSSQS	LGKFEDEQEV	FSESKSFVED	LSSSEELDL	240
	RCLSQALEEP	EDAEVFTESS	SVVEKYNTSD	DCSSSEEDLF	LRHPAQALGK	PKNQOEVSAA	300
	SNNTPEBCND	FMQQLFSRCP	SQPIMNPTVO	QQVPTSSVGT	SIKQSDSVEP	IPRHPFPQFW	360
	VNPKVEQEV	SSPKSMAVEE	SISMKPLPEK	LLCQPLMNPK	VQQNMFSGSE	DIAVERVTSV	420
	EPLLPYRSPQ	SLTDPQIRQI	SESTAVEEGT	YVEPLPPRCL	SQPSERPKFL	DSMSTSAEWS	480
	SPVAPTPSKY	TSPPWVTPKF	EELYQLSAHP	ESTTVEEDIS	KEQLLPRHLS	QLTVGNKVQQ	540
10	LSSNFERAAI	EADISGSPLP	PQYATQFLKR	SKVQEMTSRL	EKMAVEGTSN	KSPIPRRPTQ	600
	SFVKFMAQQI	FSSEALKRG	SDVAPLPPNL	PSKSLSKPEV	KHVFSDSGS	ANPKGGISSK	660
	MLPMKHPLQS	LGRPEDPQKV	FSYSERAPGK	CSSFKEQLSP	RQLSQALRKP	EYEQKVSFVS	720
	ASSPKWNRNS	KKQLPKHSS	QASDRSKFPQ	QMSKGFVNV	FVKQSSGEKH	LFSSSPFQQQ	780
	VHSSSVNAAA	RRSVFESNSD	NWFLGRDEAF	AIKTKKFSQG	SKNPIKSIPA	PATKPGKFTI	840
15	AFVRQTSTSG	GIYSKKEDLE	SGDGMNNQHA	NLSNQDDVEK	LFQVRLKRAP	PSQKYKSEKQ	900
	DNFTQLASVP	SGPISSSVGR	GHKIRSTSQG	LLDAAGNLTK	ISYVADKQOS	RPKSESMAXK	960
	QPACKTPGPK	AQQQSDYAVS	EPVWITMAKQ	KQKSFKAHIS	VKELKTKSNA	GADAETKEPK	1020
	YEGAGSANEN	QPKMFTSSV	HKQEKTAQMK	PPKPTKSVGF	BAQKILQVPA	MEKETKRSST	1080
	LPAKFQNFVE	FIEPVWFSLA	RKKAKAWSHM	AEITQ			

SEQ ID NO:49 PAB7 DNA SEQUENCE

Nucleic Acid Accession #: D87742

Coding sequence: 208-3582 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GCTTTCCTTT	CTAAAGTAGA	AGAGGATGAT	TATCCCTCTG	AAGAACTACT	AGAGGATGAA	60
	AACGCTATAA	ATGCAAAAACG	GTCTAAAGAA	AAAAACCCCTG	GGAATCAGGG	CAGGCAGTTT	120
	GATGTTAATC	TGCAAGTCCC	TGACAGAGCA	GTTTATGAGGA	CCATTCATCC	AGATCCAGAA	180
30	ATTGAAGAAA	GCAAGCAAGA	AAC TAGTAG	ATT TGGATA	GTGAAAAAAC	AAGTGAGACT	240
	GCTGCCAAAG	GGGTCAACAC	AGGAGGCAGG	GAACCAATA	CAATGGTGGG	AAAAGAACGC	300
	CCTCTGCAG	ATAAGAAAGC	ACAGAGACCA	TTTGAACGAA	GTGACTTTTC	TGACAGCATA	360
	AAAATTCAGA	CTCCAGAAAT	AGGTGAAGTG	TTTCAGAATA	AAGATTCTGA	TTATCTGAAG	420
	AACGACACCC	CTGAGGAACA	TCCTGAAGACC	TCAGGGCTTG	CAGGGGAGCC	TGAGGGAGAA	480
	CTCTCAAAAG	AGGACCATGG	GAACACAGAG	AAGTACATGG	GCACAGAAAG	CCAGGGGTCT	540
35	GCTGCTGCAG	AACCTGAAGA	TGACTCGTTC	CACTGGACTC	CACATACAAG	TGTAGAGCCA	600
	GGGCATAGTG	ACAAGAGGGA	GGACTTACTT	ATCATAGCA	GCTTCTTTAA	AGAACAACAG	660
	TCTTTTGAGC	GGTTCAGAG	GTACTTTAAT	GTCCATGAGC	TGGAAGCCTT	GCTACAAGAA	720
	ATGTCATCAA	AACCTGAAGT	AGCGCAGCAG	GAGAGCCTGC	CCTATAATAT	GGAAAAAGTC	780
40	CTAGATAAGG	TCTTCCGTGC	TTCTGAGTCA	CAAATTCTGA	GCATAGCAGA	AAAATGCTT	840
	GATACTCGTG	TGGCTGAAGA	TAGAGATCTG	GGAATGAACG	AAAATAACAT	ATTTGAAGAG	900
	GCTGCAGTGC	TTGATGACAT	TCAAGACCTC	ATCTATTTTG	TCAGGTACAA	GCCTCCACA	960
	GCAGAGAGAA	CAGCCACACT	GGTGATGGCA	CCACCTCTAG	AGGAAGGCTT	GGGTGGAGCA	1020
	ATGGAAGAGA	TGCAACCACT	GCATGAAGAT	AATTTCTCAC	GAGAGAAGAC	AGCAGAACTT	1080
45	AATGTGCAGG	TCTCTGAAGA	ACCCACCCAC	TTGGACCAAC	GTGTGATTGG	GGCACTCAT	1140
	GCCTCAGAAG	TGTCACAGAA	GCCAAATACT	GAGAAAGACC	TGGACCCAGG	GCCAGTTACA	1200
	ACAGAAAGACA	CTCCTATGGA	TGCTATTGAT	GCAAAACAAG	AACCAGAGAC	AGCCGCCGAA	1260
	GAGCCGGCAA	GTGTCACACC	TTTGAAAAAC	GCAATCCTTC	TAATATATTC	ATTCACTGTT	1320
	TATTTAACTA	AGTGCCTAGT	TGCTACATAG	CCTGATGATG	TTGACGCTGG	GCCTGATTTT	1380
50	TATGCACTGC	CATGGAAACC	TGTATTATC	ACTGCCCTCT	TGGGAATTGC	TTCTGTTGCC	1440
	ATTTTCTTAT	GGAGAACTGT	CCTTGTGTG	AAGGATAGAG	TATATCAAGT	CACGGAACAG	1500
	CAAAATTTCTG	AGAAGTTGAA	GACTATCATG	AAAGAAATA	CAGAACTTGT	ACAAAAATTT	1560
	TCAAATTATG	AACAGAAATC	CAAGGAATCA	AAGAAACATG	TTGAGGAAC	CAGGAACAA	1620
	AATATGATTC	TCTCTGATGA	AGCAATTAAA	TATAAGGATA	AAATCAAGAC	ACTTGAAAAA	1680
55	AATCAGGAAA	TTCTGGATGA	CACAGCTAAA	AACTCTCGTG	TTATGCTAGA	ATCTGAGAGA	1740
	GAACAGAAAT	TGCAAGATCA	GGACTTGTAT	TCAGAAACAA	AGAAATCTAT	AGAGAAAGTTA	1800
	AAGGATGTTA	TTTCAATGAA	TGCTTCAGAA	TTTTTCAGAG	TTGAGATGTC	ACTTAATGAA	1860
	GCTAAGCTGA	GTGAAGAGAA	GGTGAAGTCT	GAATGCCATC	GGGTTCAGAA	AGAAATGCT	1920
	AGGCTTAAGA	AGAAAAAAGA	GCAGTTGCAG	CAGGAAATCG	AAGACTGGAG	TAAATTACAT	1980
60	GCTGAGCTCA	GTGAGCAAA	CAAAATCATTT	GAGAAGTCTC	AGAAAGATTT	GGAGTAGCT	2040
	CTTACTCACA	AGGATGATAA	TATTAATGCT	TTGACTAATC	GCATTACACA	GTTGAATCTG	2100
	TTAGAGTGTG	AATCTGAATC	TGAGGGTCAA	AATAAAGGTG	GAAATGATTC	AGATGAATTA	2160
	GCAANTGGAG	AAGTGGGAGG	TGACCGGAAT	GAGAAGATGA	AAATCAAAAT	TAAGCAGATG	2220
	ATGGATGTCT	CTCGGACACA	GACTGCAATA	TCGGTAGTTG	AAGAGGATCT	AAAGCTTTTA	2280
65	CAGCTTAAGC	TAAGAGCCTC	CGTGTCCACT	AAATGTAACC	TGGAAGACCA	GGTAAAGAAA	2340
	TTGGAAGATG	ACCGCAACTC	ACTACAAGCT	GCCAAAGCTG	GACTGGAAGA	TGAATGCAAA	2400
	ACCTTGAGGC	AGAAAGTGGG	GATTCGTGAT	GAGCTCTATC	AGCAGAAAGG	GATGGCTTTG	2460
	CAAAAGAAAC	TGAGTCAAGA	AGAGTATGAA	CGGCAAGAAA	GAGAGCACAG	GCTGTCAGCT	2520
	GCAGATGAAA	AGGCAGTTTC	GGCTGCAGAG	GAAGTAAAAA	CTTACAAGCG	GAGAATTGAA	2580
70	GAAATGGAGG	ATGAATTACA	GAAGACAGAG	CGGTCAATTA	AAAACACAGT	CGTACCCAT	2640
	GAGAAAGAG	CTCATGAAAA	CTGGCTCAAA	GCTCGTCTG	CAGAAAGAGC	TATAGCTGAA	2700
	GAGAAAAGGG	AAGCTGCCAA	TTTGAGACAC	AAATTATTAG	AATTAAACAC	AAAGATGGCA	2760
	ATGCTGCAAG	AAGAACCCTG	GATTGTAAAA	CCAATGCCAG	GAAAACCAAA	TACACAAAAC	2820
	CCTCCACGGA	GAGGTCTCTC	GAGCCAGAA	GGCTCTTTTG	GCCCCATCCC	TGTGAGTGGT	2880
75	GGAGATGCT	CCCCCTCATT	GACAGTGGAG	CCACCCGTGA	GACCTCTCTC	TGCTACTCTC	2940
	AATCGAAGAG	ATATGCCTAG	AAGTGAATTT	GGATCAGTGG	ACGGGCTCTC	ACCTCATCCT	3000
	CGATGGTTCAG	TGAGGCAATC	TGGGAAACCC	TCTCCTTCTG	ATCCAGGATC	TGGTACAGCT	3060
	ACCATGATAG	ACAGCAGCTC	AAGAGGCTCT	TCCCTTACCA	GGGTACTCGA	TGAAGGCAAG	3120
	GTAAATATGG	CTCCAAAAAG	GCCCCCTCCT	TTCCCGAGAG	TCCCTCTCAT	GAGCACCCCC	3180
80	ATGGGAGGCC	CTGTACCAAC	ACCCATTCGA	TATGGACCAC	CACCTCAGCT	CTGCGGACCT	3240
	TTTGGGCCCTC	GGCCACTTCC	TCCACCCCTT	GGCCCTGGTA	TGCGTCCACC	ACTAGGCTTA	3300

5
10
15
20
25
30
35
40
45

AGAGAATTG CACCAGGCGT TCCACCAGGA AGACGGGACC TGCCTCTCCA CCCTCGGGGA 3360
TTTGTACCTG GACACGCACC ATTTAGACCT TTAGGTTTCC TTGGCCCAAG AGAGTACTTT 3420
ATTCCCTGGTA CCCGATTACC ACCCCCAACC CATGGTCCCC AGGAATACCC ACCACCACCT 3480
GCTGTAAAGAG ACTTACTGCC GTCAGGCTCT AGAGATGAGC CTCCACCTGC CTCTCAGAGC 3540
ACTAGCCAGG ACTGTTTACA GGCCTTTAAA CAGAGCCCAT AAAACATGA CCTCTGAGGT 3600
TTTATTGGAA AGAAGAGTGA CTGTGCATTA TCCATTACAG TAAAGGATTT CATTTGGCTTC 3660
AAAATCCAAA AGTTTATTTT AAAAGGTTTG TTGTTAGAAC TAAGCTGCCT TGGCAGTGTG 3720
CATTTTGTAG CCAAAACAAT CAAAAATGTC ATTTCTTCCC TAAATAAAAA TCACCTTTTA 3780
AGCTAGAGCG TCCTTTACAAC TTTGAAATGT GCAATAAAGA ATACCTGTGT TTTAGCTAAT 3840
GTAGCATATG TAATTGCAAA ATGATTAGTA ATGTCATGAA AAATATGAAC ATTTCTGTGT 3900
GAAATGCTTT AAGAACATGT ATTTCCATTA TCCCTATTTT AGGTACACCC AGCTGAATAC 3960
GGAGCAATGG TGTTTATTAAG CGTTTTTTTA AACTATCTGG TCACAAAGAC TGTACGCTA 4020
AAAATGTTTA CTAAGAGATC ACTAACTAT CTCCCTCTT GCTGAAGTTC TTTGTAGTAA 4080
TAGCTCATAA AATTTGTGTT ATTAATATTT CCCAAGTGTC TGTGTACTCA TTGGACTGTT 4140
ATGAGCGCTG TGCCATTTGG GGAACATGTA AACTCAGGCT CCCAGAACGT AAGATGGTGG 4200
CTGGTGGCAC ACTTCGGGCT GCTCCTCCGT CACCTGTGAA CTCTACAAGT GATGTCTTTT 4260
TATTTCAAAG AACTTTATTT CCCACTTGTA TAGCATTAC ATGCTTTCTT TACGATCCTC 4320
ATTGTCTATT TGAGAAATGT TTTCTGAGAG TGAGTTTACA TTAGTAGCAA GAGTTGTTTG 4380
ACCTGATGTT CCAATGTTT TACCATTCTT GTAGAAAAAG GGTGCACAC AGAAAAATGA 4440
AAATGATGTG TCAATGCCAT AAAAGTATAG AAATCTTTAA AAATTTTAAA ATGTACAGTC 4500
CCTATCTAT CTTCCTCAT CTTCGCCAT GATTTTGTAG GAATATAATA AAAAGATTGG 4560
AAGAGTATTA TGCCATGAGA AAGATGATT TAGGACTGTG AGCGTTATAA CATGCCCTAG 4620
GTCAGCAACC AAGGGTTGAA ATCAGTTCTG TTTTAGGGGG AAATGGGGGG GCGCAGAGAT 4680
ATTATTTCAA AATTAATATT AATTAATATT TAAACGTTGG TGTTTTATTT TAAAAATCAG 4740
TAACTAACCA TCTGGAATAG CACCATACTT AAAGTCTTAT CCATTACTAC ACTGTCTTTA 4800
AAACAATGTT TCTTTAAATA CTCTACAACG TTCTTAAGAA CGAAGTTTCA ACATTTTAA 4860
TACAGTAATA ATAGCACTCC TTTTAAGGAG TTTCAGATCC ACCTTAAAC TAAATTCATA 4920
AAAGGCTGAT ACTTTGTTT GCTGCTAGGC TATATCTTTC CATCTTTTGA AGTCCATGA 4980
TGTAATATT TTTGAAACCTA GTGTATGTCT TGCTACTGTT GTGATATTTA ATCGATTAAG 5040
AATACCTTGT AAAAAGGAGC AAAAGCTTCA ATGTGAAACA ATTTCTCTCT TTTTACTATA 5100
ACAACCTGAG ATAGATAGTT TAGAAGATA AGGACCTTTG AAAGAAGACA ACTCTGTCAA 5160
AGTTTATAAG GAATATAAAA ATTCTTCAGG AAAAGAGAAT TCAATCTATA TGTCCTCCCG 5220
TTTAATATCA AGAATAGAAG AAATTAAGAG GAAAACTCCA CAGAAGAGCA TAGGCCACTT 5280
TTAGCCATGT AAAAATAAGA TTAAGTCACA AATACAACCT TTGAATTTAC CTGTCAATAT 5340
CTCTTTAGGA CACAAAACAA TGCTGAAGTT AATATAATTT CTAATTTTAA ATGTCAATTA 5400
AGTGTAGATT ATGCCATCTA GGAAGGTAAG TAGGAAAGGT AAATTAATTC TATTTTAAA 5460
ATTCAAAATA TTAGAGTATT TTTCCCTCTT AAAGCCTTTT TTGGTGATTA TTCTGTATCT 5520
GACATAATTG AGAACTGGT AAGCTGTAAA GATTCCAGTG TAGCTTCTCT GAGAAGTTGT 5580
GAGCCAGTCC ATAACTGCTT CCTCACATCC ATCTGATTGC ACCATTCTCT CAGCAAACCC 5640
CAAAGCAGGG TGCCATATAT CAGATGGCAT AGGGAGTATC ATCCCTCAGC CAAATCACTT 5700
TTCCATCTCT AAAGTTTCAT CTATTTTGA AGTCATCTCC AACTAATGT GTCTGGATT 5760
AGTTGCTAAA ATGTCTTAT TTATTTATGA AGCAGCAATA TTCAGCCTGA AAGCATTTCT 5820
GCCATAGTTG TTGTAGTTAT ATCGCCAATG GCTGATTTTT TTCATTGGAA AGTAAATTTA 5880
AGTAATTCGT GGGATGTGGT ATATTCTGTG TCAACTTCAA GATAATCACT CATTTTCTCG 5940
TTATATTCAG GTCTGAATTA AAGTTAAGTT AATCAC

SEQ ID NO:50 PAB7 Protein sequence
Protein Accession #: BAA13448

50
55
60
65
70
75

1 11 21 31 41 51
| | | | |
AFLSKVEED YPSEELLEDE MAINAKRSKE KNFGNQGRQF DVNLQVPDRA VLGTIHPDPE 60
IESKQETSM ILDEKTSSET AAKGVNTGGR EPNTMVEKER PLADKKAQRP FERSDFSDSI 120
KIQTPELGEV FQNKDSYDLK NDNPEEHLKT SGLAGEPEGE LSKEDHGNTB KYMGTESQGS 180
AAAEPEDDSF HWTPHTSVEP GHSDKREDLL IISFFKEQQ SLQRFOKYFN VHELEALLQE 240
MSSKLKSAQQ ESLFYNMKV LDKVFRASES QILSLAEKML DTRVAENRDL GMNENNIFEE 300
AAVLDDIQDL IYFVRYKHST AEETATLVMA PPLEBGLGGA MEEMQPLHED NFSREKTABL 360
NVQVPEEPHT LDQRVIGDTH ASEVSQKENT EKDLDPGPVT TEDTPMDAID ANKPETAAT 420
EPASVTPLEN AILLIYSFME YLTKSLVATL PDDVQPGPDF YGLPFWKPVFI TAPLGIASFA 480
IFLWRTVLVV KDRVYQVTEQ QISEKLRTIM KENTELVQKL SNEYQKIKES KKHVQETRRQ 540
NMILSDEAIK YKDKIKTLEK NQEIILDDTA NLRVLMESER EQNVKNQDLI SENKKSIEKL 600
KDVLSMNAE FSEVQIALNE AKLSEEEKVKS ECHRVQEBNA RLKKKKEQLQ QEIEDWSKLH 660
AELSEQIKSF EKSQKDLVA LTHKDDNINA LTNCITQLNL LECESESEQ NKGNDSDDEL 720
ANGEVGGDRN EKMNQIKQM MDVSRQTAT SVVEEDLKLL QLKLRASVST KCNLEDQVKK 780
LEDDRNLSQA AKAGLEDECK TLRQKVEILN ELYQKEMAL QKKLSQEEYE RQEREHLISA 840
ADEKAVSAAE EVKTYKRRIE EMEDELQTE RSFKNQIATH EKKAHENWLK ARAAERAI 900
EKREANLRH KLEELTKQMA MLQEPVIVK PMPGKPNQON PPRRGPLSQN GSGFSPFVSG 960
GECSPPLTVE PPVRPLSATL NRRDMRSEF GSVDGPLPHP RWSAEASGKP SPSPDPSGTA 1020
TMNNSSSRGS SPFRVLDEGK VNMAFKGPPP FPGVPLMSTP MGGPVPPPIR YGPPPLCGP 1080
FGFRPLPPFF GPGRPLPLGL REFAPGVPPG RRDPLPHPRG FLPGHAPFRP LGSGLPREYF 1140
IPGTRLPPPT HGPEYFPPPP AVRDLFSGS RDEPPPASQS TSQDCSQALK QSP

SEQ ID NO:51 PAB9 DNA SEQUENCE

Nucleic Acid Accession #: NM_006457
Coding sequence: 84-1874 (underlined sequences correspond to start and stop codons)

80
1 11 21 31 41 51
| | | | |
AGACTGAGGC GGAGGCACGC CCGCGCCGCG CCGGACCCGA GCATATTTC A TTTCTGTGCA 60

5 TTGGACTTTG AGCCATTAGA ACCATGAGCA ACTACAGTGT GTCAGTGGTT GGCCAGCTC 120
 CTGGGGTTT CCGGCTGCAG GCGGTAAGG ATTTCAACAT GCCTCTGACA ATCTCTAGTC 180
 TAAAAGATGG CGGCAAGGCA GCCCAGGCAA ATGTAAGAAT AGGCGATGTG GTTCTCAGCA 240
 TTGATGGAAT AAATGCACAA GGAATGACTC ATCTTGAAGC CCAGAAATAG ATTAAGGGTT 300
 GTACAGGCTC TTTGAATATG ACTCTGCAAA GAGCATCTGC TGCACCCAG CCTGAGCCGG 360
 TTCTGTGTCA AAAGGGAGAA CCTAAAGAAG TAGTTAAACC TGTGCCATT ACATCTCTG 420
 GTGTGTCAA AGTCACTTCC ACAACAACA TGGCCTACAA TAAGGCACCA CGGCTTTTG 480
 GTCTGTGTG TACACCAAAA GTACATCCA TCCATCACC ATCGTCTGCC TTCACCCAG 540
 10 CCCATGCGAC CACCTCATCA CATGCTTCCC CTTCACCCGT GCGTGCCTGC ACTCTCCCC 600
 TGTTCGCTGC ATCTGGAGTG CATGCTAATG CCAATCTTAG TGCTGACCAG TCTCCATCTG 660
 CACTGAGCGC TGGTAAACT GCAGTTAATG TCCACGGCA GCCACAGTC ACCAGCGTG 720
 GTTCCGAGAC TTCTCAGAG CTAGCAGAG GACAGAGAAG AGGATCCAG GGTGACAGTA 780
 AACACGAAAA TGGCCACCA AGAAAACACA TTGTGGAGCG CTATACAGAG TTTTATCATG 840
 15 TACCCACTCA CAGTGATGCC AGCAAGAAGA GACTGATTGA GGATACTGAA GACTGGCGTC 900
 CAGAACCTGG AACACCTCAG TCTCGCTCTT TCCGAATCCT TGCCAGATC ACTGGGACTG 960
 AACATTTGAA AGAATCTGAA GCGGATAATA CAAAGAAGGC AAATAACTCT CAGGAGCCTT 1020
 CTCCGCAATT GGTCTCCPTG GTAGCTTCCA CACGGAGCAT GCCCGAGAGC CTGGACAGCC 1080
 CAACCTCTGG CAGACACGGG GTTACCAGCC TCACAACCTG AGCTGCCCTC AAGCCTGTAG 1140
 20 GATCCACTGG CGTCATCAAG TCACCAAGCT GGCAACGGCC AAACCAAGGA GTACCTTCCA 1200
 CTGGAAGAA CTCAACACGC GCTACTTACT CAGGATCAGT GGCACAGCC AACTCAGCTT 1260
 TGGGACAAAC CAGCCCAAGT GACCAGGACA CTTTAGTGCA AAGAGCTGAG CACATTCAG 1320
 CAGGGAACCG AACTCCGATG TGGGCCCAT GTAACAGGT CATCAGAGGA CCATTCCTAG 1380
 TGGCACTGGG GAAATCTTGG CACCCAGAAG AATTCACCTG CGCTCAGTGC AAAATACAA 1440
 25 TGGCCTACAT TGGATTGTGA GAGGAGAAAG GAGCCCTGTA TTGTGAGCTG TGCTATGAGA 1500
 AATCTCTTGC CACTGAATGT GGTCTGATCC AAAGGAAGAT CCTTGGAGAA GTCATCAATG 1560
 CGTTGAAACA ACCTTGGCAT GTTCTCTGTT TTGTGTGTGT AGCCTGTGGA AAGCCCATTC 1620
 GGAACAATGT TTTTCACTTG GAGGATGGTG AACCCACTG TGAGACTGAT TATTATGCCC 1680
 TCTTTGGTAC TATATGCCAT GGATGTGAAT TTCCCATAGA AGCTGGTGAC ATGTCTCTGG 1740
 30 AAGCTCTGGG CTACACCTGG CATGACACTT GCTTTGTATG CTCAGTGTGT TGTGAAAGTT 1800
 TGGAGGTCA GACCTTTTTC TCCAAGAAG ACAAGCCCTT GTGTAAGAAA CATGCTCAT 1860
 CTGTGAATTT TTGAAAGTCA ACAGTTCAGG AGAAGAGAAG GAATTTGAAG AGAAAAAGGA 1920
 AAATTAATAA TACTAATTA TTTTATGATT CAATATTTAT ATGGAGTTT GAAAAATAA 1980
 AGTGGCCCTG AAGGAATAAA TTCCAGCTTT AAAAACCAAG TCTGAGGAAA TATTGGCTT 2040
 35 CATAAAGTAA AGAGACGGT TGGCATTTAT TATTACTTTT TCCTGTATTT TATGCCATA 2100
 AAATAAGCTT TATAAAACC AATTTCTGTA TGGACTATTA AATTCATCTT AGAATAAAT 2160
 AGTGAGAAAT TTAATTTTAG AATAAATAA CCAATCTGAA ATAATTATAC CTCTTTCTCT 2220
 TGTTAGGTAG TTATCAGTAA ATCTGCAAAA GGCAATGAAA ATGCCTTAAA TTTTATCAAT 2280
 AACAGAAATA TTGTATTTAA AAAAAACTA ATACTTATCT TTAATAAGT AAATAGGATT 2340
 40 TTAACAGAG AATTTATATC GTAAATAGTG TCAGTTTATA AAAAATTCCT TGTAGGCTGA 2400
 GCGCGGTGGC CAGCCCTGT AATCCCAGCA CTTTGGGAGG CCAAGGTGGG TGGACACAT 2460
 GAGGTCAGGA GTTTGAGATC AGCCTGGCCA ACATGGTGAA ACCCATCTCT TACTAAAAAT 2520
 ACAAAAATA GCCCGACGCA GTGGCACGCG CCGTGAATCC CAGCTACTCA AGAGGCTGAG 2580
 GCACGAGAA CTCTGAACCG CGGAGGGAG AGGTTCAGT GAGCCAAGAT CGTACCACCTG 2640
 45 CACTCCAGCC TGGGTGACAG AGTGAGACTC CGTCTCCAAA AAAAATCTTT GCTTGTATAT 2700
 TATTTTGGC TTACAGTGGA TCATTCTAGT AGGAAAGGAC AATAAGATTT TTTATCAAAA 2760
 TGTGTACATG CAGTAAGAGA TGTATATATC TTTTCTTAT TCTTCCCTAC CCAAAAAATA 2820
 GCTACCATAT AGCTTATAAG TCTCAAATTT TTGCCCTTTA CTAATAATGT ATTGTTTCTG 2880
 TTTATTTGCT ATGCTTATC ACCTATATTA GCAAAATTC ATTTTTCCTT TTGCGCTAAG 2940
 50 GTAAAGATTT AATTAATAA TTTTGGCCTC TCATAGTTT CTCTCTCTTT AAAGAGAATA 3000
 AATAGAGGGC CAGGTGTGGT GGCTCACGCC TGTGATCCCA GCACCTTGGG AGGCCAAGAC 3060
 GGGCGGATCA TGAGGTCAAG AGATCAAGAT CATCTGGCC AACATGGTGA AACCTGTCT 3120
 CTACTAAAAA TCAAAAAATG AGCTGGCAT GGTGGGCGT GCTGTAGTC CCATGTACTT 3180
 55 GGGAGGCTGA GGCAGGAAAA TTCTTGAACC CAGGAGACGG AAGTGCAGT GAGCTGAGAT 3240
 CACACCACCTG CACTCCAGCC TGGTGACAGA GCAAGACTCC GCCTCTT

SEQ ID NO:52 PA89 Protein sequence

Protein Accession #: NP_006448

60 1 11 21 31 41 51
 1 MSNYSVSLVG PAPWGFRLQG GKDFNMPLTI SSLKDGKAA QANVRIGDVV LSIIDGINAQG 60
 61 MTHLEAQNKI KGCTGSLNMT LQRASAAFKP EPVFPQKGEP KEVVKPVPIT SPAVSKVTST 120
 121 NNMAYNKAPR PFGSVSSPKV TSIPSPSSAF TPAHATTSSH ASPSPVAATV PPLFAASGLH 180
 181 ANANLSADQS PSALSAGKTA VNVPRQPTVT SVCSETSQEL ABGQRRGSQG DSKQONGPFR 240
 65 241 KHIVERYTEF YHVPTSDAS KKRLIEDTED WRPRGTGTS RSFRILAQIT GTEHLKESEA 300
 301 DNTKKANNSQ EPSFQLASLV ASTRMPESL DSPTSGRFGV TSLTTAAAFK PVGSTGVKIS 360
 361 PSWQRNQGV PSTGRISNSA TYSGSVAPAN SALGQTQPSD QDTLVQRAEH IPAGKRTPMC 420
 421 AHCNQVIRGP FLVALGKSNH PEEFNCAHCK NIMAYIGFVE EKGALYCELC YEKFFAPECG 480
 481 RCQRKILGEV INALKQTHV SCFVCVACGK FIRNNVFHLE DGEFYCETDY YALFGTICHG 540
 70 541 CEPPIEAGDM FLEALGYTHW DTCFVCSVCC ESLEGQTFPS KKDKPLCKKH AHSVNF

SEQ ID NO:53 PBH7 DNA SEQUENCE

Nucleic Acid Accession #: AA431407

Coding sequence: 1-864 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 ATGGCCAAC GTAAAAATGAC CAAAAGCATC AGGTTCCCTG CCCTGGAGCA CTGCTATACT 60
 GCGCGGGAG TCGTGTGCC CAAGGATCAG GAGGAGTGGG AAAGACGGAC GGGCCTTCTG 120
 80 CTCTACGAGA ACTATGGGCA GTCGGAACG GAGCTAATTT GTGCCACCTA CTGGGGAATG 180

5
10
15

```

AAGATCAAGC CGGGTTTCAT GGGGAAGGCC ACTCCACCCT ATGACGTCCA GTTTCATATG 240
GAGGCCTCAG TTGAAAACCTG CATTATTGTG AGCATGAACA CCGCTGACCC TGGCAGCCAG 300
GGCATCACAC ACAGCCTCTT GCTACAGGTC ATTGATGACA AGGGCAGCAT CCTGCCACCT 360
AACACAGAAG GAAACATTTGG CATCAGAATC AAACCTGTCA GGCCTGTGAG CCTCTTCATG 420
TGCTATGAGG GTGACCCAGA GAAGACAGCT AAAGTGGAAAT GTGGGGACTT CTACAACACT 480
GGGGACAGAG GAAAGATGGA TGAAGAGGGC TACATTTGTT TCCTGGGGAG GAGTGATGAC 540
ATCATTAATG CCTCTGGGTA TCGCATCGGG CCTGCAGAGG TTGAAAGCGC TTTGGTGGAG 600
CACCCAGCGG TGGCGGAGTC AGCCGTGGTG GGCAGCCAG ACCCGATTGC AGGGGAGGTG 660
GTGAAGGCCCT TTAATGTCTT GACCCACAG TTCTGTCTCC ATGACAAGGA TCAGCTGACC 720
AAGGAAGTGC AGCAGCATGT CAAGTCAGTG ACAGCCCCAT ACAAGTACCC AAGGAAGGTG 780
GAGTTTGTCT CAGAGCTGCC AAAAACCATC ACTGGCAAGA TTGAACGGAA GGAACCTTCG 840
AAAAAGGAGA CTGGTCAGAT GTAAATCGCA GTGAAGTCAG AACGCCTGAC ACACCTGAGG 900
CAAAATCCCTG GCCACTTTAG TCTCCCACT ATGGTGAGGA CGAGGGTGGG GCATTGAGAG 960
TGTTGATTTG GGAAGTATC AGGAGTGCCA TGATTCCAAT GTTTTCCTTC TTTTAAATTA 1020
AATTCAGTTG CTCTGCTTCC TCCAAGTCTT CTGTATCTTT AGAATTTCCT AGGTGAGCAC 1080
TCATAACGCA AGTAATAAAA TACTGATATC AAAAA

```

SEQ ID NO:54 PBH7 Protein sequence

Protein Accession #: FGENESH predicted

20
25

```

1      11      21      31      41      51
|      |      |      |      |      |
MANCKMTKSI RPPALEHCYT GGEVVLPKDQ EEWKRRTGLL LYENYQOSET GLICATYWGM 60
KIKPGFMGKA TPPYDVQFHM EASVENCIV SMNTADPGSQ GITHSLLLQV IDDKGSILPP 120
NTEGNIGIRI KPVRFVSLFM CYEGDPEKTA KVECGDFYNT GDRGKMDEEG YICFLGRSDD 180
IINASGYRIG PAVESALVE HPAVAESAVV GSPDPIRGEV VKAFIVLTPQ FLSHDKDQLT 240
KELQQHVKSU TAPYKYPRKV EFVSELPKTI TGKIERKELR KKETGQM

```

SEQ ID NO:55 PBJ5 DNA SEQUENCE

Nucleic Acid Accession #: AF388200

Coding sequence: 33-137 (underlined sequences correspond to start and stop codons)

30
35
40
45

```

1      11      21      31      41      51
|      |      |      |      |      |
GAGAGAGGGA GGCAGAAGAG GAAGTCAGAG CGATGTGCTG TGAATCTTAC TACCGTTTGC 60
TGGTTTGTGA AATGGAGAAA AAGAGTGAGG AACTGAGAAA CATGGATGGC CTGGGAAACG 120
TGGAAAAGGG TCACGTAAAT GGCACGACAT GAACCTCAAG AGGCTATTTA TGACCTATGC 180
ATTGTGCAACA TGAAGAAAGC TTATCTGGAG TGAAGATAAA TGAGACCAAC AGAGATAAGA 240
GACCCGGAGA AATCCTGCTT ACACCTGCTT AATCCTGTCA GTCTATATCT GGAGTCTGTT 300
TAATACAAAA TAATAGTAAT AATCCTCTCT TTTCTTATGT TTATGCCAAC TTCAACAAAA 360
AGAAACTTGA CTAAGAGACA ATATAAGAAC TTAATGTGTA ATTAAGAAAG AACTCTCCAC 420
CACGGGGAAT GTGAAAGGTA TATGAGTCCC TTTTCACGAT GCGATGTCAT GTCTTTTAAA 480
TAAGCCATAC TTTATGTTC AATAAAGAG AATAAGCAGG A

```

SEQ ID NO:56 PBJ5 Protein sequence

Protein Accession #: AAK83352

50

```

1      11      21      31      41      51
|      |      |      |      |      |
MCCBIYYRLV VLKMEKKSEE LRNM DGLGNV EKH

```

SEQ ID NO:57 PBJ7 DNA SEQUENCE

Nucleic Acid Accession #: AA878910

Coding sequence: 1-2064 (underlined sequences correspond to start and stop codons)

55
60
65
70
75
80

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGACAGTT GCCTGCAACA TATGAGAGAC CTACTTTACC TCCTTCAGGA GCTCAGGTGT 60
TTAAATCCAG CTACACTACT CCCTGATCCA GACTCCACTA CTCCTGTTC TACTGTCTAG 120
GATCTGTGTG AAATACCAAA AACTGGCCAA CCTGATCTTC AAGATGTGCC CTAGAAAAAG 180
GCAGATGCCA CTGTGTTTCA AGATGGTAGC AGCTTCCTCG AGCAGGGAGA ACGAAAAGCT 240
GTTTCTTTTC CACAGCCAGA TCTGCCTGAC AATCCACAT ACTCAACAGA AGAAGAAAAA 300
CTGGCTTCAG ATGTTGGAGC AAATAAAAAAT CAGGAAGGAC GTGTATTTCG AAACACTACT 360
TGGAGGGCCG GTACCTCCAA GGAAGTCTCC TTTGCAGTTG ATTTATGTGT ACTGTTCCCA 420
GAGCCAGCTC GTACCCATGA AGAGCAACAT AATTGCGCG TCATAGGAGC AGGAAGTGTG 480
GACCTTGCA GAGGATTTGG ACACCTGGG AGCCAAACTG GATGTGGAAG CTCCAAAGGT 540
GCAGAAAAAG GGCTCCAAAA TGTGACTTT TACCTCTGTC CTGGAATCA CCTGACGCT 600
AGCTGTAGAG ATACTTACCA GTTTTCTGCT CCTGATGGA CATGTGTAAC TTTAGCCACC 660
TACTCTGGG GATCAACTAG ATCTTCAACT CTTTCCATAA GTCTGTCTCC TCATCTTAAA 720
TTATGTACTA GAAAAATG TAATCCTCTT ACTATAACTG TCCATGACCC TAATGCAGCT 780
CAATGGTATT ATGGCATGTT ATGGGGATTA AGACTTATA TCCCAGGATT TGATGTTGGG 840
ACTATGTTC AATCCAAAAA AAAATCTTC GTCTCATGGA GCTCCCCAA GCCAATCGGG 900
CCTTTAAGTG ATCTAGGTGA CCCTATATTC CAGAAACACC CTGACAAAGT TGATTTAACT 960
GTCTCTGCG CATCTCTAGT TCCTAGACCC CAGCTACAAC AACACATCT TCAACCCAGC 1020
CTAATGTCTA TACTAGTGG AGTACACCAT CTCCTTAACC TCACCCAGCC TAAACTAGCC 1080
CAAGATGTTT GCTATGTTT AAAAGCAAAA CCCCCTTATT ATGTAGGATT AGGAGTAGAA 1140
GCCACACTTA AACGTGGGCC TCTATCTTGT CATAACGAC CCCGTGCTCT CACAATAGGA 1200
GATGTGCTG GAAATGCTTC CTGTCTGATT AGTACCGGGT ATAACTTATC TGCTTCTCCT 1260
TTTCAGGCTA CTGTGATCA GTCCCTGCTT ACTTCCATAA GCACCTCAGT CTCTTACCAA 1320
GCACCAACA ATACCTGTTT GGCCTGCACC TCAGGTCTCA CTCGCTGCAT TAATGGAAGT 1380

```


5	GAACCAGGAC	CTCTCCTGTG	CGTGTAGTGT	CATGTACTTC	CCCAGGTATA	TGTGTACAGT	1440
	GGACCAGAAG	GACGACAAC	CATCGCTCCC	CCTGAGTTAC	ATCCCAGGTT	GCACCAAGCT	1500
	GTCCCACTTC	TGGTTCCTCC	ATTGGCTGGT	CTTAGCATAG	CTGGATCAGC	AGCCATTGGT	1560
	ACGGCTGCCC	TGGTTCAAGG	AGAACTGGA	CTAATATCCC	TGTCTCAACA	GGTGGATGCT	1620
	GATTTTAGTA	ACCTCCAGTC	TGCCATAGAT	ATACTACATT	CCCAGGTAGA	GTCCTGGCT	1680
	GAAGTAGTTC	TTCAAAACTG	CCGATGCTTA	GATCTGCTAT	TCCTCTCTCA	AGGAGGTTTA	1740
	TGTGCAGCTC	TAGGAGAAAG	TTGTTGCTTC	TATGCCAATC	AATCTGGAGT	CATAAAAGGT	1800
	ACAGTAAAAA	AAGTTCGAGA	AAATCTAGAT	AGGCACCAAC	AAGAACGAGA	AAATAACATC	1860
10	CCCTGGTATC	AAAGCATGTT	TAACCTGGAAC	CCATGGCTAA	CTACTTTAAT	CACTGGGTTA	1920
	GCTGGACCTC	TCCTCATCCT	ACTATTAAAGT	TTAATTTTGT	GGCCTTGTAT	ATTAAATTCG	1980
	TTTCTTAATT	TTATAAAACA	ACGCATAGCT	TCTGTCAAAC	TTACGTATCT	TAAGACTCAA	2040
	TATGACACCC	TTGTTAATAA	CTGA				

15 SEQ ID NO:58 PBJ7 Protein sequence
Protein Accession #: FGENSEH predicted

20	1	11	21	31	41	51	
	MDSCLQHRMD	LLYLLQELRC	LNPATLLPDP	DSTTFVHDCQ	DLLETTKTGQ	PDLQDVPLEK	60
	ADATVFTDGS	SFLQGERKA	VSFPQDLFD	NPTYSTEEK	LASDVGANKN	QEGRVFANTT	120
	WRAGTSKEVS	FAVDLCVLF	EPARTHEEQH	NLPVIGAGSV	DLAAGFGHSG	SQTGCGSSKG	180
	AEKGLQNVDF	YLCFQNHEDA	SCRDTYQFFC	PDWTCVTLAT	YSGGSTRSST	LSISRVPHPK	240
	LCTRKNCNPL	TTTVHDPNAA	QWYVGMWSGL	RLYIPGFDVG	TMFTIQKKIL	VSWSSPKPIG	300
	PLTDLGDIPI	QKHDPKVDLT	VLPFLVPRP	QLQQHQLQPS	LMSILGGVHH	LLNLTQPKLA	360
25	QDCWLCKLAK	PFYVVGLEVE	ATLKRGLPSC	HTRFRALTIG	DVSGNASCLI	STGVNLSASP	420
	FOATCNQSL	TSIGTSVSQY	APNNTWLACT	SGLTRCINGT	EPGPLLCVLV	HVLPQVYVYS	480
	GPEGRQLIAP	PELHPRHLQA	VPLLVPFLAG	LSIAGSAAIG	TAALVQGETG	LISLSQQVDA	540
	DFSNLQSAID	ILHSQVESLA	EVVLQNCRC	DLFLSQGGL	CAALGESCCF	YANQSGVIK	600
30	TVKKVRENLD	RHQQERENNI	PWYQSMFNWN	PWLTTTLITGL	AGPLLLILLS	LTFGPCIINS	660
	FLNFIKQRIA	SVKLTLYLKTQ	YDTLVN				

SEQ ID NO:59 PCC1 DNA SEQUENCE

	Nucleic Acid Accession #: NM_019005						
	Coding sequence: 182-1885 (underlined sequences correspond to start and stop codons)						
35	1	11	21	31	41	51	
	TGATGGTGGG	AATTTCCTTGA	AACCGCTCTC	GTAATTTGCC	ACGTGCTGTT	GCAAAATATTC	60
40	TGGTGAATGA	ACACAGAAAT	AGCATGGCTT	TCCTTTGCTG	AGAAATCACT	GATGGGAAGT	120
	GAGACTTGTT	AAACTTGAAA	GTGAATGGAC	CTGAGTGGAC	CCTTTGATCA	CATCAGTAAA	180
	CATGAGCGGT	ACCAAACTGT	ATATTTTATG	GGCACCACAC	CATGTTGATA	GATTTGTGTG	240
	GTGTGACTCA	GAACTAAGTC	TTTATCATGT	GGAATCTACT	GTGAATTCAG	AATCTCAAAGC	300
	TGGATCTTTA	CGTTTATCTG	AAGACTCTGC	AGCTACATTA	CTGTCAATAA	ATTCAGATAC	360
45	ACCCATATAT	AAATGTGTTG	CCTGGTATCT	TAATTATGAT	CCTGAATGTC	TGCTGGCAGT	420
	TGGACAAGCA	AATGGTCGAG	TTGTACTTAC	AAGCCTTGTT	CAAGATCATA	ACTCAAAGTT	480
	CAAAAGATTG	ATAGGAAAAG	AGTTTGTTC	AAAACATGCA	CGACAATGTA	ATACCCCTGC	540
	CTGGAATCCA	CTGGAATAGTA	ACTGGCTAGC	TGCTGGTTTA	GATAAGCACA	GAGCTGACTT	600
	TTCACTGCTA	ATATGGGATA	TCTGCAGCAA	ATATACTCCT	GATATAGTTC	CCATGGAAAA	660
50	AGTGAAACTT	TCAGCAGGTC	AAACTGAAAC	AACATTATTA	GTAAACAAAC	CACCTTTATGA	720
	GTTAGGACAG	AATGATGCTT	GTCTGCTCTC	TTGTTGGCTT	CCACGAGACC	AGAAACTTCT	780
	CCTTGCTGGT	ATGCATCGTA	ACCTAGCTAT	ATTTGATCTT	CGGAATACAA	GCCAAAAGAT	840
	GTTCGTAAT	ACAAAAGCTG	TTTCAGGGTGT	GACGGTAGAC	CCATATTTTC	ACGATCGTGT	900
	TGCTTCTCTC	TATGGAAGTC	AGGTTGCAAT	ATGGGATCTT	AGAAAATTTG	AGAAGCCAGT	960
55	TTTGACATTG	ACTGAGCAAC	CAAAACCCCT	AAACAAAAGTA	GCATGGTGTC	CCACTAGGAC	1020
	TGGTCTACTT	GCCACTTTAA	CAAGGGATAG	TAATATTATT	AGATTGTATG	ATATGCAGCA	1080
	TACACCCACT	CCCAATTGGG	ATGAAACTGA	ACCCACAATA	ATTCAAGAA	GTGTGCCAAC	1140
	TTGTGACAAT	TACATTGCTT	CCTTTGCGTG	GCATCCAACA	AGTCAAAATC	GAATGATAGT	1200
	TGTAACCTCC	AACCGCAACA	TGTCAGACTT	CACGTTTTTT	GAAAGGATAT	CTCTTGCCTG	1260
60	GAGCCCAATT	ACATCTTTAA	TGTGGGCTTG	TGGTCGTCAT	TTATATGAAT	GTACGGAAGA	1320
	AGAAAATGAT	AATTCTTTAG	AAAAAGATAT	AGCAACGAAG	ATGCGTCTTC	GGGCTTTATC	1380
	AAGGTATGGA	CTTGATACAG	AGCAGGTGTG	GAGGAACAC	ATPTTAGCTG	GAAATGAAGA	1440
	TCCACAGCTC	AAGTCACTCT	GGTATACTCT	GCACCTTATG	AAGCAATACA	CAGAAGATAT	1500
	GGATCAGAAA	TCTCCAGGCA	ACAAAGGATC	ATTGGTTTAT	GCAGGAATTA	AATCAATTGT	1560
65	AAAGTCATCG	TTGGGAATGG	TGGAAGCAG	CAGACATAAT	TGGAGTGGGT	TGGATAAGCA	1620
	AAGTGATATT	CAAAACTTAA	ATGAAGAGAG	AATCTTAGCT	TTACAGCTTT	GTGGGTGGAT	1680
	AAAGAAAGGA	ACGGATGTAG	ACGTGGGGCC	ATTTTGAAC	TCCCTTGATC	AAGAAGGGGA	1740
	ATGGGAAGA	GCTGCTGCTG	TGGCATTGTT	CAACTTGGAT	ATTCCGCCAG	CAATCCAAAT	1800
	CCTGAATGAA	GGGGCACTCT	CTGAAAAGG	CAGGAGATCT	GAATCTCAAT	GTGGTAGCAA	1860
70	TGGCTTTATC	GGGTATATAC	GATGAGAAGA	ACTCCCTTTG	GAGAGAAATG	TGTAGCACAC	1920
	TGCGATTACA	GCTAAATAAC	CCGTATTGTT	GTGTCAATGT	TGCATTTCTG	ACAAGTGAAA	1980
	CAGGATCTTA	CGATGGAGTT	TTGTATGAAA	ACAAAGTTGC	AGTACGTGAC	AGAGTGGCAT	2040
	TTGCTGTGTA	ATTCTCTAGT	GATACTCAGA	TACATCGAAA	AGTTGACCAA	TGAAATGAAA	2100
	GAGGCTGAAA	ATTTGGGAAG	AATTTTGCTT	ACAGGCTTCA	CTAAAGATGG	AGTGGACTTA	2160
75	ATGGAGAGTT	ATGTTGATAG	AACTGGAGAT	GTTCAAACAG	CAAGTTACTG	TATGTTACAG	2220
	GGTTCACCTT	TAGATGTTCT	TAAAGATGAA	AGGGTTTCACT	ACTGGATTGA	GAATTATAGA	2280
	AATTTATTAG	ATGCTCTGGG	GTTTTGGCAT	AAACGAGCTG	AATTTGATAT	TCACAGGAGT	2340
	AAGTTGGATC	CCAGTTCCAA	GCCTTTAGCA	CAAGTTTCTG	TGAGTTGCAA	TTTCTGTGGC	2400
	AAGTCAATCT	CCTACAGCTG	TTTCAGCTGTG	CCTCATCAGG	GCAGAGGTTT	TAGTCAGTAT	2460
80	GGTGTGAGTG	GCTCACCAAC	GAAATCTAAA	GTCAACAGTT	GTCTTGGCTG	TCGAAAAACA	2520
	CTTCTCTGAT	GTGCGCTTTG	TCTCATTTAT	ATGGGAACAC	CAGTTTCTAG	CTGTCTCTGA	2580

5 GGAACCAAAAT CAGATGAAAA AGTGGACTTG AGCAAGGACA AAAAATTAGC CCAATTTAAC 2640
 AACTGGTTTA CATGGTGTCA TAATTGCAGG CACGGTGGAC ATGCTGGACA TATGCTTAGT 2700
 TGGTTCAGGG ACCATGCAGA GTGCCCTGTG TCTGCATGCA CGTGATAATG TATGCAGTTG 2760
 GATACAACGG GGAATCTGGT ACCTGCAGAG ACTGTCCAGC CATAAAATGT TACCACCTTA 2820
 AGAGAACCCT TCAAGTGTGG AGCTTCTAG TAGGTGTCC TCATAGCTCA GAAACATACC 2880
 TCAGAACCAAG CCATTTCATGA CTTACCTGTA ATGGGAAAAT AAATCATCTC ATCAGAAAAA 2940
 AAAAAAAAAA AAAAAAAAAA

10 SEQ ID NO:60 PCQ1 Protein sequence
 Protein Accession #: NP_061878

15 1 11 21 31 41 51
 MSGTKPDILW APHVHDFV CDSLSLYHV ESTVNSELKA GSLRLSEDSA ATLLSINSDD 60
 PYMKCVAYWL NYDPECALLV GQANGRVLT SLGQDHNSKF KDLIGKEFVP KHARQCNTLA 120
 WNP L DSNWLA AGLDKHRADF SVLIWDICSK YTPDIVPMEK VKLSAGETET TLLVTKPLYE 180
 LGQNDACL SL CMLPRDQKLL LAGMHRLAI FDLRNTSQKM FVNTKAVQGV TVDPYFHDRV 240
 ASFYEGQVAI WDLRKFEKPV LTLTEQPKPL TKVAVCPTRT GLLATLTRDS NIIRLYDMQH 300
 20 TPTPIGDETE PTI IERSVQP CDNYIASFAW HPTSQNRMI VTPNRTMSDF TVFERISLAW 360
 SPTTSLMWRAC GRHLYECTEE ENDNSLEKDI ATKMLRLALS RYGLDTEQVW RNHILAGNED 420
 BQLKSLWYTL HFMKQYTEDM DQKSPGNKGS LUYAGIKSIV KSSLGMVESS RHNWSGLDKQ 480
 SDIQNLNEER ILALQLCGWI KKGTDVDVGP FLNSLVQEGE WERAAAVAF NLDIRRAIQI 540
 LNEGASSEKG RRSESCQGSN GFILGYG

25 Nucleic Acid Accession #: U42359
 Coding sequence: 563-775 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 TTGTACATCT TAACAACCTT AAGCTGTACA AATAGANCAA TAATATCTAA ATGGTGTGAT 60
 GATCAGCCCA CAGTACACAT CATTGATGAG AATTTCACCT GTCTCAACCT TTCTCATGCT 120
 GAGTCTCTGGC TTGTATAAAT GACTTATAAA GGTCCAAGGA TTAGAGATG ATTAAGAGAT 180
 35 AAGCTGGCAT TCTGTAAAGG CACCATCGTC TATCCCTGT CTATCTAGA TAAAGAAATGT 240
 AGTGCTAAAT CTGTATAATA TATTGTACAA ATGGAAATTC AATCTTAAGG ATTATTTTTT 300
 CCATATTGTT GTATTTCATT GTGGTGTATT GGAAAGTGAT CTGGACTTTG AGTGAGAAGA 360
 TGTGATTTGG ACCATGGCAC TTAATAACTC TATAACCTCA GGCAAGTCTT TTAATCTTCT 420
 40 CTGAGCCTCA GTTTCCTCA TTTTCAANT ATAGAGAGTA TAACATTTAT CTATATAGAC 480
 AAGTTGTAGT AAATTAAGT TTTACAAATG TAAGATAACT TTTAACTGTG AGATTCCATA 540
 TTCCAGTCTT ACATTATTAT GTTTATCTGC CACAGGGAGA AGTCCCTAGA TAAAAATGTC 600
 TACCAAAAGA CTGACACGTG GAGTTAATCA TTTGACAGAT GCAAATGCTT CCACCCCA 660
 CAAATATCT TTCTTTAATC TCTGTGTGGG TATCACTTAG GGAATAAAG CAGGCAACA 720
 45 AAATATTTTT TAATCTATC TTAGGAAAAA TTGTAGNCAA ATCTTTTNT CCCATTACA 780
 AATAATGTAA GCCTTAATAT TCAAGGGGTA ATAAAAATAC AAAGTCTTCC AACACGGTAA 840
 CTTACTTGAA AACTTT

50 SEQ ID NO:62 PDG3 Protein sequence
 Protein Accession #: AAB18375

55 1 11 21 31 41 51
 MGARGAPSR RQAGRRLRYL PTGSFFPFL LLLLCIQLGG GQKKKENLLA EKVEQLMEWS 60
 SRSIFRMNG DKFRKFKA P PRNYSIMVMF TALQPQRQCS VCRQANEYQ ILANSWRYSS 120
 AFCNKLFFSM VDYDEGDFV QQLNMNSAPT FXHXPFGKRP KRADTFDLQ IGFAAEQLAK 180
 60 WIADRTDVHI RVFREPNYSG TIALALLVSL VGGLLYXRRN NLEFIYNKTG WAMVSLCIVF 240
 AMTSGQMWNH IRGPPYAHKN PHNGQVSYIH GSSQAQFVAE SHIILVLNAA ITMGMVLLNE 300
 AATSKGDVGK RRIICLVGLG LVVFFSFLL SIFRSKYHGY PYSLDLFE

60 Nucleic Acid Accession #: AL080235
 Coding sequence: 245-453 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 GGTCGCCGCA CCGGCCGCT CCGGCCGCC GCGGCCCCA GCGCCGCCG CGCCACCGCC 60
 GGGGCCGCCA CCGCGCTGCC AGCCTACCC GCGGCCGAGC CGCCCGGCC GCTGTGGCTG 120
 CAGGGCGAGC CGCTGCATT CTGCTGCCTA GACTTCAGCC TGGAGGAGCT GCAGGGCGAG 180
 CCGGGCTGGC GGTGTAACCG TAAGCCCAT GAGTCCACGC TGGTGGCCTG CTTCATGACC 240
 70 CTGGTCATCG TGGTGTGGAG CGTGGCCGCC CTCATCTGGC CGGTGCCCAT CATCGCCGCG 300
 TTCTGCCCA ACGGCATGGA ACAGCGCCGG ACCACCGCCA GCACCAACGC AGCCACCCCC 360
 GCCGACATG CCGCAGGGAC CACCGCAGCC GCGCCGCCG CCGCGCTGC CGCCCGGCC 420
 GCGGCCGTCA CTTCCGGGGT GCGGACCAAG TGACCCGCTC CGCTCCTCCC TGTGTCCGTC 480
 CTGTGTCCGC GCGCGGGGT GCCTTTCGCC CCGGGGACTC GCGCGGTGTG CTTCGTGCTG 540
 TAGTTATCGT TAGTTCTCT TCCCGAGATG GGGCCGCCGA GAGACCCAG CGCCTTTGAA 600
 75 AAGCAAGGTT TGTCTGCGC TTCCAGTTC GAAAGCAGA TGTTTAAGCC CTGAGACTGA 660
 GGGTGGGATC GCAGCTCCGA AGACGGAGAG GAGGGAATG GGGCCCTTC CCTCTATTG 720
 CATCCCGCTG CCGGACTCCT TCCCGGCACC CACGTGCCCT AGATTCATGG CAGAAAAATGA 780
 CCAATTCCTG TGTATTGTT TTATATATTT AATAACTGTT TTAATGAAA GTTTTAGTAA 840
 80 AAAAAATACA AACACAAAG ATTAATTCG TATTGCTGTA GTAAGAGAAG CTCTTTGTAT 900
 CTGAACATAG TTGTATTTGA AATTGTGGT TTTTAAATTT ATTTAAATTT GGGGGGAGGG 960

CATGGGAAGG ATTTAACACC GATATATGT TACCGCTGAA AATGAACTTT ATGAACCTTT 1020
 TCCAAGTTGA TCTATCCAGT GACGTGGCCT GGTGGGCGTT TCTTCTTGTA CTTATGTGGT 1080
 TMTTGGCTT TTAATACAGA CATTTCCTC CAAAAAAGG

5 SEQ ID NO:64 PDG8 Protein sequence
 Protein Accession #: CAB45781

1 11 21 31 41 51
 10 GRRTRGLRPA AAPSAAAAATA GAPALPAYP AAEPPGPLWL QGEPLHFCCL DFSLEELQGE 60
 PGWRLNRKPI ESTLVACFMT LVIVVWSVAA LIWVPIIAG FLPNGMEQRR TTASTTAATP 120
 AAVPAGITAA AAAAAAAAAA AAVTSGVATK

SEQ ID NO:65 PDM1 DNA SEQUENCE

15 Nucleic Acid Accession #: NM_006765
 Coding sequence: 149-1195 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 CGGCGCGGCG CCGGGTCCCT CGCAAGCCG CTGCCATCCC GGAGGGCCCA GCCAGCGGGC 60
 TCCCGGAGGC TGGCCGGGCA GCGGTGGTGC GCGGTAGGAG CTGGGCGCGC ACGGCTACCG 120
 CGCGTGGAGG AGACACTGCC CTGCCGCGAT GGGGGCCCGG GCGGCTCCCT CACGCGCTAG 180
 25 GCAAGCGGGG CGGGGGGTGC GGTACCTGCC CACCGGGAGC TTTCCCTTCC TTCTCCTGCT 240
 GCTGCTGCTC TGCATCCAGC TCGGGGGAGG ACAGAAGAAA AAGGAGAATC TTTTAGCTGA 300
 AAAAGTAGAG CAGCTGATGG AATGGAGTTC CAGACGCTCA ATCTCCGAA TGAATGGTGA 360
 TAAATGCCGA AAATTTATAA AGGCACCACC TCGAAACTAT TCCATGATG TTAATGTTAC 420
 TGCTCTTCAG CCTCAGCGGC AGTGTCTGT GTGAGGCAA GCTAATGAAG AATATCAAA 480
 30 ACTGGCGAAC TCTGGGCGCT ATTCACTGCT TTTTGTAAAC AAGCTCTTCT TCAGTATGGT 540
 GGAATATGAT GAGGGGACAG ACCTTTTTC ACGCTCTCAC ATGAACCTCT CTCCTACATT 600
 CAYGCATTTC CCTCCAAAGG GCAGACCTAA GAGAGCTGAT ACTTTTGACC TCCAAAGAAT 660
 TGGATTTGCA GCTGAGCAAC TAGCAAAAGT GATTGCTGAC AGAACGGATG TTTATATTCG 720
 GGTTTTCAGA CCACCCAACT ACTCTGGTAC CATTTGCTTG GCCCTGTTAG TGTGCTTGT 780
 TGGAGGTTTG CTTTATINGA GAAGGAACAA CTTGGAGTTC ATCTATAACA AGACTGTTG 840
 35 GGCCATGGTG TCTCTGTGTA TAGTCTTTC TATGACTTCT GGCCAGATGT GGAACCATAT 900
 CCGTGGACCT CCATATGCTC ATAAGAACC ACACATGGA CAAGTGAGCT ACATTTCATG 960
 GAGCAGCCAG GCTCAGTTTG TGGCAGAACT ACACATTTAT CTGGTACTGA ATGCCGCTAT 1020
 CACCATGGGG ATGTTCTTTC TAAATGAAGC AGCAACTTCG AAAGGCGATG TTGAAAAAG 1080
 40 ACGGATAATT TGCCTAGTGG GATTGGGCTT GGTGGTCTTC TTCTTCAGTT TTCTACTTTC 1140
 AATATTTCGT TCCAAAGTACC ACGGCTATCC TTATAGTGAT CTGGACTTTG AGTGAGAAGA 1200
 TGTGATTTGG ACCATGGCAC TTAATAAACT TATAACCTCA GCTTTTAAAT TAAATGAAGC 1260
 CAAGTGGGAT TTGCAATAAG TGAATGTTTA CCATGAAGAT AAAGTGTTC TGAATTTATA 1320
 CTATTTTGAA TTCAATTCATT TCATTGTGAT CAGCTAGCTT ATTCTTGTGT ACTTTTTTTA 1380
 45 AACTGTGGGT TTTCTAGTGA AATTTAATTT ACAGAAATCA ATGGTAGCAT TTAGTAATCT 1440
 ACAAGGAAA TATCAAAAGT TTTTCAAGC CTGTTATATY CAGTGTGTRC CACAGGATTG 1500
 CAATAATGA CAATGTAATT A

50 SEQ ID NO:66 PDM1 Protein sequence:
 Protein Accession #: NP_006756

1 11 21 31 41 51
 55 MGARGAPRRR RQAGRRRLRYL PTGSFPFLLL LLLLCIQLGG GQKKKENLLA EKVEQLMEWS 60
 SRRSIFRMNG DKFRKFKAAP PRNYSMIVMF TALQPRQCS VCRQANEVYQ ILANSWRYSS 120
 AFCNKLFFSM VDYDEGTDVF QQLNMNSAPT FXHXPFGKRP KRADTFDLQR IGFAAEQLAK 180
 WIADRTDVHI RVFRPPNYSG TIALALLVSL VGGLLYXRRN NLEFIYNKTG WAMVSLCIVF 240
 AMTSGQMWNH IRGPPYAHKN PHNGQVSVIH GSSQAQFVAE SHIILVLNAA ITMGMVLLNE 300
 60 AATSKGDVGK RRIICLVGLG LVVFFSFLL SIFRSKYHGY PYSDLDPE

SEQ ID NO:67 PDM2 DNA SEQUENCE

65 Nucleic Acid Accession #: NM_000947
 Coding sequence: 88-1617 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 70 GGTTCATAT GAATCTTCCC GCCACCCGGG AACAGCTGGC TGCCACCGTT TGTGTTTTC 60
 GAGTTGTAT TCTTGCAGGT GACCAAGATG GAGTTTCTG GAAGAAAGCG GAGGAAGCTG 120
 AGGTGGCAG GTGACCCAGG GAATGCTTCC TACCCTCATT GCCTTCAGTT TTACTTGCAG 180
 CCACCTTCTG AAAACATATC TTTAACAGAA TTTGAAACT TGCTATTGA TAGAGTTAAA 240
 TTGTTAAAA CAGTTGAAAA TCTTGGAGTG AGCTATGTGA AAGGAACTGA ACAATACCAG 300
 75 AGTAAGTTGG AGAGTGAAGT TCGGAAGCTC AAGTTTTCCT ACAGAGAGAA GCTAGAAGAT 360
 GAATATGAAC CACGAAGAAG AGATCATATT TCTCAATTTA TTTTGGCGCT TGCTTATTCG 420
 CAGCTGGAAG AACTTAGACG CTGGTTCATT CAACAAGAAA TGGATCTCCT TCGATTTAGA 480
 TTTAGTATTT TACCCAAGGA TAAATTCAG GATTTCCTAA AGGATAGCCA ATTGCAGTTT 540
 GAGGCTATAA GTGATGAAGA GAAGACTCTT CGAGAACAGG AGATTGTTGC CTCATCACCA 600
 80 AGTTAAGTG GACTTAAGTT GGGGTTGAG TCCATTATA AGATCCCTTT TGCTGATGCT 660
 CTGGATTGTT TTCGAGGAAG GAAAGTCTAT TTGGAAGATG GCTTTGCTTA CGTACCACTT 720

5	AAGGACATTTG	TGGCAATCAT	CCTGAATGAA	TTTAGAGCCA	AACTGTCCAA	GGCTTTGGCA	780
	TTAACAGCCA	GGTCTTGCC	TGCTGTGCAG	TCTGATGAAA	GACTTCAGCC	TCTGCTCAAT	840
	CACCTCAGTC	ATTCCTACAC	TGGCCAAGAT	TACAGTACCC	AGGGAAATGT	TGGGAAGATT	900
	TCCTTAGATC	AGATGATTT	GCTTCTACC	AAATCCTTCC	CACCTTGCA	GCCTCAGTTA	960
	CATAAAGCCT	TGCGGAAAA	TCACCATCTT	CGTCATGGAG	GCCGAATGCA	GTATGGCCTA	1020
	TTTCTGAAGG	GCATTTGGTT	AACCTTTGAA	CAGGCATTGC	AGTTCTGGAA	GCAAGAATTT	1080
	ATCAAAGGAA	AGATGGATCC	AGACAAGTTT	GATAAAGGTT	ACTCTTACAA	CATCCGTCAC	1140
	AGCTTTGGAA	AGGAAGGCAA	GAGGACAGAC	TATACACCTT	TCAGTTGCCT	GAAGATTATT	1200
10	CTGTCCAAATC	CACCAAGCCA	AGGGGATTAT	CATGGGTGCC	CATTCCGTC	CAGTGATCCA	1260
	GAGCTGCTGA	AGCAAAAGTT	GCAGTCATAC	AAGATCTCTC	CTGGAGGGAT	AAGCCAGATT	1320
	TTGGATTTAG	TAAAGGGGAC	ACATTACCAG	GTAGCCTGTC	AAAAATACTT	TGAGATGATA	1380
	CACAATGTGG	ATGATTTGGG	CTTTCTTTTG	AATCATCCTA	ATCAGTTCTT	TTGTGAGAGC	1440
	CAACGTATTCC	TAAATGGTGG	TAAAGACATA	AAGAAGGAAC	CTATCCAACC	AGAAACTCCT	1500
15	CAACCCAAAC	CAAGTGTCCA	GAAAACCAAG	GATGCATCAT	CTGCTCTGGC	CTCTTTAAAT	1560
	TCCTCTCTGG	AAATGGATAT	GGAAGGACTA	GAAGATTACT	TTAGTGAAGA	TTCTTAGGCA	1620
	GTTTATAAAC	CTTTTTCCTT	CAATAGCCTG	TTTCTGTGTT	TAAAGATTTT	GCCTTTGTTG	1680
	TTGAAAAAAG	GTTTCACTGT	CACCAAGGCT	TAGTGCAAGT	ACACAATTAC	AGCTGATTGC	1740
	AGCCTTGACC	TTCCCAAGCTC	AAGTGATCCT	CCTACCTCAG	CCTCCCAAGT	AGTTAGGACA	1800
20	CACAGGTGTG	CACCTCATAT	CCAGATAATT	TTTTTCAATT	TTTTTTTGTA	GAGGTGGGGG	1860
	GTCTCCCTAT	GTGTCACAGG	CAGATCTCAG	ACTCCTGGGC	TCAAGCGATC	CTCACACCTC	1920
	AGCGTCCAC	AGTGTCTGGG	TTACAGTTGT	GAGCCACTGT	GCCTGGCCTT	TTTTTTTTTT	1980
	TAACTTTTTC	GTTTAACTTC	TCTCTTCACT	GCATCCCAAT	CCATCTACAG	GCATGCACAC	2040
	TTATTAGGAA	AGGAGGTTTG	AGGTAACAAC	AGAGACTTTC	ACTATATTTT	GCTTTGACAG	2100
25	AAGGAAAGAG	GAGGAGTTTC	TATTAATAATC	TGTCACTTGA	GTGATGTCAT	TTAAGTCCCTA	2160
	TTTTAGGAGA	TAAAAACAGC	TTTGGGGACT	GTTTAAAGTC	CCCCAGAAAC	TACAATAAAG	2220
	AACAACCTTT	GTTTAACTC	TTAATCACTT	TGTAATTTTG	ACTCAATCCT	TTTCTGGACC	2280
	ATTTTGTGTA	ATAAATATCA	AAGTGT				

30 **SEQ ID NO:68 PDM2 Protein sequence:**
 Protein Accession #: NP_000938

35	1	11	21	31	41	51	
	MEFSGRKRRK	LRLAGDQRNA	SYPHCLQFYL	QPPSENISLT	EFENLAIDRV	KLLKSVENLG	60
	VSYVKGTEQY	QSKLESELRK	LKFSYREKLE	DEYEPRRRDH	ISHFILRLAY	QSQBELRRWF	120
	IQQEMDLLRF	RFSILPKDKI	QDFLKDSQLQ	FEAISDEEKT	LREQEIVASS	PSLSGLKLGF	180
	BSIYKIFPAD	ALDLFRGRKV	YLEDGFAYVP	LKDIVAILLN	EFRAKLSKAL	ALTARSLPAV	240
40	QSDERLQPLL	NHLSHSTYQ	DYSTQGNVVK	ISLDQIDLLS	TKSFPPCMRK	LHKALRENNH	300
	LRHGGRRQVQ	LFLKIGLITL	EQALQFWKQE	FIKGMKDPDK	FDKGYSYNIR	HSFGKEGKRT	360
	DYTFPFSLKI	ILSNFPGSQD	YHCGPFRHSD	PELLKQKLQS	YKISFPGISQ	ILDLVKGYTHY	420
	QVACQKYFEM	IHNVDCCGFS	LNHPNQPFCE	SQRILNGGKD	IKKEPIQPST	PQPKPSVQKT	480
	KDASSALASL	NSSLEMDMEG	LEDYFSEDS				

45 **SEQ ID NO:69 PDM3 DNA SEQUENCE**
 Nucleic Acid Accession #: NM_024840
 Coding sequence: 108-491 (underlined sequences correspond to start and stop codons)

50	1	11	21	31	41	51	
	AAATCATACA	GGAGAGAAGT	CATATATATG	CAGTGATTGT	GGAAAAGGCT	TCATCAAGAA	60
	GTCTCGGCTC	ATTAAATCATC	AGAGAGTTCA	TACAGGAGAG	AAACCACATG	GATGCGCCT	120
	GTGTGGGAAG	GCCTTTCCCA	AAAGGTCCAG	GCTCACTGAA	CACCAGAGAA	CTCATACAGG	180
55	AGAGAAGCCC	TATGAATGCA	CTGAATGTGA	CAAAAGCATTC	CGCTGGAAAT	CACAGCTCAA	240
	TGCACATCAG	AAAGCTCACA	CAGGAGAGAA	GTCAATATATA	TGCCGTGATT	TGGGAAAAGG	300
	CTTCATTCAG	AAGGGAATC	TCATTGTACA	TCAGCGAATT	CATCTGGGAG	AAAAACCCCTA	360
	TATATGCAAT	GAATGTGGAA	AAGGCTTCAT	CCAAAAGGGC	AACCTCCTTA	TTCATCGACG	420
	TACTCACACT	GGAGAGAAAC	CCTATGAATG	CAATGAATGT	GGGAAAGGCT	TCAGCCAGAA	480
60	GACATGTTTA	ATATCCCATC	AGAGATTCCA	CACAGGAAG	ACACCTTTTG	TATGTACTGA	540
	GTGTGGAAAA	TCCTGTCTAC	ACAAGTCAGG	TCTCATTTAA	CACCAGAGAA	TTACACACAGG	600
	AGAGAAACCC	TATACATGCA	GTGACTGTGG	GAAAGCTTTC	AGAGATAAAT	CATGTCTCAA	660
	CAGACATCGG	AGAACTCATTA	CAGGGGAGAG	ACCGTATGGA	TGCTCTGATT	GTGGGAAAGC	720
	TTTCTCCAC	TTGTCATGCC	TTGTTTATCA	TAAGGGAATG	CTGCATGCAA	GAGAGAAATG	780
65	TGTAGGTTCA	GTCAAAATGG	AAAAATCCTG	CTCAGAGAGT	CATAGCTTAT	CACATACACG	840
	TGATCTCATA	CAGGATAAAG	ACTCTGTATA	CATGGTGACT	CTGCAGATGC	CTTCTGTGGC	900
	AGCTCAGACC	TCATTAACTA	ACAGTGCCTT	CCAAGCAGAG	AGCAAAGTAG	CCATTGTGAG	960
	CCAGCCTGTT	GCCAGAAGTT	CAGTCTCAGC	AGATAGTAGA	ATTTGCACAG	AATAAAAACC	1020
	ATATGAATGC	AGTGAATGTG	GTAGTGCTTT	CAGTGATCAA	TTACATCATA	TGTCACAAAA	1080
70	AACACAGAGG	AACAACTGA	TATATTCAAG	GTGGAAAGCC	CTTGAATAAA	ACCTTATGGC	1140
	TAATAAGCAT	ATACTCAGAG	AAAAATAGTA	TGAAGTGGAG	ACTGGGAAAT	TCTTTTATGG	1200
	GAAGATAGAT	CTTCTCATCA	GTGACCATAG	ATCACATCTT	CAGTGAGCTT	ATAGTTGGTA	1260
	GAATATATAAT	GATCATGGAA	AAGTCCCTGT	TCAGAAACAG	TACGCCAGTA	GGTATCAGGG	1320
	GGTTTACACA	GAGAGAGAAC	TTTTGGAAGA	CCTTTGAAGG	CTATGAATGT	GGCAGGGTTG	1380
75	CTAGTGGTAC	ATTCCTGCCCT	ATCCTCAGAG	GGAATCATAT	AGAAAATAAA	CTATGAAAAT	1440
	GTAACATAGA	CATCTTCATC	AAAATATGAA	AGAACACACG	AAGCAAAATA	CCCTGTGTA	1500
	AAGGAGTATT	TTAGAGATTT	CGATCAGAAA	TCTAACATCA	TTATATGGCA	GATATATATC	1560
	AGGATGTGTA	TTTTAGGACA	ATATACCTTG	AATCACTAGT	TGATATGTCA	ATGACTAATT	1620
	AAAAGGGGTT	GTCAAGTTTA	CACATCATTG	GTTAAATTTA	TAGCACAATG	TACCTCTTCC	1680
80	CCCTTTTTTG	ATAAGAGTCT	TCTATTTCCA	ACCAAGATCA	TTATATGATT	AGCTCTTGTT	1740
	TTTCTTTGAT	TCCAAATTTT	TTCACTTGTT	ATTTCAGACT	ACTGAAGCTC	TTCAAAAGGA	1800

AAAATGTATT TAATTTAATA ATGTAACACA ACAAGTTTGG ATGTGTTTAA CTTTATAAAT 1860
AATCACCCCA GAGGAATGAA GTTCAAACT TGTGAATAAC C

5 SEQ ID NO:70 PDM3 Protein sequence:
Protein Accession #: NP_079116

1 11 21 31 41 51
10 MDAACVGRPS PKGPGSLNTR ELIQERSPMN ALNVTKHSAG NHSSMHIRKL TQERSHIYAV 60
IVEKASFRRE ISLYISEFIL EKNPIYAMNV EKASSKRATS LFIDVLTLEL NPMNAMNVGK 120
ASARRHV

15 SEQ ID NO:71 PDM8 DNA SEQUENCE
Nucleic Acid Accession #: NM_018455
Coding sequence: 341-955 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
20 AATTTCGGCA CGGGGGGGAG GCACAGTGAG TCCACTGGGG CACGGCAGCG TCTAAGCCAC 60
AAGCCGACTG ACATAAGCCA GGTCCCTAACG GAGCCTATGT GTAAGTCCAC TACTGGTGCA 120
AGGTTCGACA CTTCTAAGAA GAGCGGCTCGG GGGGGCTCGG CGACCTTCGC TTCAGTCGCT 180
CCCCCGTGCA GTCCCTCTGT CCCAAGACAC AGCCTGATGC TTGTGCTCCG GTGGGCGGAC 240
TTGGAGGCGG CGGGAAGTGC AATTGGTGGC TTTGAAGGCG GCGGAGCGGG AACAGCTCTT 300
25 GAGGAGTGAG ACTGCAAGAG ATGTGGGCCG TGCCAAAGAG ATGGATGAGA CTGTTGCTGA 360
GTTTCATCAAG AGGACCATCT TGAAAATCCC CATGAATGAA CTGACAACAA TCCTGAAGGC 420
CTGGGATTTT TTGTCTGAAA ATCAACTGCA GACTGTAAAT TTCCGACAGA GAAAGGAATC 480
TGTAAGTTCAG CACTGTATCC ATCTGTGTGA GGAAGAGCGT GCAAGTATCA GTGATGCTGC 540
30 CCTGTTAGAC ATCATTTATA TGCAATTTC AAGAGTTCAG AAAGTTTGGG ATGTTTTCAT 600
GATGAGTAAA GGACAGGCTG AAGATGTTGA CCTTTTGAT ATGAAACAAT TTAATAATTC 660
GTTCAAGAAA ATTCATTCAGA GAGCATTAAA AAATGTGACA GTCAGCTTCA GAGAACTGA 720
GGAGAATGCA GTCTGGATTG GAATTGCCTG GGGAAACACG TACACAAAGC CAAACAGTA 780
CAAACCTACC TACGTGGTGT ACTACTCCCA GACTCCGTAC GCCTTCACGT CCTCCTCCAT 840
35 GCTGAGGCGC AATACACCGC TTCTGGGTCA GGAGTTAGAA GCTACTGGGA AAATCTACCT 900
CCGACAAGAG GAGATCATTT TAGATATTAC CGAAATGAAG AAAGCTTGCA ATTAGTGAAC 960
ATGAAGGAA AATAAAAAAT CCTCACAGTC AAAAAAAAAA AAAAA

40 SEQ ID NO:72 PDM8 Protein sequence:
Protein Accession #: NP_060925

1 11 21 31 41 51
40 MDETVAEFIK RTILKIPMNE LTTILKAWDF LSENQLQTVN FRQRKESVVQ HLIHLCEEKR 60
45 ASISDAALLD IYMQFHQHQ KVVWVFQMSK GPGEDVDLFD MKQPKNSFKK ILQRALKNVT 120
VSFRETENA VVIRLAWGTQ YTKPNQYKPT YVYYYSQTPY APTSSSMLRR NTPPLGQLE 180
ATGKIYLRQE EILIDITEMK KACN

50 SEQ ID NO:73 PDM9 DNA SEQUENCE
Nucleic Acid Accession #: NM_016192
Coding sequence: 1-1125 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
55 ATGGTGCTGT GGGAGTCCCC GCGGCAGTGC AGCAGCTGGA CACTTTGCGA GGGCTTTTGC 60
TGGCTGTGTC TGCTGCCCGT CATGCTACTC ATCGTAGCCC GCCCGGTGAA GCTCGCTGCT 120
TTCCTTACCT CCTTAAGTGA CTGCCAAACG CCCACCGGCT GGAATTGCTC TGGTTATGAT 180
GACAGAGAAA ATGATCTCTT CCTCTGTGAC ACCAACACCT GTAAATTGTA TGGGGAATGT 240
TTAAGAAATG GAGACACTGT GACTTGCCTC TGTCAGTTCA AGTCAACAA TGAATATGTG 300
60 CCTGTGTGTG GCTCCAATGG GGAGAGCTAC CAGAATGAGT GTTACCTGCG ACAGGCTGCA 360
TGCAAACAGC AGAGTGAGAT ACTTGTGGTG TCAGAAGGAT CATGTGCCAC AGATGCAGGA 420
TCAGGATCTG GAGATGGAGT CCATGAAGGC TCTGGAGAAA CTAGTCAAAA GGAGACATCC 480
ACCTGTGATA TTTGCCAGTT TGGTGCAAGT TGTGACGAAG ATGCCGAGGA TGCTGTGGTGT 540
GTGTGTAATA TTGACTGTTC TCAAACCAAC TTCAATCCCC TCTGCGCTTC TGATGGGAAA 600
65 TCTTATGATA ATGCATGCCA ATCAAGAA GCATCGTGTC AGAAACAGGA GAAATTTGAA 660
GTCATGTCTT TGGGTCGATG TCAAGATAAC ACAACTACAA CTAATAAGTC TGAAGATGGG 720
CATTATGCAA GAACAGATTA TGCAAGAAAT GCTAACAAAT TAGAAGAAAG TGCCAGAGAA 780
CACCACATAC CTTGTCCGGA ACATTACAAT GGCTTCTGCA TGCAATGGGA GTGTGAGCAT 840
TCTATCAATA TGCAGGAGCC ATCTTGCAGG TGTGATGCTG GTTATACTGG ACAACACTGT 900
70 GAAAAAAGG ACTACAGTGT TCTATACGTT GTTCCCGGTC CTGTACGATT TCAGTATGTC 960
TTAATCGCAG CTGTGATTGG AACAAATCAG ATTGCTGTCA TCTGTGTGGT GGTCTCTGTC 1020
ATCACAAGGA AATGCCCCAG AAGCAACAGA ATTCACAGAC AGAAGCAAAA TACAGGCGAC 1080
TACAGTTCAG ACAATACAAC AAGAGCGTCC ACGAGGTTAA TCTGA

SEQ ID NO:74 PDM9 Protein sequence:
Protein Accession #: NP_057276

```

5      1      11      21      31      41      51
      1 MVLWESPRQC SSWTLCEGFC WLLLLFVMLL IVARPVKLAA FPTSLSDCQT PTGWNCSGYD 60
      61 DRENDFELCD TNTCKFDGEC LRIGDTVTCV CQFKCNNDYV FVCGSNGESY QNECYLRQAA 120
      121 CKQOSEILVV SEGSCATDAG SSGSDGVHEG SGETSQKET'S TCDICQFGAE CDEDAEDVWC 180
      181 VCNIDCSQTN FNPLCASDGK SYDNACQIKE ASCQKQEKIE VMSLGRCDQN TTTTTSKSEDG 240
      241 HYARTDYAEN ANKLEESARE HHIPCPPEHYN GFCMHGKCEH SINMQEPSRC CDAGYTGQHC 300
      301 EKKDYSVLV VPGFVRQYV LIAAVIGTIQ IAVICVVVLC ITRKCPRSNR IHRQKQNTGH 360
      361 YSSDNTTRAS TRLI

```

SEQ ID NO:75 PDO1 DNA SEQUENCE

Nucleic Acid Accession #: NM_014324
Coding sequence: 89-1237 (underlined sequences correspond to start and stop codons)

```

20      1      11      21      31      41      51
      1 GCGCGCGGGA TTGGGAGGGC TCTCTGCAGG CTGCTGGGCT GGGGCTAAGG GCTGCTCAGT 60
      21 TCTCTTCAGC GGGGCACTGG GAAGCGCCAT GGCACGTGAG GGCATCTCGG TCGTGGAGCT 120
      31 GTCCGGCCTG GCCCGGGGCC GTNCTCTGTC TATGGTCCCTG GCTGACTTCG GGGCGCGTGT 180
      41 GGTACGCGTG GACCGGGCCG GCTCCCGCTA CGACGTGAGC CGCTTGGGCG GGGGCAAGCG 240
      51 CTGCGTAGTG CTGGACCTGA AGCAGCCGCG GGAGCCGCGT GCTGCGGCGT CTGTGCAAGC 300
      61 GGTGCGATGT GCTGCTGGAG CCTTCCGCC CCGGTGTCTAT GGAGAAATC CAGCTGGGCC 360
      71 CAGAGATTCT GCAGCGGGAA AATCCAAGGC TTATTTATGC CAGGCTGAGT GGATTTGGCC 420
      81 AGTTCAAGAA AGCTTCTGCG GGTTAGCTGG CCACGATATC AACTATTGG CTTTGTGCTCAGG 480
      91 TGTTCTCTCA AAAATTGGCA GAAGTGGTGA GAATCCGTAT GCCCGCTGTA ATCTCGTGGC 540
      101 TGACTTTGCT GGTGGTGGCC TTATGTGTGC ACTGGGCATT ATAATGGCTC TTTTGTACCG 600
      111 CACACGCACT GACAAGGGTC AGGTCAATTGA TGCAAAATATG GTGGAAGGAA CAGCATATTT 660
      121 AAGTTCTTTT CTGTGGGAAA CTCAGAAATC GAGTCTGTGG GAAGCACCTC GAGGACAGAA 720
      131 CATGTTGGAT GGTGGAGCAC CTTTCTATAC GACTTACAGG ACAGCAGATG GGGATTTCTAT 780
      141 GGTGTTGGA GCAATAGAAC CCCAGTTCTA CGAGCTGCTG ATCAAAGGAC TTGGACTAAA 840
      151 GTCTGATGAA CTTCCCAATC AGATGAGCAC GGATGATTGG CCAGAAATGA AGAAGAAGTT 900
      161 TGCAGATGTA TTTGCAAAAG AGACGAAGGC AGAGTGGTGT CAAATCTTTG ACGGCACAGA 960
      171 TGCTCTGTGG ACTCCGGTTC TGACTTTTGA GGAGGTTGTT CATCATGATC ACAACAGGA 1020
      181 ACGGGCTCG TTTATACCCA GTGAGGAGCA GGACGTGAGC CCCCCTGCTG CACCTCTGCT 1080
      191 GTTAAACACC CCAGCCATCC CTTCTTCCAA AGGGGATCCT TTCATAGGAG AACACACTGA 1140
      201 GGAGATACTT GAAGAATTG GATTACAGCG AGAAGAGATT TATCAGCTTA ACTCAGATAA 1200
      211 AATCATTGAA AGTAATAAGG TAAAGCTAG TCTCTAACTT CCAGGCCAC GGCTCAAGTG 1260
      221 AATTTGAATA CTGCATTATC AGTGTAGAGT AACACATAAC ATTGTATGCA TGGAAACATG 1320
      231 GAGGAACAGT ATTACAGTGT CTTACCACTC TAATCAAGAA AAGAATTACA GACTCTGATT 1380
      241 CTACAGTGAT GATTGAATTC TAAAAATGGT TATCATTAGG GCTTTTGATT TATAAACTT 1440
      251 TGGGTACTTA TACTAAATTA TGGTAGTTAT TCTGCCTTCC AGTTTGCTTG ATATATTTGT 1500
      261 TGATATTAG ATTCTTGACT TATATTTTGA ATGGGTTCTA GTGAAAAGG AATGATATAT 1560
      271 TCTTGAGAGC ATCGATATAC ATTTATTATC ACTCTTGATT CTACAATGTA GAAATAGAG 1620
      281 AAATGCCACA AATTGTATGG TGATAAAGT CACGTGAAC AGAGTGATTG GTTGCAATCA 1680
      291 GGCCTTTTGT CTTGGTGTTC ATGATCTCCC TCTAAGCACA TTCCAAACTT TAGCAACAGT 1740
      301 TATCACACTT TGTAATTGTC AAAAGAAAGT TTCACCTGTA TTGAATCAGA ATGCTTCAA 1800
      311 CTGAAAAAAA ATATCCAAA ATAATGAGGA AATGTGTTGG CTCACTACGT AGATCCAGA 1860
      321 GGGACAGTCA GTTTTAGGGT TGCTGTATC CAGTAACCG GGGCTGTGTT CCCCTGGGT 1920
      331 CTCTGGGCTG TCAGCTTTCC TTTCTCCATG TGTTTGATTT CTCCTCAGGC TGGTACCAAG 1980
      341 TTCTGGATCT TATACCAAC ACACAGCAAC ATCCAGAAAT AAGATCTCA GGACCCCA 2040
      351 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

```

SEQ ID NO:76 PDO1 Protein sequence:
Protein Accession #: NP_055139

```

60      1      11      21      31      41      51
      1 MALQGISVVE LSLGAPGRXC AMVLADFGAR VVRVDREGSR YDVSRLGRGK RSLVLDLKQP 60
      61 REPRAAASVQ AVGCAAGALP PRCHGETPAG PRDAAAGSK AYLCQAEWIW PVQESFCRLA 120
      121 GHDINYLALS GVLSKIGRS ENPYAPNLV ADFAGGGLMC ALGIIMALFD RTRTDKQVI 180
      181 DANMVEGTAY LSSFLWKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEF MAVGAIEPQF 240
      241 YELLIKLGL KSDLPNQMS TDDWPEMKK FADVFAKKTK AEWCQIFDGT DACVTPVLTF 300
      301 EEVVHHDH NK ERGSFITSEE QDVSPRLAP LLNTPAIPSS KGDFPIGEHT EEILEEFGFS 360
      361 REEIVQLNSD KIIESNKVKA SL

```

SEQ ID NO:77 PDO3 DNA SEQUENCE

Nucleic Acid Accession #: AB028951
Coding sequence: 97-1128 (underlined sequences correspond to start and stop codons)

```

75      1      11      21      31      41      51
      1 GTTAAATCCT TACTTTACCA GATTCCTGAT GGTATCCATT ACCTCCATGC AAATTGGGTG 60
      21 CTTCACAGAG ACTTGAAACC AGCAATATC CTAGTAATGG GAGAAGTCC TGAGAGGGGG 120
      31 AGAGTCAAAA TAGCTGACAT GGGTTTGGCC AGATTATTCA ATCTCCTCTT AAAGCCACTA 180
      41 GCAGATTGG ATCCAGTAGT TGTGACATTT TGGTATCGGG CTCCAGAACT TTTGCTTGGT 240
      51 GCAAGGCAIT ATACAAAGGC CATTGATATA TGGGCAATAG GTTGATATAT TGCTGAATTG 300
      61 TTGACTTCGG AACCTATTTT TCACTGTCGT CAGGAAGATA TAAAACAAG CAATCCCTTT 360

```

	CATCATGATC	AACITGGATCG	GATATTTAGT	GTCTATGGGGT	TTCTTCGAGA	TAAAGACTGG	420
	GAAGATATTA	GAAAGATGCC	AGAATATCCC	ACACTTCAAA	AAGACTTTAG	AAGAACAACG	480
	TATGCCAACA	GTAGCCCTCAT	AAAGTACATG	GAGAAACACA	AGGTCAAGCC	TGACAGCAAA	540
5	GTGTCTCTCT	TGCTTCAGAA	ACTCTTGACC	ATGGATCCAA	CCAAGAGAAT	TACCTCGGAG	600
	CAAGCTCTGC	AGGATCCCTA	TTTTTCAGGAG	GACCCTTTGC	CAACATTAGA	TGTATTTGCC	660
	GGCTGCCAGA	TTCCATACCC	CAAACGAGAA	TTCTTTAATG	AAGATGATCC	TGAAGAAAAA	720
	GGTGACAAGA	ATCAGCAACA	GCAGCAGAAC	CAGCATCAGC	AGCCACACAG	CCCTCCACAG	780
	CAGGCAGCAG	CCCTCCACCA	GGCGCCCCCA	CCACAGCAGA	ACAGCACCCA	GACCAACGGG	840
10	ACCGCAGGTG	GGGCTGGGGC	CGGGGTCGGG	GGCACCAGGAG	CAGGGTTGCA	GCACAGCCAG	900
	GACTCCAGCG	TGAACCAAGT	GCCTCCAAAC	AAGAAGCCAC	GGCTAGGGCC	TTCAGGCGCA	960
	AACITCAGGAT	TGCTGAGCAT	GCCCTCGGAT	TATCAGCACT	CCAGTTCTCG	CCTGAATTAC	1020
	CAAGCAGCG	TTCCAGGATC	CTCTCAGTCC	CAGAGCACAC	TTGGCTACTC	TTCTCTGCTCT	1080
	CAGCAGAGCT	CACAGTACCA	CCCATCTCAC	CAGGCCACCC	GGTACTGACC	AGCTCCCGTT	1140
	GGGCCAGGCC	AGCCCAAGCC	AGAGCACAGG	CTCCAGCAAT	ATGTCTGCAT	TGAAGAAGAC	1200
15	CAAAAAATG	CAAACTATGA	TGCCATTAA	AACTCATACA	CATGGGAGGA	AAACCTTATA	1260
	TACTGAGCAT	TGTCGAGGAC	TGATAGCTCT	TCTTTATTGA	CTTAAAGAAG	ATTCTTGTGA	1320
	AGTTTCCCCA	GCACCCCTTC	CCTGCATGTG	TTCCATGTGT	ACTTCTCTGA	TAAAGCGTCT	1380
	GATCTAATCC	CAGCATTTCT	GTAACTTTCA	GCATTTCTTT	GAAGGATTTC	CTGGTGCACC	1440
20	TTTCTCATGC	TGTAGCAATC	ACTATGGTTC	ATCTTTTCAA	AGCTCTTTTA	ATAGGATTTT	1500
	AATGTTTATG	AAACAGGATT	CCAGTGGTGT	ATAGTTTAT	ACTTCTATGA	CTGATTTAGC	1560
	AAACACAGTA	AAAATGCAAC	TTTTAAAGCA	CTACGTTTTC	ACAGACAATA	ACTGTTCTGC	1620
	TCAITGGAAT	CTTAAACAGA	AACTGTTACT	GTCCCAAGT	ACTTTACTAT	TACGTTCTGA	1680
	TTTATCTAGT	TTCCAGGGAAG	GTCTAATAAA	AAGACAAGCG	GTGGGACAGA	GGGAACCTAC	1740
25	AAACCAAAAC	TGCCATAGATC	TTTGCAAGTA	TGTGCTTTAT	GCCACGAAGA	ACTGAAGTAT	1800
	GTGGTAATTT	TTATAGAATC	ATTCATATGG	AACTGAGTTC	CCAGCATCAT	CTTATTTCTGA	1860
	ATAGCATTTA	GTAATTAAGA	ATTACAATTT	TAACCTTCAT	GTAGCTAAGT	CTACCTTAAA	1920
	AAGGGTTTCA	AGAGCTTTGT	ACAGTCTCGA	TGGCCACAC	CAAAACGCTG	AAGAGAGTAA	1980
	CAACTGCAC	AGGATTTCTG	TAAGGAGTAA	TTTTGATCAA	AAGACGTGTT	ACTTCCCTTT	2040
30	GAAGGAAAG	TTTTTATGTT	GTATTTGTAC	TAAAGTCCGC	TTCTCTAAAG	AACCATTTGT	2100
	TTCTTACAT	CTGGGTCTGC	GTGAGTAACT	TTCTTGCAAT	ATCAAGGTTA	CTCAAGTAGA	2160
	AGCCTGAATA	TAAATCTGCT	TTTTAAATAA	AGAGCAGTGT	TCTCCATTTC	TATTTGTATP	2220
	AGATATAGAG	TGACTATTTT	TAAAGCATGT	TAAAAATTTA	GGTTTTATTC	ATGTTTAAAG	2280
	TATGTATTTA	TGATGCAATA	TTTTTGCTGT	GTACTGAAA	CTTAAATCTA	TCAAGAACTT	2340
35	TTTTCTATGC	ACTGAAATGAT	TTCTTTTGCC	CCTAGGAGAA	AACTTAATAA	TTTGCTCTAA	2400
	AAACTATGGG	CGGATAGTAT	AAGACTATAC	TAGACAAAGT	GAATATTTGC	ATTTCCATTA	2460
	TCTATGAATT	AGTGGCTGAG	TTCTTTCTTA	GCTGCTTTAA	GGAGCCCCCT	ACTCCCCAGA	2520
	GTCAAAAGGA	AATGTAAAAA	CTTAGAGCTC	CCATTGTAAAT	GTAAAGGGCA	AGAAATTTGT	2580
	GTCTCTCTGA	ATGCTACTAG	CAGCACCAGC	CTTGTTTTAA	ATGTTTCTCT	GAGCTAGAAG	2640
40	AAATGAGCTA	TATTTGTATA	TGCAAAATAC	ATGCATTTTT	AAAAACTAAT	CTTTCTGAAC	2700
	TTATCTACCT	GGTTATGATA	CTGTGGGTCC	ATACACAAGT	AAATAAGAT	TAGACAGAAG	2760
	CCAGTATACA	TTTTGCACTA	TTGATGTGAT	ACTGTAGCCA	GCCAGGACCT	TACTGATCTC	2820
	AGCATATATA	TGCTTACTAA	TAAATGAAGTC	TGCTAGTGA	CACCTCATCA	GACTGAAGAT	2880
	GAAGCAGGTT	ACGTGCTCCA	TTGGAAGGAG	TTTCTGATAG	TCTCTGCTGT	TTTTACCCCT	2940
45	TCCATTTTTT	TAAATAAGAA	ATTAGCAGCC	CTCTGCATAA	TGTAGCTGCC	TATATGCAGT	3000
	TTTATCTCTG	GCCCTAAAGC	CTCACTGTCC	AGAGCTGTTC	GTCTATCAGAT	GCTTATGCA	3060
	CCCTCACCAT	GTGCTCTGGT	CCCTGCTGGG	TAGAGAACAC	AGAGGACAGG	GCATACTTCT	3120
	TGCTCTTAAG	GAGCTTTGTA	TCTGTGACAG	TAAAGCCCTCC	TGGGATGTCT	GTGCCATGTC	3180
	ATTGACTTAC	AAGTGAAACT	GTCTTATAAT	ATGAAGGTCT	TTTTGTTTAC	TTCTAAACCC	3240
50	ACTTGGGTAG	TTACTATCCC	CAAACTGTTC	CTGTAAATAA	TATTAAGGAA	GGGTTTCTAT	3300
	GTCACTCTAC	CTTCAAGAAA	GCCAGTGATT	CAATATCACA	AAAGGCATTG	ACGTATCTTT	3360
	GAAATGTTCA	CAGCAGCCTT	TTAAACAACA	CTGGGTGGTC	CTTGTAGGCA	GAACATACTC	3420
	TCCTAAGTGG	TGTAGGAAA	TTGCAAGGAA	AATAGAAGGT	CTGTTCTTGC	TCTCAAGGAG	3480
	GTTACCTTTA	ATAAAGAAG	ACAAACCCAG	ATAGATATGT	AAACCAAAAT	ACTATGCCCC	3540
55	TTAATACTTT	ATAAGCAGCA	TTGTTAAATA	GTCTTACG	TTATACATTC	ACAGAACTAC	3600
	CCTGTTTTCC	TGTATATATA	TGACTTTTGC	TGGCAGAACT	GAAATATAAA	CTGTAAAGGG	3660
	ATTTCGTCTG	TGCTCCAG	TATACAATAT	CCTCCAGGAC	ATAGCCAGAA	ATCTCCATTC	3720
	CACACATGAC	TGACTTCTCA	TCCCTGCCT	GGTACTGGCT	CTTTCTCTCT	CTTTCTTTGC	3780
	CTCAGGGTTC	GTGCTACCCA	CTGATTCCTT	TTACCTTTAG	TAATAATTTT	GGATCATTTT	3840
60	CTTTCCTTTA	AAGGGGAACA	AAGCCTTTTT	TTTTTTTGAG	ACGGAGTGT	GCTCTGTAC	3900
	CCAAGCTGGA	GTGCAAGTGG	ACGATCTTGG	CTCACTCCAA	CCTCCACCTT	CCAGGTTCAA	3960
	GTGATTTCTC	TGCCCTCAGC	TCCCGAGTAG	CTGGGACTAC	GGGCACGCAC	CACCACGCTC	4020
	GGCTAATTTT	TGTATTTTTA	GTAGAGATGG	GGTTTCAACC	TATTTGGTCAG	GCTGGTCTTG	4080
	AATTTCTCAC	CTCAGGTCAAT	CCGCTGTCT	CGGCTCCCG	AAGTGTGGG	ATTATAGGTG	4140
65	TGAGCCACCG	CACCCAGTTG	GGAAACAAAG	CTTTTAAACA	CACGTAAGGG	CCCTCAAAAC	4200
	GTGGGACCTC	TAAGGAGACC	TTTGAAGCTT	TTTGAGGGCA	AACTTTACCT	TTGTGTTCC	4260
	CAAAATGATG	CATTTCTCTT	TGAAATTTAT	TAGATACTGT	TATGTCCCCC	AAGGGTACAG	4320
	GAGGGGCATC	CCTCAGCCTA	TGGGAACACC	CAAACTAGGA	GGGGTTAATG	ACAGGAAGGA	4380
	ATGAATCCAA	TGGAAGGCTT	TCTGCTCTTC	GTGTTACAAA	CCAGTTTCAG	AGTTAGCTTT	4440
70	CTGGGGAGGT	GTGTGTTTGT	GAAAGGAATT	CAAGTGTGTC	AGGACAGATG	AGCTCAAGGT	4500
	AAGGTAGCTT	TGGCAGCAGG	GCTGATACTA	TGAGGCTGAA	ACAATCCCTG	TGATGAAGTA	4560
	GATCTGTGAG	TGACATACAA	AGACCAAGGA	TTATGTATAT	TTTTATATCT	CTGTGTTTTC	4620
	GAAACTTTAG	TACTTGAAT	TTTGCCCTTC	TGCACTACTC	TTTTGCTCTT	ACGAACATAA	4680
	TGGACTCTTA	AGAAATGAAA	GGGATGACAT	TTACCTATGT	GTGCTGCCTC	ATTCCTGGTG	4740
75	AAGCAACTGC	TACTTGTCTT	CTATGCCTCT	AAATGATGTC	TGTTTCTCTT	GCTAAAGGTA	4800
	AAAGAAAAGA	AAAAATAGT	TGGAAAATTA	GACATGCAAC	TTGATGTGCT	TTTGAGTAAA	4860
	TTTATGTCAG	AGAAACTATA	CAATGAAGGA	AGAATTTCTAT	GGAAATTACA	AATCCAAAC	4920
	TCTATGATGA	TGTCTTCTTA	GGGAGTAGAG	AAAGGCAGTG	AAATGGCAGT	TAGACCAACA	4980
	GAGGCTTGAA	GGATTCAAGT	ACAAGTAATA	TTTTGTATAA	AACATAGCAG	TTTAGTCCCC	5040
80	CATAATCTCT	AAAAATAGTC	ACAAATATAA	CAAAGTTCAT	TGTTTTAGGG	TTTTTAAAAA	5100
	ACGTGTTGTA	CCTAAGGCCA	TACTTACTCT	TCTATGCTAT	CAGTCAAGG	GGGTGATATG	5160

5 TATGTATTAT ATAAAAA AAACCCTTAA TGCACGTGTA TCTCCTAAAT ATTTAGTAAA 5220
 TTAATACATAT TTAATTTTTT TAAAGATTG TCTGTGTAGA CACTAAAAGT ATTACACAAA 5280
 ATCTGGACTG AAGGTGTCCT TTTTAAACA AATTAAAGT ACTTTTATA TATGTTATGT 5340
 AGTATATCCT TTCTAAACTG CCTAGTTTGT ATATTCCTAT AATTCCTATT TGTGAAGTGT 5400
 ACCTGTTCTT GTCTCTTTTT TCAGTCATTT TCTGCACGCA TCCCCCTTTA TATGTTATA 5460
 GAGATGACTG TAGCTTTTTCG TGCTCCACTG CGAGGTTTGT GCTCAGAGCC GCTGCACCCC 5520
 AGCGAGGCTT GCTCCATGGA GTGCAGGACG AGCTACTGCT TTTGAGCGAG GGTTCCTGTC 5580
 TTTTGAGTTG ACCTGACTTC CTTCTTGAAA TGAAGTTTAA AACTAAATA AATTACATTG 5640
 CATTATTTTT ATATTCCTGG TTGAAATAAA ATTTAATTGA CTTTG

SEQ ID NO:76 PDQ3 Protein sequence:

Protein Accession #: BAA82980

15 1 11 21 31 41 51
 VKSLLYQILD GIHYLHANWV LHRDLKPANI LVMGEGPERG RVKIADMGFA RLFNSPLKPL 60
 ADLDFVVVTF WYRAPELLLG ARHYTKAIDI WAIGCIFAEI LTSEPIFHCR QEDIKTENPF 120
 HHDQLDRIF VMGFPAKDW EDIRKMEYFP TLQKDFRRIT YANSSSLIKY EKHKVKPDSK 180
 20 VFLLQLKLLT MDPTKRITSE QALQDPYFQE DPLPTLDVFA GCQIPYFKRE FLNEDDPBEK 240
 GDKNQQQQON QHQQPTAFPO QAAAPFPAPP PQONSTQING TAGGAGAGVG GTGAGLQHSQ 300
 DSSLNQVPPN KKPRLGPSGA NSGGPVMPSD YQHSRRLNY QSSVQSSQS QSTLGYSSSS 360
 QQSSQYHPSH QAHRV

SEQ ID NO:79 PDQ5 DNA SEQUENCE

Nucleic Acid Accession #: XM_002922

Coding sequence: 1-2190 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTACACCTGT CTCCATTGAA 60
 GAGGTACCAC CTGACCCACC TAGCCCTCCA AAGAGCCAT CTCCGACAAAT CTGTGGCTCC 120
 AACTATCCAC TGAGCATTTGC CTTCAATGTG TGGAATGAAT TCTGCGAGCG CTTTTCCTAT 180
 TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTGATT TCCTGCACCTG GAATGAAGAT 240
 35 ACCTCCACAT CTATATACCA TGCCTTCAGC AGCCTCTGTT ATTTTACTCC CATCCTGGGA 300
 GCAGCCATG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCTTGGTG 360
 TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCTTAC CAATACTGGG AGGACAAAGT 420
 GTACACACAG TCCATATCAT GATCGGCTG AGTCTAATAG CTTTGGGGAC AGGAGGCATC 480
 AAACCTCTGT TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAACATGCG AGAGGAACGG 540
 40 ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATT 600
 ATCACACCCA TGGTGAAGAG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCATTGGCT 660
 TTTGAGATTC CAGGACTGCT CATGGTAATT GCACCTTGTG TGTTTGCAAT GGGAGCAAA 720
 ATATACATAA AACCAACCCC TGAAGGAAAC ATAGTGGCTC AAGTTTTCAA ATGTATCTGG 780
 TTTGCTATTT CCAATCGTCT CAAGAACCGT TCTGGAGACA TTCCAAAGCG ACAGCACTGG 840
 45 CTAGACTGGG CAGCTGAGAA ATATCCAAAG CAGCTCATTA TGGATGTAAA GGCCTGACC 900
 AGGGTACTAT TCCTTTATAT CCCATTGCCC ATGTTCTGGG CTCTTTTGGG TCAGCAGGCT 960
 TCACGATGGA CTTTGCAGCG CATCAGGATG AATAGGAATT TGGGGTTTTT TGTGCTTAC 1020
 CCGGACCAGA TGCAGGTTCT AAATCCCTTT TGTGTTCTTA TCTTCATCCC GTTGTGAGC 1080
 TTTGTCTATT ATCGTCTGGT CTCCAAGTGT GGAATTAAC TCTCATCACT TAGGAAAATG 1140
 GCTGTGTGTA TGAATCTAGC GTGCTGGCA TTTGCAGTTG CGGCAGCTGT AGAGATAAAA 1200
 50 ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCTTACA AGTCTTGAAT 1260
 CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAATG AAAACAATTC TCTGTGTATA 1320
 GAGTCCATCA AATCCCTTCA GAAACACCA CACTATTTCCA AACTGCACCT GAAACAAAA 1380
 AGCCAGGATT TTCACTTCCA CCTGAAATAT CACATTTTGT CTCTCTACAC TGAGCATTC 1440
 GTGCAAGGAG AGAATCTGTA CAGTCTGTTC ATTCGTGAAG ATGGGAACAG TATCTCCAG 1500
 55 ATGATGTTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGT 1560
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CATGTTGGT 1620
 GAAGACTATG GTGTGCTGCT TTATAGAACT GTGCAAGAG GAGAATACCC TGCAGTGCAC 1680
 TGTAGAACAG AAGATAAGAA CTTTCTCTG AATTGGGTC TTCTAGACTT TGGTGCAGCA 1740
 TATCTGTTTG TTATTAATAA TAAACCAAT CAGGCTCTTC AGGCTTGAA GATTGAAGAC 1800
 60 ATTCCAGCCA ACAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
 GGGGAGGTCA TGTCTCTGCT CACAGGTCTT GAGTTTCTTT ATTCTCAGGC TCCCTCTAGC 1920
 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCTGT 1980
 CTGTGTTGGG CACAGTTCAG TGGCTGGTA CAGTGGGCGG AATTCATTTT GTTTTCTGTC 2040
 65 CTCTGCTGCG TGAATCTGCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100
 ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC 2160
 AAACCTAGTA CCAAGAAGAC AAAACTCTGA

SEQ ID NO:80 PDQ5 Protein sequence:

Protein Accession #: XP_002922

70 1 11 21 31 41 51
 MNFFQKNESE ETLFSFVSIE EVPRPSPFP KKPSPTICGS NYPLSIATFV VNEFCERFSY 60
 YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPILG AAIADSWLKG FKTIILYLSLV 120
 75 YVLGHVIKSL GALPITGGQV VHTVLSLIGL SLIALGTGGI KPCVAAGFGD QPEEKHAER 180
 TRYFSVFYLS INAGCSLSTF ITPMLRGDVQ CFGECDYALA FGVPGLLMVI ALVVFAMGSK 240
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIKFRQHW LDWAAEKYFK QLIMDVKALT 300
 RVLFLYIPLP MFALLDQQG SRWPLQAIM NRNLGFFVLQ PDQMQLNPF LVLIFLPLFD 360
 80 FVIYRLVSKC GINFSLRKM AVGMILACLA FAVAAAEIK INEMAPAQSG PQEVFLQVLN 420
 LADDEVKVTV VGNENNSLIL ESISFKFKTP HYSKHLKTK SQDFHFHLKY HNLSLYTEHS 480

VQERNWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSNLVNG 540
 EDYGVSAVRT VORGEYPAPH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
 IPANKMSIAW QLPQVALVTA GEVMPFSVTGL EFSYSQAPSS MKSVLQAAWL LTIAVGNIIIV 660
 LVVAQFSGLV QWAEFILEFSC LLLVICLIFFS IMGYYYVPVK TEDMRGPADK HIPHIQGNMI 720
 KLETRKTKL

SEQ ID NO:81 PD06 DNA SEQUENCE

Nucleic Acid Accession #: NM_020448

Coding sequence: 1-1221 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGGACGGAT CCCACAGCGC AGCCCTGAAG CTGCAGCAGC TGCCTCCCAC AAGTAGCTCC 60
 AGCGCCGTAA GCGAGGCCTC CTTCCTCTAC AAGGAAAACC TGATTGGCGC CCTCTTGGCG 120
 ATCTTCGGGC ACCTCGTGGT CAGCATTGCA CTTAACCTCC AGAAGTACTG CCACATCCGC 180
 CTGGCAGGCT CCAAGGATCC CCGGGCCTAT TTCAAGACCA AGACATGGTG GCTGGGCGCT 240
 TTCTGTATGC TTCTGGGCGA GCTGGGTGTG TTGCGCTCCT ACGCCTTCGC GCCCGTGTCA 300
 CTCATCTGTC CCCTCAGCGC AGTTTCTGTG ATAGCTAGTG CCATCATAGG AATCATATTC 360
 ATCAAGGAAA AGTGGAAACC GAAAGACTTT CTGAGGCGCT ACGTCTTGTG CTTTGTGGCG 420
 TGCCTTTTGG CTGTCTGTGG TACCTACCTG CTGGTGACAT TCCGACCCAA CAGTCACGAG 480
 AAGATGACAG GCGAGAATGT CACCAGGCAC CTGCTGAGCT GGCCTTTCCT TTTGTACATG 540
 CTGCTGAGAG TCATCTCTGT CTGCTGTCTG CTCTACTTCT ACAAGGAGAA GAACGCCAAC 600
 AACATTTCTG TGATCTCTCT CTGTGTGGCG TTACTTGGCT CCATGACAGT GGTGACAGTC 660
 AAGGCCCTGG CTGGGATGCT TGTCTTGTCC ATTCAAGGGA ACCTGCAGCT TGACTACCCC 720
 ATCTCTACAG TGATGTTCGT GTGCATGGTG GCAACCGCCG TCTATCAGGC TGCCTTTTTC 780
 AGTCAAGCCT CACAGATGTA CGACTCCTCT TTGATTGCCA GTGTGGGCTA CATCTGTGCC 840
 ACAACCATGT CTATCACAGC AGGTGCAATA TTTTACCTGG ACTTCATCGG GGAGGACGTG 900
 CTGCACATCT GCAATGTTTC ACTGGGTGTC CTCAATTGCAT TCTTGGCGCT CTTCTTAATC 960
 ACGCGTAACA GGAAGAAGCC CATTCCATTT GAGCCCTATA TTTCCATGGA TGCCATGCCA 1020
 GGTATGCAGA ACATGCAACG TAAAGGGATG ACTGTCCAGC CTGAACCTAA AGCTTCTTTT 1080
 TCCTATGGGG CTCGTGAAAA CAATGACAAC ATTCTTGAGA TCTACGCTCC TGCCACCCCTG 1140
 CCAGTCATGC AAGAAGAGCA CGGCTCCAGA AGTGCTCTCT GGGTCCCTTA CCGAGTCTTA 1200
 GAGCACACCA AGAAGGAATG A

SEQ ID NO:82 PD06 Protein sequence

Protein Accession #: NP_065181

1 11 21 31 41 51
 | | | | |
 MDGSHSAALK LQQLPPTSSS SAVSEASFYS KENLIGALLA IFGHLVVSIA LNLQKYCHIR 60
 LAGSKDPRAY FKTKTWLGL FLMLLGELGV FASYAFAPLS LIVPLSAVSV IASAIIGIIF 120
 IKEKWKPKDF LRRYVLSFVG CGLAVVGTYL LVTFAFNSHE KMTGENVTRH LVSWFFLLYM 180
 LVEIILFCLL LYFYKEKNAN NIVVILLLLVA LLGSMTVVTV KAVAGMLVLS IQGNLQLDYP 240
 IFYVMFVCMV ATAVYQAFL SQASQMYDSS LIASVGYILS TTIATAGAI FYLDFIGEDV 300
 LHICMFALGC LIAFLGVFLI TRNRKKPIPF EPYISMDAMP GMQNMHDKGM TVQPELKASF 360
 SYGALENNDN ISEIYAPATL PVMQEHEGSR SASGVYPYRVL EHTKKE

SEQ ID NO:83 PD08 DNA SEQUENCE

Nucleic Acid Accession #: NM_032712

Coding sequence: 555-908 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CACTCATTAA GAACAGAGGA GGCTGCCTGT TACTCTTGGT GTTGCACTCCC TCCAGACACT 60
 CTGCTGTTTC CTGCTTAGGC GTGGCTGCAG CCATGGCTAG GAAAGCGCTG CCACCCACCC 120
 ACCTGGGCCA GAGCTGGTTC TGCTCTGCTG GCAGGGACAC TGAGCTGGCT ATCTCGGCGC 180
 TTCTGGCAAG AACTGCAACA GGCTCTCCTG GGTCTGTCAG GTGTACAGCC GGGCCCTGTC 240
 CTGTGCTCCT AGCTCTCGAG AGCTGCTGCT GCCGGGTGAC CTGATCCAAC CTGATAAGGT 300
 GCCATCTTCA GCTACCACTG CAAGGCCCTG AGGGCAACAG CAGCAGGGCA CTGCCCACCC 360
 GGCTGCTGAT GGCCTGTGTC CAGCTGGGAG TCCTCCCGCG ACTTCGAGGC CACTGAGCCA 420
 CCCTCCAGC CCCAGCCAC CATGGACAGG GGTATCCAGC TTCTCTCTCA ACCTCGTCTT 480
 CTGCCCTTGA GCCAGTGACG CCAAGGACA TGCTGTCTAC CAGGTCTCTG TACCAGCACT 540
 AGCTGGTCAA GGGCATGACA GTGCTGGAGG CCGTCTTGGA GATCCAGGCC ATCACTGGCA 600
 GCAGGCTGCT CTCATGGTGT CCAGGGCCCG CCAGGCCACC AGGCTCATGC TGGGACCCAA 660
 CCCAGTGCAC AAGGACTTGG CTGCTGAGCC ACACACCCAG GAGAAGGTGG ATAAGTGGGC 720
 TACCAAGGGC TTCTGTGAGG CTAGGGGAGG AGCCACCCCG CTTCTCTCTAT TGTGACCAGG 780
 CCTATGGGGA GGAGCTGTCC ATACGCCACC GTGAGACCTG GGCCTGGCTC TCAAGGACAG 840
 ACACCGCTTG GCCTGTGTCT CCAGGGGTGA AGCAGGCCAG AATCCTGGGG GAGCTGTCTC 900
 TGGTTTGGAG TGCATTGAGG AAGTGCAGGA CATGGTAGGG GAGGCAAAAA GCCTTGGGCA 960
 CTACCTCTCC TGTGGAGCTG TTGGGTGTCC GTGAGCTAG CCACACCCCT ACACCATGTT 1020
 CAAGGGTACC GGAAGAGAAG GGTGCTGTCC CCCAACCTCT CCTGTGGGTG TCACTGGCCA 1080
 GATCTCATGA GGAAGAGCAG CCTTGTGAGT GGACACTGAC CATGAGTCCC TGGGGGGAGT 1140
 GATCCCGCAG GCATCTGTGT CCATGTTGCA CTCTTGCCCA GGCAGCAGGG TGGGTGGGTA 1200
 CCATGGGTGC CCACCCCTCC ACCACATGGG GCCCAAGAG ACTGCAGGCC AAGCAGGGCA 1260
 ACCCCACACC CTTGACATTA AAGCATCTTG AAGCTTTTAA AAAAAAAAAA AAAAAA

SEQ ID NO:84 PD08 Protein sequence

Protein Accession #: NP_116101

1 11 21 31 41 51

MTVLEAVLEI QAITGSRLLS MYPGPAPPPG SCWDPQTQCTR TWLLSHTPRR RWISGLPRAS 60
CRLGEEPPPL PYCDQAYGEE LSIRHRETWA WLSRTDTAWP GAPGVKQARI LGLELLLV

5

SEQ ID NO:85 PDT1 DNA SEQUENCE

Nucleic Acid Accession #: NM_000693

Coding sequence: 53-1591 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
AGCCGGTTCG CCGCAGACTA GGGCGCCTCG GGCCAGGGAG CGCGGAGGAG CCATGGCCAC 60
CGCTAACGGG GCGCTGGAAA ACGGCGAGCC GGACGGGAAG CCGCCGGCCC TGCCGCGCCC 120
CATCCGCAAC CTGGAGGTCA AGTTCACCAA GATATTTATC AACAAATGAAT GGCACGAATC 180
CAAGAGTGGG AAAAAGTTTG CTACATGTAA CCCTTCAACT CGGGAGCAAA TATGTGAAGT 240
GGAAGAAGGA GATAAGCCCG ACGTGGACAA GGCTGTGGAG GCTGCACAGG TTGCCTTCCA 300
GAGGGGCTCG CCATGGCGCC GGCTGGATGC CCTGAGTCGT GGGCGGCTGC TGCACCAAGT 360
GGCTGACCTG GTGGAGAGGG ACCGCGCCAC CTTGGCCGCC CTGGAGACGA TGGATACAGG 420
GAAGCCATTT CTTCATCGTT TTTTCATCGA CCTGGAGGGC TGTATTAGAA CCCTCAGATA 480
CTTTGCAGGG TGGCGAGACA AAATCCAGGG CAAGACCATC CCCACAGATG ACAACGTCGT 540
ATGCTTCACC AGGCATGAGC CCATTTGGTGT CTGTGGGGCC ATCACTCCATG GGAACCTCCC 600
CCTGCTGATG CTGGGTGTGA AGCTGGCACC CGCCCTCTGC TGTGGGAACA CCATGGTCCT 660
GAAGCCTCGG GAGCAGACAC CTCTCACC GCCTTATCTC GGCTCTCTGA TCAAAGAGGC 720
CGGGTTCCCT CCAGGAGTGG TGAACATTTG GCCAGGATTC GGGCCACAG TGGGAGCAGC 780
AATTTCTTCT CACCCCTCAGA TCAACAAGAT CGCCTTCACC GGCTCCACAG AGGTTGGAAA 840
ACTGGTTAAA GAAGCTGCGT CCGGAGACAA TCTGAAGCGG GTGACGCTGG AGCTGGGGGG 900
GAAGAACCCC TGCACTCGTG GTGCGGACGC TGACTTGGAC TTGGCAGTGG AGTGTGCCCA 960
TCAGGGAGTG TTCTTCAACC AAGGCCAGTG TTGCACGGCA GCCTCCAGGG TGTTCGTGGA 1020
GGAGCAGGTG TACTCTGAGT TTGTCAAGCG GAGCGTGGAG TATGCCAAGA AACGCCCGT 1080
GGGAGACCCC TTCCGATGCA AACACAGAACA GGGCCCTCAG ATTGATCAAA AGCAGTTCTGA 1140
30 CAAATCTTA GAGCTGATCG AGAGTGGGAA GAAGGAAGGG GCCRAGCTGG AATGCGGGGG 1200
CTCAGCCATG GAAGACAAGG GGCTCTTCAT CAARCCCACT GTCTTCTCAG AAGTCACAGA 1260
CAACATGCGG ATTGCCAAG AGGAGATTTT CGGCCAGTG CAACCAATAC TGAAGTTCAA 1320
AAGTATCGAA GAAGTGATAA AAAGAGCGAA TAGCACCGAC TATGGATCTA CAGCAGCCGT 1380
GTTCAACAAA AATCTCGACA AAGCCCTGAA GTTGGCTTCT GCCTTAGAGT CTGGAACGGT 1440
35 CTGGATCAAC TGCTACAACG CCCTCTATGC ACAGGCTCCA TTTGGTGGCT TTAATATGTC 1500
AGGAAATGGC AGAGAACTAG GTGAATACGC TTTGGCCGAA TACACAGAAG TGAATCTGT 1560
CACCATCAAA CTGGCGGACA AGAACCCTCG AAGGAAGGC GGGGCTCCTT CCTCAACATC 1620
CGGACGCGGG AATGTGGCAG ATGAAATGTG CTGGAGGAAA AAAATGACAT TTCTGACCTT 1680
CCCAGGACAC ATTCTTCTGG AGGCTTTACA TCTACTGGAG TTGAATGATG GCTGTTTCC 1740
40 TCTCACTCTC CTGTTTATTC ACCAGACTGG GGATGCCAT AGGTGTGCTG TGAATCGCA 1800
GTCCTGCTCG GGGAGGGAGC TGTTGGCCAT TTCTGTGTTT CCCTTTAAAC CAGATCCTGG 1860
AGACAGTGGG ATACTCAGGG CGTTGTAAAC AGGGAGTGGT ATTTGAAGTG TCCAGCAGTT 1920
GCTTGAATG CTTGCCGAAA TCTGACTCCA GTAAGAATGT GGGRAAACCC CCTGTGTGTT 1980
45 CTGCAAGCAG GGCTCTTGCA CCAGCGGTCT CCTCAGGCTG GACCTGCTTA CAGAGCAAGC 2040
CACGCCCTCT TCCGAGGTGA AGGTGGGACC ATTCCTTTGG AAAGGATPCA CAGTAAGGTT 2100
TTTGGTPTT TGTTTTTTGT TTCTTGTGTT TTAATAAAG GATTTCACAG TGAGAAAGTT 2160
TTGTTAGTG CATACCGTGG AAGGGCGCCA GGGTCTTTGT GSATTGCTATG TTGACATTGA 2220
CCGTGAGATT CGGCTTCAAA CCAATACTGC CTTTGAATA TGACAGAATC AATAGCCCAG 2280
AGAGCTTAGT CAAAGACGAT ATCAGGCTCT ACCTTAACCA AGGCACCTTC TTAAGCAGAA 2340
50 AATATTTGTG AGGTTCACCT TGCTGCTAAA GATCCAATCT TCTAACGCCA CAACAGCATA 2400
GCAATCTCTA GGATAATCA CCTCTCAAT TGACAAATCA GAGCTGTAAT TCACTTTAAC 2460
AAATTAACCA TTTCTATCAC GTTCACTAAC AGCTTATGAT AAGTCTGTGT AGTCTTCTCT 2520
TTCTCCAGTT CTGTTACCCA ATTTAGATTA GTAAAGCGTA CACAACCTGA AAGACTGCTG 2580
TAATAACACA GCCTTGTGAT TTTTAAGTCC TATTTTGATA TTAATTTCTG ATTAGTTAGT 2640
55 AAATAACACC TGGATTCTAT GGAGGACCTC GGCTCTCAAT CAAGTGGCCT GAGTATTTCA 2700
CTGGCAGGTT GTGAATTTT CTTTCTCTCT TTGGGAATCC AAATGATGAT GTGCAATTTT 2760
ATGTTTAAAC TTGGGAAACT GAAAGTGTTC CCATATAGCT TCAAAAAACA AAACAAATGT 2820
GTTATCCGAG GGATACCTTT ATGGTTACTA ACTAGTACTT TCCTAATTTG GAAAGTAGTG 2880
CTTAAGTTTG CAAATTAAGT TGGGAGGGGC AATAATAAAA TGAGGGCCCG TAACGAGAAC 2940
60 AGTGTGTGTA TAACGAAAC CATGTATAAA ATGGGCTAT CACCCTTGTC AGAGATATAA 3000
ATTACCACAT TTGGCTTCCC TTCATCAGCT AACACTTATC ACTTATACTA CCAATAACTT 3060
GTTAAATCAG GATTTGGCTT CATACACTGA ATTTTCAGTA TTTTATCTCA AGTAGATATA 3120
GACACTAACC TTGATAGTGA TACGTTAGAG GGTTCCTAT CTTCCTATGT ACGATAATGT 3180
CTTTAATATG AAATGCTACA TTATTATATA TTGGTAGAGT TATTGTATCT TTTTATAGTT 3240
65 GTAAGTACAC AGAGGTGGTA TATTTAACT TCTGTAAAT ACTGTATTTA GAAATGGAAA 3300
TATATATAGT GTTAGGTTTC ACTTCTTTTA AGGTTTACCC CTGTGGTGTG GTTTAAAAAT 3360
CTATAGGCCT GGAATTTCCG ATCCTAGCTG CAGATCGCAT CCCCAATGCG GAGAAATGATA 3420
AAATAAAATT GGATATTGGA GA

70 SEQ ID NO:86 PDT1 PROTEIN SEQUENCE

Protein Accession #: NP_000684

75 1 11 21 31 41 51
MATANGAVEN GQPDGKFPAL PRPIRNLEVK FTKIFINNEW HESKSGKKFA TCNPFSTREQI 60
CEVEEGDKED VDKAVEAAQV AFQRGSPWRR LDALSRGRL HQLADLVERD RATLAALBTM 120
DTGKPFLLHAF FIDLEGCIRT LRYFAGWADK IQGKTIPTDD NVVCFTRHEP IGVCGLAITPW 180
NFPLMLLVVK LAPALCCGNT MVLKPAEQTP LTALYLGSLI KEAGFPFGVV NIVFGFGPTV 240
GAAISSHPQI NKIAFTGSTV VGKLVKEAAS RSNLKRVTLE LGKNKPCIVC ADADLDLAVE 300

CAHQGVFFNQ GQCCTAASRV FVEEQVYSEF VRRSVEYAKK RPYGDPFDVK TEQGPQIDQK 360
 QFDKILELIE SGRKEGAKLE CGGSAMEDKG LFIKPTVFSE VTDNMRIAKE BIFGPVQPIIL 420
 KFKSIEEVIK RANSTDYGLT AAVFTKNLDK ALKLASALEK GTVWINCYNA LYAQAFFGGF 480
 KMSGNGRELG EYALAERYTEV KTVPTIKLGDK NP

5

SEQ ID NO:87 PDV3 DNA SEQUENCE

Nucleic Acid Accession #: NM_032642

Coding sequence: 184-1263 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 | | | | | |
 GACCATTAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC 60
 TAGTTTGAAC CTAGGAACCTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG 120
 ACAGAGGGAA CCCTACTCTG GAAACTGTCA GTCCACGGGC ACTGGGGAGG GCTGAGGCCG 180
 15 ACCATGCCCA GCCTGCTGCT GCTGTTACAG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240
 CTGACAGAGC CCAACTCCTG GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300
 TTTATCATCG GTGCCACGCC CGTGTGCAGT CAGCTTCCCC GGCTCTCCCC TGGCCAGAGG 360
 AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420
 20 ATCAGGAAT GCCAGCACCA GTTCCGGCAG CGCGGTGGA ATTGCAGCAC AGCGGACAAAC 480
 GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACGG 540
 GTGAGCGCCG CGGGCTGCTG CAACGCCATC AGCCGGGCTT GCCCGAGGG CGAGCTCTCC 600
 ACCTGCGGCT GCAGCGGAGC GGCCTGGCCC AAGGACCTGC CCGGGGAGTG GCTGTGGGGC 660
 GGCTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG 720
 25 GAGCGAGAGA AGAACTTTGC CAAAGGATCA GAGGAGCAGG GCCGGGTGCT CATGAACCTG 780
 CAAAACAACG AGGCCGGTGC CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAAAATG 840
 CACGGCGTCT CGGGGTCTTG CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCTC 900
 AAGGTCGGGG ACCGGGTGAA GGAGAAGTAC GACAGCGCGG CCGCCATGCG CGTCACCCGC 960
 AAGGGCCGGC TGGAGCTGGT CAACAGCCGC TTCAACCCAGC CCACCCCGGA GGACCTGGTC 1020
 TATGTGACC CCAGCCCCGA CTACTGCCCTG CGCAACGAGA GCACGGGCTC CCGGGCAGC 1080
 30 CAGGGCCCGC TCTGCAACAA GACCTCGGAG GGCACTGGATG GCTGTGAGCT CATGTGCTGC 1140
 GGGCGTGGCT ACAACGAGTT CAAGAGCGTG CAGGTGGAGC CTGCCCAGTG CAAGTTCAC 1200
 TGGTGTCTGT TCGTCAGGTG TAAGAAGTGC ACGGAGATCG TGGACCAGTA CATCTGTAAA 1260
 TAGCCCGGAG GGCTGCTCTC CGGCCCCCCC TGCACCTTGC CTCACAAAGG TCTATATTAT 1320
 35 ATAAATCTAT ATAAATCTAT TTTATATTG TATAAGTAAA TGGGTGGGTG CTATACAATG 1380
 GAAAGATGAA AATGGAAAGG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG 1440
 GACTTTGCTG GTTCTCTCCT CTTGGTGGGT GGGAGACAGG GCTTTTCTC TCCCTCTGGC 1500
 GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCCTGGAG 1560
 GAGGGAGGTT GTGGTTGGAT GGAGGAGATG ATCTTGTCTG GAAGTCTAGA GTCTTTGTGT 1620
 40 GTTAGAGGAC TGCTCTGTAT CCTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680
 ACTCAGCTTC AACCTCGATG TCTTCAGGCT CTGTCCAGA ATGTAGATGG GTTCCGTAAG 1740
 AGGCCTGGTG CTCTCTTACT CTTTCATCCA CGTGCACTTG TCGGCATCTT GCAGTTTACA 1800
 GGAACGGCTC CTTCCTTAAA ATGAGAAGTC CAAGGTCATC TCTGGCCAG TGACCACAGA 1860
 GAGATCTGCA CTTCCCGGAC TTTAGGCGCT CTTTCCAGC GAGAATCTT CATCTCCAC 1920
 45 GGTTCACAT CTCTACCTG AAGAGGAAAG GGGGCCATT GACCTGACAT GTCAGGAAAG 1980
 CCCTAAACTG AATGTTTTCG CCTGGGCTGC AGAAGCCAGG GTGCATGACC AGGCTGCGTG 2040
 GAGGTTATAC TGTCTTCCCC CACCCCGGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100
 CTCACCGAG TGAAGGCTCA CAAACACAG GACGCTGCAA CGGGTCAGGC TGGCGGGCCC 2160
 GCGTGTCTCA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220
 50 TGGAAAAAAA AAAAAGAAAA AAAAAAAAAA AA

SEQ ID NO:88 PDV3 Protein sequence

Protein Accession #: NP_116031

55 1 11 21 31 41 51
 | | | | | |
 MPSELLLFTA ALLSSWAQLL TDANSWWSLA LNFVORPEMF IIGAOPVCSQ LPGLSPGQRK 60
 LCQLYQEHMA YIGEGAKTGI KECQHQRQR RWNCTADNA SVFGRVMQIG SRETAETHAV 120
 SAAGVVNAIS RACREGELST CGCSRTARPK DLFRDWLWGG CGDNVEYGYR FAKEFVDARE 180
 60 REKNFAKGSE EQGRVLMNLQ NNEAGRRVAV KMDAVACKCH GVSQSCSLKT CWLQLAEFRK 240
 VGDRLEKEKYD SAAAMRVTRK GRLELVNSRF TQFTPEDLVY VDESPDYCLR NESTGSLGTQ 300
 GRLCNKTSSE MDGCELMCCG RGYNQFKSVQ VERCHCKPHW CCFVRCKKCT EIVDQYICK-

SEQ ID NO:89 PDT9 DNA SEQUENCE

Nucleic Acid Accession #: NM_033280

Coding sequence: 58-636 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 | | | | | |
 GGCAGCGCTC TGTGCCACCC AGAGCCGGCG GGCCGCTAGG TCCCGGAGAG CCCTGCTATG 60
 GTGCGTGGCG GCGCCGTGGG GGCTCATCTC CCGCGCTCCG GCTTGGATAT CTTCCGGGAC 120
 CTGAAGAAGA TGAACAAGCG CCAGCTCTAT TACCAGGTTT TAAACTTCGC CATGATCGTG 180
 TCTTCTGCAC TCATGATATG GAAAGGCTTG ATCGTGCTCA CAGGCAGTGA GAGCCCATC 240
 75 GTGGTGGTGC TGAAGTGGCAG TATGGAGCCG GCCTTTCACA GAGGAGACCT CCGTTCCTC 300
 ACAAAATTCG GGAAGAGACC AATCAGAGCT GGTGAATATG TTGTTTTTAA AGTTGAAGGA 360
 CGAGACATTC CAATAGTTCA CAGAGTAATC AAAGTTCATG AAAAGATATA TGGAGACATC 420
 AAATTTCTGA CTAAAGGAGA TAATAATGAA GTTGATGATA GAGGCTTGTA CAAAGAAAGC 480
 CAGAAGTGGC TGAAGAAAGG GACGCTGGTG GGAAGAGCAA GAGGGTTTTT ACCATATGTT 540
 80 GGTATGGTCA CCATAATAAT GAATGACTAT CCAAAATFCA AGTATGCTCT TTTGGCTGTA 600
 ATGGGTGCAT ATGTGTTACT AAAACGTGAA TCCTAAATG AGAAGCAGTT CCGGGACCA 660
 GATTGAAGTG AATCTGTTTG AAAAAGAGAA AAATAATAT ATTTGAGATG TTCCATTTTC 720

TGTATAAAG GGAACAGTGT GGAGATGTTT TTGTCCTGTC CAAATAAAG ATTACCAGT 780
 AAAAAAAAAA AAAA

5 **SEQ ID NO:90 PDV9 Protein sequence**
 Protein Accession #: NP_150596

1 11 21 31 41 51
 | | | | |
 10 MVRAGAVGAH LPASGLDIFG DLKMMNKRQL YYQVLNFAMI VSSALMIWKG LIVLTGSESP 60
 IVVVLSGSME PAFHRGDLLE LTNFREDPIR AGEIVVFKVE GRDIPIVHRV IKVHEKDNGD 120
 IKFLTSGDNN EVDDRGLYKE GQNWLEKKDV VGRARGFLPY VGMVTIIMND YPKFKYALLA 180
 VMGAYVLLKR ES

15 **SEQ ID NO:91 PDV5 DNA SEQUENCE**
 Nucleic Acid Accession #: NM_016590
 Coding sequence: 691-975 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 20 GATTACTCAC ACAGTCTTGA AGATGCAATG TCAGCTATTT AGGACAGAAA CATCCAAGGC 60
 CGTGTACAGAA CTCAATTACG ACTACATATG CATTAAAGCA GGAAGTGGCA GGCCTCAGGG 120
 TACGCCAACT ATAGAGACTCG TGCTTCTCGT ACGCTGGGCT ATAATCTATG AAAGTGAAGT 180
 CCAGAGCCAG CCAATCACTT AGCTCCTCAT AACAAGTCTA ACTGGCTCTG GAAAGCTGAA 240
 AGGGCTGCAC TGAACACACA CAGATGAGAT ATTCTACACA TTAATCTACT TATCTGGAAT 300
 25 CACTTTGCCT CTAAAGGCCA GAGAAAAATC ACAGCTTCCT TGTCGGAGGG GAAAGGAGCA 360
 GGTGATCTGG GGAAGACGCA GCTACACCTG GAGCAAGGTC TCTTCCCGGC TTGGCAATCT 420
 CAGCTGTGCC GGCCTGACGG GACCCGAGCC GTCCCAGAAA CCAAGGGGCA GGCACGGCAG 480
 CAAACGCGCT AGTGTCTGCT CCTTCGGTGA CTATATGAGA ATGGAAACTT CTAAAGGAAGC 540
 CAGGTTGTTA GAATTGPTAC CCCCTTTACT CAGAGATAAC ATAGATTATC CAGGCTGAGA 600
 30 TGGAAACAA GGCCTTTATT GAATTTTCAA CACAGACTCC CTGCTTCTCA TCTCTTAAT 660
 AAAATTTCAT TAAATTCCTC TTGAATCTCC ATGTTTCAAT CTCCATTGTG TGACAGACAA 720
 AGCCAACAAT ACTCTAAACT GAGGCTTGCA AGTCATTTC TTTGTATTTT TGTCAGAGAA 780
 TTTCCCATAG GAAGACTTCA CCTCTACAAA CTCCGAAGAA AACCTTACT GTCCAAGACC 840
 GTCACCAACA ACCATCCGCA GTCATTCAAG TGAAGGCTTT CACAGCTTTT GTACATTCTC 900
 35 TGTGTCATA TACAACFGAG TTACAGACTG TCCCTTGGCT CCCTGACCTT TACAACACT 960
 AAAAGTTTGT TTTGACTCAA CTTCAGCTG CTCATCTGTT AGTAAGTGAT GTTCACTCCA 1020
 GAACACATTC ATGATGAGAA CTTCCTAATA GACCAAGCACT GCTCTTCCCT TCCTATAATC 1080
 ATAATAATCA TGATAACCTG AAACATGTTA CTGGGACTCG ACATTTTCTT GGGGATTGAA 1140
 ATCTTTAGTC CTTTGAGCTG TCACATAGCA GGGGCAACCT CACACTGAAA CAAAGGAAGT 1200
 40 GATGTCCCAT TATTATCCAC CCTGAGCCAC CATAATATGC TGTPTTACAT TATTTCCTC 1260
 AGCCTGTGCA AAACAAAGCA ATGGAAGAGG AAACATAAAA ATATACATAC TAGTACCATT 1320
 ATCTTCTTPT GCTTAAATTT ACTAATGCAC CACGTCAGTC TGCTTCTCTC AGGCATCATT 1380
 CTCATTTTCT CAGGACTTGT ATTAGCAGGT TCTGGCTAGA GAGACTATCT CCGTTCATCA 1440
 CGATCAATTA ATGTTTCTGT GTGATCACAT CAGGCCCTAT CTAAGAAGCT CATGGTATAC 1500
 45 AAGGGTCACC CAAATAGCTG AGTGAGTCC TTGCTCATAT TCTCTTCATC TTAACCCCGC 1560
 AAACAGAAAT TAAGATGATC CCAATAAAG AAAAATTTGCT CAGGAAACTG AACCTTTTTC 1620
 TGAACCAAGC ACTGTGAGCA AATCTCAGGT ATTAGAGCAA CTATGGTTGA TTGAAAAGTG 1680
 TCTCAAAATC TGGGCCAAGA ATGATTGCTA GGTCCATAAG CTAATTTGTC TGGCCTTGCC 1740
 ATTTACGTAA GCCAAGAGAA GTCACTCATG AGTAAACTAT AGAAAACGTT CAGACCCATC 1800
 50 CTGTTAGTAT GTCAAAATCAA CTAAGACTGG CAGGGTATTA ACTCCATTC AGGTGACATG 1860
 GATAAAGAGC CCCATTTATT TCACAGTGCC AGCCTCTACC TAAGGAAACC CTAGACCTTG 1920
 GAACCAAGTT CCTGTGAGG AACTGCTGAC AGTTTCAATG CTGACAGTTG GAGCCAATGC 1980
 CTCATAGTGT AAACGAGAG AAAAATAGTT GCTTTTAAAA ATGTACAGCA GAAGGCTGTC 2040
 55 CTCATCTTAA CAAAGCAAAA AAAAATGCTT TAATTCAAAT TAAAAATCAT GATACTAAAA 2100
 AAAAAAAA

SEQ ID NO:92 PDV5 Protein sequence
 Protein Accession #: NP_057674

60 1 11 21 31 41 51
 | | | | |
 MQCQLFRTE SKAVSELNYD YICIKAGTGR PQGTPTIGLV LLVRWAIHYE TELQSQFIT

65 **SEQ ID NO:93 PEE6 DNA SEQUENCE**
 Nucleic Acid Accession #: NM_002606
 Coding sequence: 61-1842 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 70 CGCGGCGGCT GCGCTCGGGA AAGTACAGTA AAAAGTCCGA GTGCAGCCGC CGGGCGCAGG 60
 ATGGGATCCG GCTCCTCCAG CTACCGGCC CAGGCCATCT ACCTGGACAT CGATGGACGC 120
 ATTCAGAAAG TAATCTTCAG CAAGTACTGC AACTCCAGCG ACATCATGGA CCGTCTCTG 180
 ATCGCCACCG GCGTCCCTCG GAACACGACC ATCTCCCTGC TGACCAACCGA CGACGCCATG 240
 75 GTCTCCATCG ACCCCACCAT GCCCGCGAAT TCAGAACGCA CTCGCTACAA AGTGAGACCT 300
 GTGGCCATCA AGCAACTCTC CGCTGGTGTG GAGGACAAGA GAACCAACA CCGTGGCCAG 360
 TCTGCTGAGA GACCACTGAG GGACAGACGG GTTGTGGGCC TGGAGCAGCC CCGGAGGGAA 420
 GGAGCATTTG AAAGTGGACA GGTAGAGCCC AGGCCAGAG AGCCCCAGGG CTGCTACCG 480
 GAAGGCCAGC GCATCCCTCC AGAGAGAGAA GAATTAATCC AGAGCGTGCT GGCGCAGGTT 540
 GCAGAGCAGT TCTCAAGAGC ATTCAAAATC AATGAACCTA AAGCTGAAGT TGCAAAATCA 600
 80 TTGGCTGTCC TAGAGAAACG CGTGAATATG GAAGGACTAA AAGTGGTGGG GATTGAGAAA 660

5
10
15
20
25

```

TGCAAGAGTG ACATTAAGAA GATGAGGGAG GAGCTGGCGG CCAGAAGCAG CAGGACCAAC 720
TGCCCCCTGTA AGTACAGTTT TTGGGATAAC CACAAGAAGT TGA CTCTCCG AC GCGATGTT 780
CCCACTTACC CCAAGTACCT GCTCTCTCCA GAGACCATCG AGGCCCTGCG GAAGCCGACC 840
TTTGACGTCT GGGTTTGGGA GCCCAATGAG ATGCTGAGCT GCCTGGAGCA CATGTACCAC 900
GACCTCGGGC TGGTCAGGGA CTTCAGCATC AACCTGTCA CCCTCAGGAG GTGGCTGTTC 960
TGTGTCCACG AACACTACAG AAACAACCCC TTCCACAAC TCCGGCACTG CTTCTGCGTG 1020
GCCAGATGTA TGTACAGCAT GGTCTGGCTC TGCAGCTCC AGGAGAAGTT CTCACAAACG 1080
GATATCCTGA TCCTAATGAC AGCGGCCATC TGCCACGATC TGGACCATCC CGGCTACAAC 1140
AACACGTACC AGATCAATGC CCGCACAGAG CTGGCGGTCC GCTACAATGA CATCTCACCG 1200
CTGGAGAAC ACCACTGCGC CGTGGCCTTC CAGATCCCTG CCGAGCCTGA GTGCAACATC 1260
TTCTCCAACA TCCCACTGA TGGGTTCAG CAGATCCGAC AGGGAATGAT CACATTAATC 1320
TTGGCCACTG ACATGGCAAG ACATGCGAAG ATTATGGATT CTTTCAAGA GAAATGGAG 1380
AATTTTGA CTACAGCAACG GGAGCACATG ACCCTGTGTA AGATGATTTT GATAAAATGC 1440
TGTGATATCT CTAACGAGGT CCGTCCAATG GAAGTCGCAG AGCCTTGGGT GGACTGTTTA 1500
TTAGAGGAAT ATTTTATGCA GAGCGACCGT GAGAAGTCAG AAGGCCTTCC TGTGGCACC 1560
TTTATGGACC GAGACAAAGT GACCAAGGCC ACAGCCAGA TTGGGTTCAT CAAGTTTGTC 1620
CTGATCCCAA TGTTTGAAC AGTGACCAAG CTCTTCCCA TGGTTGAGGA GATCATGCTG 1680
CAGCCACTTT GGAATCCCG AGATCGCTAC GAGGAGCTGA AGCGGATAGA TGACGCCATG 1740
AAAGAGTTAC AGAAGAGAGC TGACAGCTTG ACGTCTGGGG CCACCGAGAA GTCCAGAGAG 1800
AGAAGCAGAG ATGTGAAAAA CAGTGAAGGA GACTGTGCTT GAGGAAAGCG GGGGGCGTGG 1860
CTCAGTTCTT GGACGGGCTG GCCGAGCTGC GCGGGATCCT TGTGCAAGGA AGAGCTGCC 1920
TGGGCACCTG GCACCAAG ACCATGTTTT CTAAGAACCA TTTTGTTCAC TGATACAAA 1980
AAAAAAAAA A

```

SEQ ID NO:94 PEE6 Protein sequence
Protein Accession #: NP_002597

30
35
40

```

1 11 21 31 41 51
| | | | |
MGSSSSSRP KAIYLDIDGR IQKVIKSKYC NSSDIMDLFC IATGLPRNTT ISLLTTDDAM 60
VSIDTPMPAN SERTPYKVRP VAIKQLSAGV EDKRTTSRGQ SAERPLRRR VVGLEQPRRE 120
GAFESGQVEP RPREFQGCYQ EGQRIPPERE ELIQSVLAQV AEQFSRAFKI NELKAEVANH 180
LAVLEKRVBL EGLKVVEIEK CKSDIKMKRE ELAARSSRTN CPCKYSFLDN HKKLTERRDV 240
PTYPKYLLSP ETIEALRKPT FDVWLWEPNE MLSCLEHMYH DLGLVRDFSI NPVTLLRWLF 300
CVHDNYRNPN FHNFRHCFVQ AQMMYSMVWL CSLQEKFSQT DILILMTAAI CHLDLHFGYN 360
NTYQINARTE LAVRYNDISP LENHHCVAFA QILAEPECNI FSNIPDGFK QIRQGMITLI 420
LATDMARHAE IMDSFKKME NFDYSNEEHM TLLKMILIKC CDISNEVRPM EVAEPWVDCL 480
LBEYFMQSDR EKSEGLFPVAP FMDRDKVTKA TAQIGFIKIV LIPMFETVTK LFPMVBEIML 540
QPLWESDRDY EELKRIDDAM KELQKKTDSL TSGATEKSRE RSRDVKNSEG DCA

```

SEQ ID NO:95 PEG4 DNA SEQUENCE

Nucleic Acid Accession #: none
Coding sequence: 41-559 (underlined sequences correspond to start and stop codons)

45
50
55
60

```

1 11 21 31 41 51
| | | | |
CAGTCACAGG CGAGAGCCYT GGGATGCACC GGCCAGAGGC ATGCTGCTGC TGCTCACGCT 60
TGCCCTCTCTG GGGGGCCCA CCGTGGCAGG GAAGATGTAT GGCCCTGGAG GAGGCAAGTA 120
TTTCAGCACC ACTGAAGACT ACGACCATGA AATCACAGGG CTGCGGGTGT CTGTAGGTCT 180
TCTCCTGGTG AAAAGTGTCC AGGTGAAACT TGGAGACTCC TGGGACGTGA AACTGGGAGC 240
CTTAGGTGGG AATACCCAGG AAGTACCCTT GCAGCCAGGC GAATACATCA CAAAAGTCTT 300
TGTCGCCCTTC CAAGCTTTCC TCCGGGGTAT GGTCTATGAT ACCAGCAAGG ACCGCTATTT 360
CTATTTTGGG AAGCTTGATG GCCAGATCTC CTCTGCCCTAC CCCAGCCAAG AGGGGCAGGT 420
GCTGTGGGGG ATCTATGGCC AGTATCAACT CCTTGGCATC AAGAGCATTG GCTTTGAATG 480
GAATATATCCA CTAGAGGAGC CGACCACTGA GCCACCACTT AATCTACATC ACTCAGCAAA 540
CTCACCCGTG GGTGCGTAGG GTGGGGTATG GGGCCATCCG AGCTGAGGCC ATCTGTGTGG 600
TGATGGCTGA TGGTACTGGA GTAACTGAGT CGGGACGCTG AATCTGAATC CACCAATAAA 660
TAAAGCTCTT GCAGAATCAG TGAAAAAAA A

```

SEQ ID NO:96 PEG4 Protein sequence
Protein Accession #: FGENSEH predicted

65
70

```

1 11 21 31 41 51
| | | | |
MLLLLTALL GGPTWAGKMY GPGGKYFST TEDYDHEITG LRVSVGLLLV KSVQVKGDS 60
WDVKLGALGG NTQEVTLQPG EYITKVFVAF QAFLRGMVMY TSKDRYFYFG KLDGQISSAY 120
PSQEGQVLVG IYGYQLLGI KSIGFEWNYF LBPPTTEPFV NLITYANSFV GR

```

SEQ ID NO:97 PEL9 DNA SEQUENCE

Nucleic Acid Accession #: NM_006953
Coding sequence: 33-896 (underlined sequences correspond to start and stop codons)

75
80

```

1 11 21 31 41 51
| | | | |
CCGTTCGCGG CTCGGCGGCG TCCTCCCGGG CGATGCCTCC GCTCTGGGCC CTGCTGGCCC 60
TCGGCTGCCT CCGGCTTCGGC TCGGCTGTGA ACCTGCAGCC CCAACTGGCC AGTGTGACTT 120
TCGCCACCAA CAACCCACACA CTTACCACTG TGGCCTTGGG AAAGCCTCTC TGCATGTTTG 180
ACAGCAAGA GGCCTCTACT GGCACCCACG AGGTCTAOC TGTATGTCCTG GTCGACTCAG 240
CCATTTCCAG GAATGCCTCA GTGCAAGACA GCACCAACAC CCCACTGGGC TCAACGTTCC 300

```

TACAAACAGA GGGTGGGAGG ACAGGTCCCT ACAAAGCTGT GGCCTTTGAC CTGATCCCCT 360
 GCAGTGACCT GCCCAGCCTG GATGCCATTG GGGATGTGTC CAAGGCCTCA CAGATCCTGA 420
 ATGCCTACCT GGTGAGGGTG GGTGCCAACG GGACCTGCCT GTGGGATCCC AACTCCAGG 480
 GCCTCTGTAA CGCACCCCTG TCGGCAGCCA CGGAGTACAG GTTCAAGTAT GTCTGGTCA 540
 ATATGTCCAC GGGCTTGGA GAGGACCAGA CCCTGTGGTC GGACCCCATC CGCACCAACC 600
 AGCTCACCCC ATACTCGACG ATCGACACGT GGCCAGGCCG GCGGAGCGGA GGCATGATCG 660
 TCATCACTTC CATCTGGGCT TCCCTGCCCT TCTTTCTACT TGTGGGTMTT GCTGGCGCCA 720
 TTGCCCTCAG CCTCGTGGAC ATGGGGAGTT CTGATGGGGA AACGACTCAC GACTCCCAA 780
 TCACTCAGGA GGCTGTTCCT AAGTCGCTGG GGGCTTCGGA GTCTTCTTAC ACGTCCGTGA 840
 ACCGGGGGCC GCCACTGGAC AGGGCTGAGG TGTATTCAG CAAGCTCCAA GACTGAGGCC 900
 AGCACCACCC CTGGGCAGCA GCATCTCCTT CTCTGGCCTT GCCCAGGCC CTGCAGCGGT 960
 GGTGTGCACA CCTGACTTTC AGGGAAGGTG AAACAGGGCT TGTCCCTCCA ACTGCAGGAA 1020
 AACCCCTAAT AAAATCTTCT GATGAGTTC TAAAAA

SEQ ID NO:98 PEN9 Protein sequence
 Protein Accession #: NP_008884

1 11 21 31 41 51
 | | | | |
 MPPLWALLAL GCLRFGSAVN LQPQLASVTF ATNNPTLITV ALEKPLCMFD SKEALTGTHE 60
 VYLYLVDSIA ISRNASVQDS TNTPLGSTFL QTEGGRTGPY KAVAFDLIPC SDLESLDAIG 120
 DVSKASQILN AYLVVRVGANG TCLWDPNFQG LCNAPLSAAT EYRFKYVLVN MSTGLVEDQT 180
 LWSDPRTNTQ LTPYSTIDTW PRRSNGMIV ITSILGSLPF FLVGVFAGAI ALSLVDMGSS 240
 DGETTHDSQI TQEAVPKSLG ASESSYTSVN RGPPLDRAEV YSSKLQD

SEQ ID NO:99 PEN1 DNA SEQUENCE

Nucleic Acid Accession #: NM_012391
 Coding sequence: 416-1423 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GTCTGACTTC CTCCAGCAC ATTCTGCAC TCTGCCGTGT CCACACTGCC CCACAGACCC 60
 AGTCTCCCAA GCCTGCTGCC AGCTCCCTGC AAGCCCTTCA GGTGCGGCTT TGCACCGGTG 120
 CCAGCAGGCA GCCTGGGCT GGGGGTAGGG GACTCCCTAC AGGCACGCAG CCCTGAGACC 180
 TCAGAGGGCC ACCCTTGAG GGTGGCCAGG CCCCAGTGG CCAACTGAG TGTGCTCTCT 240
 GCCACAGCAG CTGCTGGCCC CTGGTTCCGC TGGCCCCCA GATGCTTGGC TGAGACACGC 300
 CAGTGGCCTC AGCTGCCCA ACCTCTTCCC GGCCCTGAA GTTGGCACTG CAGCAGACAG 360
 CTCCCTGGGC ACCAGGCAGC TAACAGACAC AGCCGCCAGC CCAACAGCA GCGGCATGGG 420
 CAGCGCCAGC CCGGCTCTGA GCAGCGTATC CCCCAGCCAC CTCTGCTGTC CCCCCGACAC 480
 GGTGTGCGCG ACAGGCTTGG AGAAGGCGGC AGCGGGGCA GTGGGTCTCG AGAGACGGGA 540
 CTGGAGTCCC AGTCCACCG CCACGCCCGA GCAGGGCCTG TCCGCTTCT ACCTCTCTTA 600
 CTTTGACATG CTGTACCCTG AGGACAGCAG CTGGGCAGCC AAGGCCCTG GGGCCAGCAG 660
 TCGGGAGGAG CCACCTGAGG AGCCTGAGCA GTGCCCCGTG ATTGACAGCC AAGCCCCAGC 720
 GGGCAGCCTG GACTTGGTGC CCGCGGGCTT GACCTTGGAG GAGCACTCGC TGGAGCAGGT 780
 GCAGTCCATG GTGGTGGGCG AAGTGTCAA GGACATCGAG ACGGCTGCA AGCTGTCTAA 840
 CATCACCGCA GATCCCATGG ACTGGAGCCC CAGCAATGTG CAGAAGTGGC TCCTGTGGAC 900
 AGAGCACCAA TACCGGTGTC CCCCATGGG CAAGGCTTC CAGGAGCTGG CGGGCAAGGA 960
 GCTGTGCGCC ATGTGCGAGG AGCAGTCCG CCAGCGCTCG CCCCTGGGTG GGGATGTGCT 1020
 GCACGCCACG CTGTACATCT GGAAGTCAGC GGCTTGGATG AAAGAGCGGA CTTCACCTGG 1080
 GGCAGTTCAC TACTGTGCTT GCACCATGTA GGAGAGCTGG ACCGACAGCG AGGTGGACTC 1140
 ATCATGCTCC GGGCAGCCCA TCCACCTGTG GCAGTTCCTC AAGGAGTTGC TACTCAAGCC 1200
 CCACAGCTAT GGGCGCTTCA TTAGGTGGCT CAACAAGGAG AAGGGCATCT TCAAAATTGA 1260
 GGACTACAGC CAGTGTGGCC GGCTGTGGGG CATCCGCAAG AACCCTCCCG CCATGAACCTA 1320
 CGACAAGCTG AGCCGCTCCA TCCGCCAGTA TTACAAGAG GGCATCATCC GGAAGCCAGA 1380
 CATCTCCAGC CGCTCGTCT ACCAGTTCGT GCACCCATC TGAGTGCCCT GCCCAGGGCC 1440
 TGAACCCCGC CCTCAGGGGC CTCTCTCTG CCTGCCCTGC CTCAGCCAGG CCTGTAGATG 1500
 GGGGAAACG GGCAGTCTGC TCTGCTGCTC TGACCTTCCA GAGCCCAAG TCAGGGAGGG 1560
 GCAACCAACT GCCCCAGGGG GATATGGGTC CTCTGGGGCC TTCGGGACCA TGGGGCAGGG 1620
 GTGCTTCTCT CTCAGGCCCA GCTGCTCCCC TGGAGGACAG AGGGAGACAG GGCTGTCTCC 1680
 CAACACCTGC CTCGACCCCT AGCATTTCCA GAGCAGAGCC TACAGAAGGG CAGTGAAGCT 1740
 ACAAAAGGCC CAGGCAGTCC AGGCCTCTCT CTGCTCCATC CCCCTGCCCT CCATTCTGCA 1800
 CCACACCTGG CATGGTGCAG GGAGACATCT GCACCCCTGA GTTGGGCAGC CAGGAGTGCC 1860
 CCCGGGAATG GATAATAAAG ATACTAGAGA ACTG

SEQ ID NO:100 PEN1 Protein sequence
 Protein Accession #: NP_036523

1 11 21 31 41 51
 | | | | |
 MGSASPLGSS VSPSHLLPP DIVSRTGLEK AAAGAVGLER RDWSPSPFPAT PEQQLSAFYL 60
 SYFDMLYPED SSWAAKAPGA SSREPFPEEP EQCPVIDSQA PAGSLDLVFG GLTLEHSLE 120
 VQQSMVVGEV LKDIETACKL LNITADPMDW SPSNVQKWLL WTEHQYRLFP MGKAFQELAG 180
 KELCAMSEEQ FRQRSPLGGD VLHAHLDIWK SAAMWKERTS PGAIHYCAST SEESWTDSEV 240
 DSSCSQPHH LWQFLKELL KHFSYGRFIR WLNKEKGIFK IEDSAQVARL WGIRKKNRPAM 300
 NYDKLSRSTR QYYXKGIIRK PDLSQRLVYQ FVHPI

SEQ ID NO:101 PEN3 DNA SEQUENCE

Nucleic Acid Accession #: NM_000742
 Coding sequence: 555-2144 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GAGAGAACAG CGTGAGCCTG TGTGCTTGTG TGCTGAGCCC TCATCCCCCTC CTGGGGCCAG 60
 GCTTGGGTTT CACCTGCAGA ATCGCTTGTG CTGGGCTGCC TGGGCTGTCC TCAGTGGCAC 120
 5 CTGCATGAAG CCGTTCCTGGC TGCCAGAGCT GGACAGCCCC AGGAAAACCC ACCTCTCTGC 180
 AGAGCTTGCC CAGCTGTCCC CGGGAAGCCA AATGCCTCTC ATGTAAGTCT TCTGCTCGAC 240
 GGGGTGTCTC TAAACCCCTC ACTCTTCAGC CTCTGTTTGA CCATGAAATG AAGTGACTGA 300
 GCTCTATTCT GTACCTGCCA CTCTATTCTT GGGGTGACTT TTGTGAGCTG CCCAGAATCT 360
 10 CCAAGCCAGG CTGGTTCTCT GCATCCTTTC AATGACCTGT TTTCTTCTGT AACCACAGGT 420
 TCGGTGGTGA GAGGAAGCCT CGCAGAAATC AGCAGAAATC TCACAGAAATC CAGCAGCAGC 480
 TCTGCTGGGG ACATGGTCCA TGGTGCAACC CACAGCAAAG CCCTGACCTG ACCTCCTGAT 540
 GCTCAGGAGA AGCCATGGGC CCCTCCTGTC CTGTGTTCTT GTCTTCCACA AAGCTCAGCC 600
 TGTGGTGGCT CCTTCTGACC CCAGCAGGTG GAGAGGAAGC TAAGCGCCCA CCTCCCAGGG 660
 15 CTCTCGGAGA CCCACTCTCC TCTCCCAGTC CCACGGCATT GCCGCAGGGA GGCTCGCATA 720
 CCGAGACTGA GGACCGGCTC TTCAAACACC TCTTCCGGGG CTACAACCGC TGGGCGCGCC 780
 CGGTGCCCCA CACTTCAGAC GTGGTGATTG TGGGCTTTGG ACTGTCCATC GCTCAGCTCA 840
 TCGATGTGGA TGAGAAGAAC CAAATGATGA CCACCAACGT CTGGCTAAAA CAGGAGTGGA 900
 GCGACTACAA ACTGCGCTGG AACCCCGCTG ATTTTGGCAA CATCACATCT CTCAGGTTCC 960
 20 CTTCTGAGAT GATCTGGATC CCCGACATTG TTCTCTACAA CAATGCAGAT GGGGAGTTTG 1020
 CAGTGACCCA CATGACCAAG GCCCACTCTT TCTCCACGGG CACTGTGACG TGGGTGCCCC 1080
 CGGCCATCTA CAAGGACTCC TGCAGCATCG ACGTCACTTT CTCCCCCTTC GACCAGCAGA 1140
 ACTGCAAGAT GAAGTTTGGC TCCTGGACTT ATGACAAGGC CAAGATCGAC CTGGAGCAGA 1200
 TGGAGCAGAC TGTGGAGCTG AAGGACTACT GGGAGAGCGG CGAGTGGGCC ATCGTCAATG 1260
 25 CCACGGGCAC CTACCAACAGC AAGAAGTACG ACTGCTGGCC CGAGATCTAC CCCGACGTCA 1320
 CCTACGCCCT CGTCATCCGG CGGCTGCCGC TCTTCTACAC CATCAACCTC ATCATCCCTT 1380
 GCCTGCTCAT CTCTTGCTTC ACTGTGCTGG TCTTCTACCT GCCCTCCGAC TCGGCGCAGA 1440
 AGATCACGCT GTGCAATTCG GTGCTGCTGT CACTCACCGT CTTCTGCTG CTATCACTG 1500
 AGATCATCCC CTCCACCTCG CTGGTCAATC CGCTCATCGG CGAGTACCTG CTGTTCACCA 1560
 30 TGATCTTCTG TACCCTGTCC ATCGTCAATC CCGTCTTCTG GCTCAATGTG CACCACCGCT 1620
 CCCCCAGCAC CCACACCATG CCCCACCTGG TCGGGGGGGC CTTCTTGGGC TGTGTGCCCC 1680
 GGTGGCTTCT GATGAACCGG CCCCCACCAC CCGTGGAGCT CTGCCACCCC CTACGCCCTGA 1740
 AGCTCAGGCC CTCTTATCAC TGGCTGGAGA GCAACGTGGA TGCCGAGGAG AGGGAGGTGG 1800
 TGGTGAGAGA GAGGGACAGA TGGGCATGTG CAGGTCAATG GGGCCCCCTT GTGGGCACCC 1860
 35 TCTGAGGAGA CGGCCACTG CACTCTGGGG CTTCAAGTCC CAAGGCTGAG GCTCTGCTGC 1920
 AGGAGGGTGA GCTGCTGCTA TCACCCACCA TGCAGAAGGC ACTGGAAGGT GTGCACTACA 1980
 TTGCCAGACA CTTGCGCTCT GAGGATGCTG ACTCTTCCGT GAAGGAGGAC TGAAGTATG 2040
 TTGCCATGGT CATCGACAGG ATCTTCTCTT GGCTGTTTAT CATCGTCTGC TTCTTGGGGA 2100
 CCATCGGCCCT CTTTCTCCCT CCGTTCCTAG CTGGAATGAT CTGACTGCAC CTCCTTCGAG 2160
 40 CTGGCTCCCA GGGCAAAGGG GAGGGTTCTT GGATGTGGAA GGGCTTTGAA CAATGTTTAG 2220
 ATTTGGAGAT GAGCCCAAAG TGGCAGGGAG AACAGCCAGG TGAGGTGGGA GGTTCGAGAG 2280
 CCAGGTGAGG TCTCTCTAAG TCAGGCTGGG GTTGAAGTTT GGAGTCTGTC CGAGTTTGCA 2340
 GGGTGTCTAG CTGTATGGTC CAGCAGGGGA GTAATAAGGG CTCTTCCGGA AGGGGAGGAA 2400
 GCGGGAGGCA GGCCTGCACC TGATGTGGAG GTACAGGCAG ATCTTCCCTA CCGGGGAGGG 2460
 45 ATGGATGGTT GGATACAGGT GGCTGGGCTA TTCCATCCAT CTGGAAGCAC ATTTGAGCCT 2520
 CCAGGCTTCT CPTTGACGTC ATTCTCTTCC TTCTTGTCTG CAAATGGCT CTGCACCAGC 2580
 CGGCCCCAG GAGGTCTGGC AGAGCTGAGA GCCATGGCT GCAGGGGCTC CATATGTCCC 2640
 TACGCGTGA CAGGCCAAAC AAGA

SEQ ID NO:102 PEN3 Protein sequence

Protein Accession #: NP_000733

1 11 21 31 41 51
 | | | | |
 MGPSCFVFLS FTKLSLWLL LTPAGGEEAK RPPPRAPGDP LSSPSPTALP OGGSHETED 60
 55 LRFKHLFRGY NRWARFVPT SDVVIVRFL SIAQLIDVDE KNQMTTNVW LKQWSDYKL 120
 RWNPADFGNI TSLRVPSEMI WIPDIVLYNN ADGEFAVTHM TKAHLFSTGT VHWVPPAIYK 180
 SSCSIDVTFF PFDQONCKMK FGSWTYDKAK IDLEQMEQTV DLKDYWESGE WAIVNATGTY 240
 NSKKYDCCAE IYPDVTFYAF IRRLEFLYTI NLIIFCLLIS CLTVLVFVLP SDGGEKITLE 300
 60 ISVLLSLTVF LLLITELIIP TSLVIPLIGE YLLFTMIFVT LSIVITVFVL NVHRSFSTH 360
 TMPHWVRGAL LGCVPRWLLM NRPPFPVELC HPLRLKLSPS YHWLESNVDA BEREVVVEE 420
 DRWACAGHVA PSVGTLCSHG HLHSGASGPK AEALLQEGEL LLSPHMOKAL EGVHYIADHL 480
 RSEDADSSVK EDWKYVAMVI DRIFLWLFII VCLGTIGLFL LPFFLAGMI

SEQ ID NO:103 PEU4 DNA SEQUENCE

Nucleic Acid Accession #: NM_018670

Coding sequence: 87-893 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CACGAGGCTG GAAGGGGCCA CTTACACACT CGGGCTCGGC ATAAAGCGGC CGCCGGCCGC 60
 CGGCCCCAG ACGCCGCCGC GCTGCCATGG CCCAGCCCTT GTGCCCGCCG CTCTCCGAGT 120
 CCTGGATGCT CTTCTCGGCC TGGGGCCCAA CTCGGCGGCC GCCGCCCTCC GACAAGGACT 180
 GCGGCGCTCT CCTCTCTCTG TCCCCAGACT CATGGGCGAG CACCCAGGCC GACAGCCCTG 240
 75 TGGCGAGCCC CGCGCGGCCA GGCACCTTCC GGGACCCCGC CGCCCTCTCC GTAGGTAGGC 300
 GCGGCGCGCG CAGCAGCCGC CTGGGCGAGC GGCAGAGGCA GAGCGCCAGT GAGCGGGAGA 360
 AACTGCGCAT GCGCAGCCTG GCCCGCGCCC TGCACGAGCT GCGCGCGCTT CTACCGCGCT 420
 CCGTGGCGCC CGCGGGCCAG AGCCTGACCA AGATCGAGAC GCTGCGCCTG GCTATCCGCT 480
 ATATCGGCCA CTGTCTGGCC GTGCTAGGCC TCAGCGAGGA GAGTCTCCAG CGCCGGTGCC 540
 80 GGCAGCGCGG TGACCGGGGG TCCCTCGGG GCTGCCCGCT GTGCCCGGAG GACTGCCCGC 600
 CGCAGATGCA GACACGGACG CAGGCTGAGG GGCAGGGGCA GGGGCGCGGG CTGGGCTTGG 660

5 TATCCGCCGT CCGCGCCGGG GCGTCTGGG GATCCCCGCC TGCCTGCCCC GGAGCCCGAG 720
 CTGCACCCGA GCCCGCGGAC CCGCCTGCGC TGTTCGCCGA GCGGGCGTGC CCGGAAGGGC 780
 AGGCGATGGA GCCAAGCCCA CCGTCCCCGC TCCTTCCGGG CGACGTGCTG GCTCTGTGG 840
 AGACCTGGAT GCCCTCTCG CCTCTGGAGT GGCTGCTGA GGAGCCCAAG TGACAAGGGA 900
 CAACTGACGC CGTCTCTGTG AGCACCAGG CTTTMTGGCC TCAGCACCTT CGAAGTGGTT 960
 CCTTGGCAGA CTGCCTTTCC TGGAAAGAGG CACGGGCGAT CCCGACGGGG GCATTCTGTC 1020
 GGGTAGAGC CGTCCCCACC GCGGCGGGCC TTCTCAGCCC CTCCCTCCAT GGAGGGACCC 1080
 ATAGGGCTAG ACACTTTGAG GCAAGCAGGA GGCTCTGCCT AATGTGAATT TATTATTATG 1140
 10 TGAATAAACT GTACTGTGT CAAAAA AAAA A A

SEQ ID NO:104 PEU4 Protein sequence

Protein Accession #: NP_061140

15 1 11 21 31 41 51
 MAQPLCPPLS ESWMLSAAWG PTRRPPPSDK DGRSLVSSP DSWGSTPADS FVASPARPGT 60
 LRDPFRAPSVG RRGARRSRLG SGQRQSASER EKLRMTLAR ALHELRRFLP PSVAPAGQSL 120
 TKIETPLRLAI RYIGHLSAVL GLSEESLQRR CRQRGDAGSP RGCPLCPDDC PAQMOTRTQA 180
 20 EGQGGQGRGLG LVSAYRAGAS WGSPPACPGA RAAPEPRDPP ALFAEAACPE GQAMEPSPPS 240
 PLLPGDVLAL LETWMLSPSL EWLPEEPK

SEQ ID NO:105 PEU5 DNA SEQUENCE

Nucleic Acid Accession #: NM_017636

Coding sequence: 324-3374 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 CCACGGAGAA GCCCACCAGT GCCTACGGAG AGCTGGACTT CACGGGGGCC GGCCGCAAGC 60
 ACAGCAATTT CTTCCGGCTC TCTGACCGAA CGGATCCAGC TGCAGTTTAT AGTCTGGTCA 120
 30 CACGCACATG GGGCTTCCGT GCCCCGAACC TGGTGGTGTG AGTGTCTGGG GGATCGGGGG 180
 GCGCCGTCTT CCAGACCTGG CTGCAGGACC TGCTGCGTCG TGGGCTGGTG CCGGCTGCCC 240
 AGAGCACAGG AGCCTGGATT GTCACTGGGG GTCTGCACAC GGGCATCGGC CGGCATGTTG 300
 GTGTGGCTGT ACGGGACCAT CAGATGGCCA GCACTGGGGG CACCAAGGTG GTGGCCATGG 360
 GTGTGGCCCC CTGGGGTGTG GTCCGGAATA GAGACACCTT CATCAACCCC AAGGGCTCGT 420
 35 TCCCTGCGAG GTACCGGTGG CGGGGTGACC CGGAGGACGG GGTCCAGTTT CCCCTGGACT 480
 ACAACTACTC GGCCCTTCTT CTGGTGGACG ACGGCACACA CGGCTGCCGT GGGGGCGAGA 540
 ACCGCTTCCG CTTCGCGCTG GAGTCTTACA TCTCACAGCA GAAGACGGGC GTGGGAGGGA 600
 CTGGAATTGA CATCCTCTTC CTGCTCTCTC TGATTGATGG TGATGAGAAG ATGTTGACGC 660
 40 GAATAGAGAA CGCCACCAGG GCTCAGCTCC CATGTCCTCT CTGGCTGGC TCAGGGGGAG 720
 CTGCGGAGG CTGGCGGAG ACCCTGGAAG ACACCTTGGC CCCAGGGAGT GGGGGAGCCA 780
 GGCAAGGCGA AGCCCGAGAT CGAATCAGGC GTTCTCTTCC CAAAGGGGAC CTGAGGTGCC 840
 TGCAGGCCCA GGTGGAGAGG ATTATGACCC GGAAGGAGCT CCTGACAGTC TATTCTTCTG 900
 AGGATGGGTC TGAGGAATTC GAGACCATAG TTTTGAAGGC CCTTGTGAAG GCCTGTGGGA 960
 45 GCTCGGAGGC CTCACCTTAC CTGGATGAGC TGGCTTTGGC TGTGGCTTGG AACCGCTGG 1020
 ACATTGCCCC GAGTGAACCT TTTCCGGGGG ACATCCAATG GCGGTCTCTC CATCTCGAAG 1080
 CTTCCTCTAT GGACGCCCTG CTGAATGACC GGCCTGAGTT CGTGCCTTGT CTCAATTCCC 1140
 ACGGCCCTAG CTGGGCCAC TFCCTGACCC CGATGCGCCT GSCCAACTC TACAGCGCGG 1200
 CGCCCTCCAA CTCGCTCATC CGCAACCTTT TGGACCAGGC GTCCACAGC GCAGGCACCA 1260
 50 AAGCCCCAGC CTTAAAGGGG GGAGCTGCGG AGCTCCGGCC CCTGACGCTG GGGCATGTGC 1320
 TGAGGATGCT GCTGGGGAAG ATGTGCGCGC CGAGGTACCC CTCCGGGGGC GCCTGGGACC 1380
 CTCACCCAGG CCAGGGCTTC GGGGAGAGCA TGTATCTGCT CTCCGACAAG GCCACCTCGC 1440
 CGCTCTCGCT GGATGCTGGC CTGCGGCAGG CCCCTGGAG CGACCTGCTT CPTTGGGCAC 1500
 TGTGTCTGAA CAGGCGACAG ATGGCCATGT ACTTCTGGGA GATGGGTTC AATGCAGTTT 1560
 55 CCTCAGCTCT TGGGGCTGTG TFGCTGCTCC GGGTGAATGC ACGCCTGGAG CCTGACGCTG 1620
 AGGAGGCAGC ACGGAGGAAA GACCTGGCGT TCAAGTTTGA GGGGATGGGC GTTGACCTCT 1680
 TTGGCGAGTG CTATCCGAGC AGTGAAGTGA GGGCTGCCCG CCTCTCTCTC CPTCGCTGCC 1740
 CGCTCTGGGG GGAATGCCACT TGCCTCCAGC TGGCCATGCA AGCTGACGCC CGTGCCTTCT 1800
 60 TTGCCAGAG TGGGGTACAG TCTCTGCTGA CACAGAAAGT GTGGGAGAT ATGGCCAGCA 1860
 CTACACCCAT CTGGGCCCTG GTTCTCGCCT TCTTTTGGCC TCCACTCATC TACACCCGCC 1920
 TCATCACTTT CAGGAAATCA GAAGAGGAGC CCACACGGGA GGAGCTAGAG TTTGACATGG 1980
 ATAGTGTCTA TAATGGGGAA GGGCTGTGCG GGACGGCGGA CCCAGCCGAG AAGACGCCGC 2040
 TGGGGGTCCC GCGCCAGTGG GGCCTGCCGG GTTGTGCGG GGGCGCTGCG GGGGGCGGCC 2100
 GGTGCTTACG CCGCTGGTTC CACTTCTGGG GCGCGCCGGT GACCATCTTC ATGGGCAACG 2160
 65 TGGTCACTA CTGCTGTTC TTGCTGCTTT TCTCGCGGGT GCTGCTCGTG GATTTCACG 2220
 CGGCGCGGCC CGGCTCCCTG GAGCTGTGTC TCTATTCTTG GGCCTTCACG CTGCTGTGCG 2280
 AGGAACTGCG CCAGGGCCTG AGCGGAGGCG GGGGAGCCCT CGCCAGCGGG GGGCCCGGGC 2340
 CTGGCCATCG CTCACTGAGC CAGCGCCTGC GCCTCTACCT CGCCGACAGC TGGAAACGAT 2400
 70 GCGACTAGT GCGCTCTACC TGCTTCCTCC TGGGCGTGGG CTGCGGCTG ACCCGGGTT 2460
 TGTACCACCT GGGCCGCACT GTCCCTGCA TCGACTTCAT GGTTTTCACG GTGCGGCTGC 2520
 TTCACATCTT CACGGTCAAC AAACAGCTGG GGGCCAAGAT CGTCATCGTG AGCAAGATGA 2580
 TGAAGACCT GTTCTTCTTC CTCTTCTTCC TCGGCGTGTG GCTGGTAGCC TATGGCGTGG 2640
 CCACGGAGGG GTCTCTGAGG CCACGGGACA GTGACTTCCC AAGTATCCTG CGCCGCTCTT 2700
 75 TCTACCTGCC CTACCTGACG ATCTTCTGGG AGATCCCCA GGAGGACATG GACGTGGGCC 2760
 TCATGGAGCA CAGCAACTGC TCCTCGGAGC CCGGCTTCTG GGCACACCTT CCTGGGGCCC 2820
 AGGCGGGCAG CTGCGTCTCC CAGTATGCCA ACTGGCTGGT GGTGCTGCTC CTGCTCATCT 2880
 TCTGTCTGCT GCGCAACATC CTGCTGGTCA ACTGCTCAT TGCCATGTTT AGTTACACAT 2940
 TCGGCAAGT ACAGGGCAAC AGCGATCTCT ACTGGAAGGC GCAGGCTTAC CGCCTCATCC 3000
 GGGAAATCCA CTCTCGGCC GCGCTGGCCC CGCCCTTTAT CGTCATCTCC CACTTGGCCG 3060
 80 TCGCTCGAG GCAATTGTGC AGGCGACCCC GGAGCCCCA GCGCTCTCTC CGGCGCTCG 3120
 AGCATTTCCG GGTTCACCTT TCTAAGGAAG CCGAGCGGAA GGTGCTAACG TGGGAATCGG 3180

5
10
15
20
25
30
35

```

TGCGATAAGGA GAACCTTCTG CTGGCAGCG CTAGGGACAA GCGGGAGAGC GACTCCGAGC 3240
GTCTGGAGCG CACGCTCCAG AAGGTGGACT TGGCACTGAA ACAGCTGGGA CACATCCGCG 3300
AGTACGAACA GCGCTGAAA GTGCTGGAGC GGGAGGTCCA GCAGTGTAGC CCGCTCCTGG 3360
GGTGGGTGAC GTAGGCGGTT AGCAGCTCTG CCATGTTGCC CTCAGGTGGG CCGCCACCCC 3420
TTGACCTGCA TGGGTCCAAA GAGTGAGCCA TGCTGGCGGA TTTAAGGAG AAGCCCCCAC 3480
AGGGGATTTT GCTCTTAGAG TAAGGCTCAT GTGGGCCTCG GCCCCCCGAC CTGGTGGCCT 3540
TGTCCTTGAG GTGAGCCCCA TGTCCATCTG GGCCACTGTC AGGACCACCT TTGGGAGTGT 3600
CATCCTTACA AACCACAGCA TGCCCGGCTC CTCCCAGAAC CAGTCCCAGC CTGGGAGGAT 3660
CAAGCCCTGG ATCCCGGGCC GTTATCCATC TGGAGGCTGC AGGGTCTCTG GGGTAACAGG 3720
GACCACAGAC CCTCACCAC TCACAGATTC CTCACACTGG GGAATAAAG CCATTTCAGA 3780
GGAAAAAAA AAAAAAAA AAAAAAAA

```

SEQ ID NO:106 PEU5 Protein sequence

Protein Accession #: NP_060106

15
20
25
30
35

```

1 11 21 31 41 51
| | | | |
MASTGGTKV AMGVAPWGV RNRDTLINPK GSFPARYRWR GDPEDGVQFP LDYNYSAFFL 60
VDDGTHGCLG GENRFLRLLE SYISQKQKTV GGTGIDIPVL LLLIDGDEKM LTRINATQA 120
QLPCLLVAGS GGAADCLAET LEDTLAPGSG GARQGEARDR IRRFFPKGDL EVLQAQVERI 180
MTRKELLTVY SSEDGSEEF TIVLKALVKA CGSSEASAYL DELRLAVAWN RVDIAQSELF 240
RGDTQWRSFH LEASTMDALL NDRPEFVRLL ISHGLSLGHF LTPMRLAQLY SAAPSNLSLR 300
NLLDQASHSA GTKAPALKGG AAELRPPDVG HVLRLMLGKM CAPRYPSSGA WDFHFGQFG 360
ESMYLLSDKA TSPLSLDAGL GQAPWSDLLL WALLLNRAQM AMYFWEMGSN AVSSALGACL 420
LLRVMARLEP DAEAAARRKD LAFKFEQMGV DLFGEQYRVS EVRAARLLLR RCPLWGDATC 480
LQLAMQADAR AFFAQDGVQS LLTQKWWGDM ASTPIWALV LAFFCPPLIY TRLITFRKSE 540
BEPTREELEF DMDSVINGEG FVGTADPAEK TPLGVPRQSG RPGCCGGRGC GRRLRRNFH 600
FWGAPVTIFM GNVVSYLLFL LLFSRVLLVD FQAPPFSGLE LLLYFWAFTL LCEELRQGLS 660
GGGGLASGG PPGPHASLSQ RLRLYLADSW NQCDLVALTC FLLGVGCRLT PGLYHLGRTV 720
LCIDEMVETV RLLHFTVWVK QLGPKIVIVS KMMKDVFFFL FFLGVWLVA VVATEGLLRP 780
RDSDFPSLLR RVFYRPLYQI FGQIPQEDMD VALMEHSNCS SEPFCFWAHP GAQAGTCVSQ 840
YANWLVLVLL VIFLLVANIL LVNLLIAMFS YTFGKVQGNS DLYWKAQRYR LIREFHSRPA 900
LAPPFIVISH LRLRLRQLCR RPRSPQSPSS ALEHFRVYLS KEAERKLLTW ESHKFNFL 960
ARARDKRESL SERLETSQK VDLALKQLGH IREYEQRLKV LEREVQQCSR VLGMWT

```

SEQ ID NO:107 PEW3 DNA SEQUENCE

Nucleic Acid Accession #: NM_005982

Coding sequence: 276-1130 (underlined sequences correspond to start and stop codons)

40
45
50
55
60
65

```

1 11 21 31 41 51
| | | | |
GGTAGCAGCA TCCACCGGCG GGGAGGTCGG AGGCAGCAAG GCCTTAAAGG CTACTGAGTG 60
CGCCGGCGCGT TCCGTGTCCA GAACCTCCCC TACTCCTCCG CCTTCTCTTC CTGGCCGCC 120
CACCGCCAAC TTCCGACTCC GGTTTTCGCC TTTGCAAGC CTAAGGAGGA GGTAGGAAC 180
AGCCGCGCCC CCCTCCCTGC GGCCTGCTCT CGGCTCTGCT CCTGCGCGC 240
TGCGCCTGGG CCGTGGCGCC CGGCAGGCGC CAGCCATGTC GATGCTCCGC TCGPTTGCT 300
TTACGCAAGG CCAAGTGGCG TCGGTGTGCG AGGTCTGTGA GCAAGGCGGA AACCTGGAGC 360
GCCTGGGCGG GTCTCTGTGG TCACTGCCCG CCTGCGACCA CCTGCACAAG AACGAGAGCG 420
TACTCAAGGC CAAGGCGGTG GTCCGCTTCC ACCGCGGCAA CTTCCTGTAG CTCTACAAGA 480
TCCTGGAGAG CCACCAATTC TCGCCTCACA ACCACCCCAA ACTGCAGCAA CTGTGGCTGA 540
AGGCGCATTA CGTGGAGGCC GAGAAGCTGC GCGGCCGACC CCTGGGCGCC GTGGGCAAAT 600
ATCGGGTGCG CCGAAAATTT CCACTGCCGC GCACCATCTG GGACGGCGAG GAGACCACT 660
ACTGCTTCAA GGAGAAGTCG AGGGGTGTCC TGCGGGAGTG GTACGCGCAC AATCCCTACC 720
CATCGCCGCG TGAGAAGCGG GAGCTGGCCG AGGCCACCGG CCTCACCAAC ACCCAGGTCA 780
GCAACTGGTT TAAGAACCGG AGGCRAAGAG ACCGGGCCCG GGAGGCCAAG GAAAGGGAGA 840
ACACCGAAAA CAATAACTCC TCCTCCAACA AGCAGAACCA ACTCTCTCCT CTGGAAGGGG 900
GCAAGCCGCT CATGTCCAGC TCAGAAGAGG AATCTCACC TCCCCAAAGT CCAGACCAGA 960
ACTCGGTCCT TCTGTGTCAG GGCAATATGG GCCACGCCAG GAGCTCAAAC TATTCTCTCC 1020
CGGGCTTAAC AGCCTCGCAG CCCAGTCAGC GCCTGCAGAC CCACCAAGCAT CAGCTCCAAG 1080
ACTCTCTGCT CGGCCCTCTC ACCTCCAGTC TGGTGGACTT GGGGTCTCTA GTGGGGAGGG 1140
ACTGGGCGCT CGAAGGGATT CCTGGAGCAG CAACCACTGC AGCGACTAGG GACACTTGTA 1200
AATAGAAATC AGGAACATTT TTGCAGCTTG TTTCTGGAGT GTTTTGCGCA TAAAGGAATG 1260
GTGGACTTTC ACAAATATCT TTTTAAAAAT CAAAACCAAC AGCGATCTCA AGCTTAATCT 1320
CCTCTTCTCT CCAACTCTTT CCACTTTTGC ATTTTCTCTC CCAATGCAGA GATCAGGG

```

SEQ ID NO:108 PEW3 Protein sequence

Protein Accession #: NP_005973

70
75

```

1 11 21 31 41 51
| | | | |
MSMLPSFGFT QEQVACVCEV LQGGNLERL GRFLWSLPAC DHLHKNESVL KAKAVVAFHR 60
GNFRELYKIL BSHQSPFNH PKLQQLWLKA HYVEAEKLRG RPLGAVGKYR VRRKFPLPRT 120
IWDGEETSYC FKEKSRGVLR EWAHNPVPS FREKRELAEA TGLTTQVSN WFKNRRQRDR 180
AAEAKERENT ENNNSSSNKQ NQLSPLEGK PLMSSSEEF SPPQSPDQNS VLLQGNMGH 240
ARSSNYSLPG LTASQPSHGL QTHQHLQDS LLGLTSSLV DLGS

```

SEQ ID NO:109 PFJ8 DNA SEQUENCE

Nucleic Acid Accession #: NM_005069

Coding sequence: 57-2060 (underlined sequences correspond to start and stop codons)

80

SEQ ID NO:110 PFJ8 Protein sequence:
Protein Accession #: NP_005060.1

75 1 11 21 31 41 51
MKEKSKNAAK TRREKENGEF YELAKLLPLP SAITSQLDKA SHRLTTSYL KMRAVFPEGL 60
GDAWQGPSRA GPLDGVAKEL GSHLLQTLDG FVFVVASDVGK IMYISETASV IHLGLSQVELT 120
GNSIYEYIHP SDHDEMTAVL TAHQPLHHHL LQYEYIERSF FLRMKCVLAK RNAGLTCSGY 180
KVHICSGYLK IROYLDMSL YVDSQYOVGL VAVGOSLPPS AITEIKLYSN MFMFRASLDL 240

KLIFLDSRVTVTGYEPQDL IEKTLYHHVH GCDVFHLRYA HLLLLVKQV TTKYRLLSK 300
 RGGWVWVQSY ATVVHNSRSS RPHCIVSVNY VLTEIEYKEL QLSLEQVSTA KSQDSWRTAL 360
 STSQETRLKLV KPKNTKMKTK LRTNPYPQQ YSSFQMDKLE CGQLGNWRAS PPASAAAPPE 420
 LQPHSESSDL LYTPSYSLPF SYHYGHFPLD SHVFSSKKPM LPAKFGQPG SPCEVARFFL 480
 STLPAEGECQ WHYANPLVPS SSSPAKNPPE PPANTARHSL VPSYEAPAAA VRRFGEDTAP 540
 PSFPSCGHYR EEPALGPAKA ARQAARDGAR LALARAAPEC CAPPTPEAPG APAQLPFVLL 600
 NYHRVLARRG PLGGAAPAS GLACAPGGPE AATGALRLRH PSPAATSPPG APLPHYLGA 660
 VIITNGR

SEQ ID NO:111 PFJ7 DNA SEQUENCE

Nucleic Acid Accession #: NM_008549

Coding sequence: 1-1254 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGAACGGAC GCTGCATCTG CCCGTCCTG CCTACTCAC CCGTCAGCTC CCCGAGTCC 60
 TCGCCTCGGC TCGCCCGCGG GCCGACAGTG GAGTCTCACC ACGTCTCCAT CACGGGTATG 120
 CAGGACTGTG TGCAGCTGAA TCAGTATACC CTGAAGGATG AAATTGGAAA GGGCTCCTAT 180
 GGTGTGCTCA AGTTGGCCTA CAATGAAAAT GACAATACCT ACTATGCAAT GAAGGTGCTG 240
 TCCAAAAGA AGCTGATCCG GCAGGCCGGC TTCCACGTC GCCCTCCACC CCGAGGCACC 300
 CGGCCAGCTC CTGGAGGCTG CATCCAGCCC AGGGGCCCCA TTGAGCAGGT GTACCAGGAA 360
 ATTGCCATCC TCAAGAAGCT GGACCACCCC AATGTGGTGA AGCTGGTGA GGTCTGGAT 420
 GACCCCAATG AGGACCATCT GTACATGGTG TTGCAACTGG TCAACCAAGG GCCCGTGATG 480
 GAAGTGCCCA CCTCAAACC ACTCTTGAA GACCAGGCC GTTCTACTT CCAGGATCTG 540
 ATCAAAGGCA TCGAGTACTT AACTACCAG AAGATCATCC ACCGTGACAT CAAACCTTCC 600
 AACCTCTGG TCGGAGAAGA TGGGCACATC AAGATCGCTG ACTTGGTGT GAGCAATGAA 660
 TTCAAGGGCA GTGACGCGCT CCTCTCAAC ACCGTGGGCA CGCCGCCCTT CATGGCACCC 720
 GAGTCTGCT CTGAGACCG CAAGATCTT TCTGGGAAG CCTTGGATGT TTGGGCCATG 780
 GGTGTGACAC TATACTGCTT TGCTTTGGC CAGTGCCCAT TCATGGACGA GCGGATCATG 840
 TGTTTACACA GTAAGATCAA GAGTCAGGCC CTGGAATTC CAGACCAGCC CGACATAGCT 900
 GAGGACTTGA AGGACCTGAT CACCGTATG CTGGACAAGA ACCCCGAGTC GAGGATCGTG 960
 GTGCCGAAA TCAAGCTGCA CCCCTGGGTC ACGAGGCATG GGGCGGAGCC GTTGGCGTCG 1020
 GAGGATGAGA ACTGCACGCT GGTGGAAGTG ACTGAAGAGG AGGTGAGAA CTCAGTCAAA 1080
 CACATCCCA GCTTGGCAAC CGTGATCCTG GTGAAGACCA TGATACGTA ACGCTCCTTT 1140
 GGGAAACCAT TCGAGGGCAG CCGGCGGGAG GAACGCTCAC TGTACGCGCC TGGAAACTTG 1200
 CTCACCAAAA AACCAACCAG GGAATGTGAG TCCCTGCTG AGCTCAAGAC CTAGAAAATA 1260
 AGTCCCTTC CTGCTGTTG CAAAGTAACG TAAGAGTTCC CTCACCCGAG TGGATGCAGA 1320
 CGTTCTTGCT GTCAGCCACC TTCCTTCATA CACATAGCCA GCCCAGGCTG ACCAGAACGT 1380
 CCCAGGACAG ATGAGGCTTT GTGTCTTAT GAGAGTGGGA GAACCTGGTG GGCACCCCTG 1440
 GTGCAGGTGC TGTGGTGGGT GGGGACCCCA CTGCCTTCC CACTGAGCAC ATCATGGCTA 1500
 CCTGACTTGG TGGGAGTTCC ATTCAGTCAC TTCTGTTTCT TAAACATAGC TTTACTGAGG 1560
 TACAATTCAC ATACCATGTA ATTCACCCAC GGGGAAGTGA TGATTCACTG GTTCTTAATA 1620
 CACACTTCTG CAGCATTAC CACCGTCAAC TTACGACAT TTTCATCAGC CCAAGAAGAC 1680
 ACCCTACACT CCTTAGCTGT CCCCATCCA CTCCCCACC CCAGTAACCA CTCAGAAATG 1740
 GTATGGATTG GCCTATTCTG GACGTTTCGT ATAAATGGCG TCATACACTA AAAAAAAAAA 1800
 AAAA

SEQ ID NO:112 PFJ7 Protein sequence:

Protein Accession #: NP_008540.1

1 11 21 31 41 51
 MNGRCICPSL PYSPVSPQS SPRLPRRPTV ESHVSIITGM QDCVQLNQYT LKDEIGKGSY 60
 GVVKLAYNEN DNTYYAMKVL SKKKLIRQAG FPRRPPRGT RPAPGCIQP RGPVYVQE 120
 IAILKLDHP NVVKLVEVLD DPNEHDLYMV FELVNQGPVM EVPTLKPLSE DQARFYFQDL 180
 IKGIEYLHYQ KIHHRDIKPS NLLVGEDGHI KIADFGVNS FKGSALLSN TVGTPAFMAP 240
 ESLSETRKIF SGKALDVWAM GVTLYCFVFG QCPFMDERIM CLHSKIKSQA LEFPDQPDIA 300
 EDLKDILTRM LDKNPESRIV VPEIKLHPWV TRHGAEPLPS EDENCTLVEV TEEEVNSVK 360
 HPSLATVIL VKTMRKRSF GNPFEGRRE ERSLSAPGNL LTKKPTRECE SLSELKT

SEQ ID NO:113 PFJ6 DNA SEQUENCE

Nucleic Acid Accession #: NM_021810

Coding sequence: 1-429 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGAAACCTC TGATATGGAC ATGGTCAGAT GTTGAAGGCC AGAGGCCGGC TCTGTCATC 60
 TGCACAGCTG CAGCAGGACC CACGACGGGA GTTAAGGGTT ATGGCAAGCC CTTTGAGCCA 120
 AGAAGTGTGA AAAACATACA CTCTACTCCT GCTTACCCAG ATGCCACAAT GCACAGACAA 180
 CTCCTGGCTC CGGTGGAAGG AAGGATGGCA GAGACATTGA ATCAGAACT CCATGTTGCC 240
 AATGTGCTGG AAGATGACCC CGGCTACCTA CCTCAGTCT ACAGCGAGGA AGGGGAGTGT 300
 GGAGGGGCCC CATCCCTCAG CTCTCTGGCC AGCTTGGAAC AGGAGTTGCA ACCTGATTG 360

CTGGACTCTT TGGGTTCAAA AGCGACTCCG TTTGAGGAAA TATATTCAGA GTCAGGTGTT 420
 CCTTCCTAA

5 SEQ ID NO:114 PFJ6 Protein sequence:
 Protein Accession #: NP_068582.1

1 11 21 31 41 51
 10 MKPLIWTWSD VEGQRPALLI CTAAAGPTQG VKGYGKPFEP RSVKNIHSTP AYPDATMHRQ 60
 LLAPVEGRMA ETLNQKLHVA NVLEDDPGYL PHVYSEEGEC GGAPSLSSLA SLEQELQPD 120
 LDSLGSKATP FEEIYSESGV PS

15 SEQ ID NO:115 PFJ5 DNA SEQUENCE

Nucleic Acid Accession #: NM_006361
 Coding sequence: 131-985 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 CGAATGCAGG CGACTTGCGA GCTGGGAGCG ATTAAAAACG CTTTGGATTC CCCCGGCCTG 60
 GGTGGGGAGA GCGAGCTGGG TGCCCCCTAG ATTCCCGGCC CCCGCACCTC ATGAGCCGAC 120
 25 CCTCGGCTCC ATGGAGCCCG GCAATTATGC CACCTTGGAT GGAGCCAAGG ATATCGAAGG 180
 CTGTCTGGGA GCGGGAGGGG GGCGGAATCT GGTGCGCCAC TCCCCTCTGA CCAGCCACCC 240
 AGCGGCGCCT ACCTGTATGC CTGCTGTCAA CTATGCCCCC TTGGATCTGC CAGGCTCGGC 300
 GGAGCCGCCA AAGCAATGCC ACCCATGCC TGGGGTGCCC CAGGGGACGT CCCAGCTCC 360
 CGTGCCCTAT GGTACTTTG GAGGCGGGA CTACTCTGC CGAGTGTCCC GGAGCTCGCT 420
 30 GAAACCCTGT GCCCAGGCAG CCACCCTGGC CGCGTACCCC GCGGAGACTC CCACGGCCGG 480
 GGAAGAGTAC CCCAGTCGCC CCACTGAGTT TGCCTTCTAT CCGGGATATC CGGGAACCTA 540
 CCACGCTATG GCCAGTTACC TGGACGTGTC TGTGGTGAG ACTCTGGGTG CTCCTGGAGA 600
 ACCGCGACAT GACTCCCTGT TGCCTGTGA CAGTTACCAG TCTTGGGCTC TCGCTGGTGG 660
 CTGGAACAGC CAGATGTGT GCCAGGGAGA ACAGAACCCA CCAGTCCCT TTTGGAAGGC 720
 35 AGCATTTGCA GACTCCAGCG GGCAGCACCC TCCTGACGCC TCGCCTTTC GTCGCGGCCG 780
 CAAGAAACGC ATTCCGTACA GCAAGGGGCA GTTGCGGGAG CTGGAGCGGG AGTATGCGGC 840
 TAACAAGTTC ATCACCAGG ACAAGAGGCG CAAGATCTCG GCAGCCACCA GCCTCTCGGA 900
 GCGCCAGATT ACCATCTGGT TTCAGAACC GCGGGTCAA GAGAAGAAGG TTCTCGCCAA 960
 GGTGAAGAAC AGCGCTACCC CTTAAGAGAT CTCCTTGCCT GGGTGGGAGG AGCGAAAGTG 1020
 40 GGGGTGTCT GGGGAGACCA GAAACCTGCC AAGCCCAGG TGGGGCCAAG GACTCTGCTG 1080
 AGAGGCCCT AGAGACAACA CCCTTCCAG GCCACTGGCT GCTGGACTGT TCCTCAGGAG 1140
 CGGCTGGGT ACCCAGTATG TGCAGGGAGA CGGAACCCA TGTGACAGGC CCACTCCACC 1200
 AGGGTTCCCA AAGAACCTGG CCCAGTCATA ATCATTATC CTCACAGTGG CAATAATCAC 1260
 GATAACCACT

45 SEQ ID NO:116 PFJ5 Protein sequence:
 Protein Accession #: NP_006352.1

50 1 11 21 31 41 51
 MEPGNYATLD GAKDIEGLL AGGGRNLVAH SPLTSHAAP TLMPAVNYAP LDLPGSAEPP 60
 KQCHPCPGVP QGTSPAPVPY GYFGGYYSC RVSRSCLKFC AQAATLAAYP AETPTAGEEY 120
 55 PSRPTAFYF PGYPTGYHAM ASYLDVSVVQ TLGAPGEPRH DSLLPVDSYQ SWALAGGWNS 180
 QMCCQGEQNP PGPFWKAFA DSSGQHPDA CAFRRGRKKR IPYSKQQLRE LEREYAANKF 240
 ITKDKRRKIS AATSLSERQI TIWFQNRVK EKKVLAKVKV SATP

60 SEQ ID NO:117 PFJ4 DNA SEQUENCE

Nucleic Acid Accession #: NM_005628
 Coding sequence: 591-2216 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 GTAACCGCTA CTCCCGGACA CCAGACCACC GCCTTCCGTA CACAGGGGCC CGCATCCAC 60
 CCTCCCGGAC CTAAGAGCCT GGGTCCCTG TTTCCGGAGG TCCGCTTCCC GGCCCCAGA 120
 TTCTGGCATC CCAGCCCTCA GTGTCCAAGA CCCAGGCAGC CCGGGTCCCC GCCTCCGGA 180
 70 TCCAGGCGTC CGGATCTGC GCCACCAGAA CCTAGCCTCC TGCAGACCTC CGCATCTGG 240
 GGGCACTCAA CCTCTGGAG CCAAGGGCCC CAGTCCAC CCAGAGAAAC TCTCGTATTC 300
 CCAGCTCTCA GGCCAAGGA ACCCGGGCGC TCGAACTCC CAGCTTTCGG ACATCTGGCA 360
 CACGGGGCAG AGCAGAGAAG CTCAGCGCCC AGCCTGGGGA ATTAAACAC TCCAGCTTCC 420
 AAGAGCCAAG GAATTCAGT GCTGTGAAC CACAACCTA AGGAGCCCTC CAAAGTTCCA 480
 GTCTCCAGGT GCTGTACTC AACTCAGTCC TAGGAACGTC GGGTCTGGG AAGGAGCCCA 540
 75 AGCGTCCCA GCCAGCTTC AGGCGCTAAG AAACCCCGGT GCTTCCCATC ATGCTGGCCG 600
 ATCTCTCTCG AGACTCCAAG GGGCTCGAG CGGCGGAGCC CACCGCCAAC GGGGGCCTGG 660
 CGCTGGCCTC CATCGAGGAC CAAGGCGCGG CAGCAGGCGG CTACTGCGGT TCCCGGGACC 720
 AGGTGCGGCC CTGCTTCTGA GCCAACCTGC TTGTGCTGT GACAGTGGTG GCCGTGGTGG 780
 CCGGCTGGC GCTGGGACTG GGGGTGTGCG GGGCCGGGGG TCGCTGGCG TTGGGCCCGG 840

AGCGCTTGAG CGCCTTCGTC TTCCCCGGCG AGCTGCTGCT GCGTCTGCTG CGGATGATCA 900
 TCTTGCCGCT GGTGGTGTGC AGCTTGATCG GCGGCGCCGC CAGCCTGGAC CCCGGCCGCG 960
 TCGGCCGTCT GGGCGCCTGG GCGCTGCTCT TTTTCTGGT CACCACGCTG CTGGCGTCGG 1020
 CGCTCGGAGT GGGCTTGGCG CTGGCTGTGC AGCCGGGGCG CGCCTCCGCC GCCATCAACG 1080
 CCTCCGTGGG AGCCGCGGGC AGTGCCGAAA ATGCCCCAG CAAGGAGGTG CTCGATTTCG 1140
 TCCTGGATCT TCGAGAGAAAT ATCTTCCCTT CCAACCTGGT GTCAGCAGCC TTTCGCTCAT 1200
 ACTCTACCAC CTATGAAGAG AGGAATATCA CCGGAACCAG GGTGAAGGTG CCCGTGGGGC 1260
 AGGAGGTGA GGGGATGAAC ATCCTGGGCT TGGTAGTGT TGCCATCGTC TTTGGTGTGG 1320
 CGCTCGGAA GCTGGGGCT GAAGGGGAGC TGTCTATCCG CTCTTCAAC TCCTTCAATG 1380
 AGGCCACCAT GGTCTGGTC TCCTGGATCA TGTGTACGC CCCTGTGGGC ATCATGTTC 1440
 TGGTGGCTGG CAAGATCGTG GAGATGGAGG ATGTGGGTTT ACTCTTGGC CGCCTTGGCA 1500
 AGTACATTCT GTCTGCTG CTGGGTACG CCAATCCATGG GTCCTGGTA CTGCCCTCA 1560
 TCTACTTCT CTTCACCCG AAAAAACCCCT ACCGCTTCT GTGGGGCATC GTGACGCCGC 1620
 TGGCCACTGC CTTTGGGACC TCTTCCAGT CCGCCACGCT GCCGTGATG ATGAAGTGGC 1680
 TGGAGGAGAA TAATGGCGTG GCCAAGCACA TCAGCCGTTT CATCTGCCC ATCGCGGCCA 1740
 CCGTCAACAT GGACGGTGCC GCGCTCTTCC AGTGGCTGGC CGCAGTGTTC ATTGCACAGC 1800
 TCAGCCAGCA GTCCTGGAC TTCGTAAAGA TCATCACCAT CCTGGTCACG GCCACAGCGT 1860
 CCAGCGTGGG GGCAGCGGGC ATCCTGCTG GAGGTGTCTT CACTCTGGC ATCATCTCG 1920
 AAGCAGTCAA CCTCCCGTC GACCATATCT CTTGATCCT GGCTGTGGAC TGGCTAGTCG 1980
 ACCGCTCCTG TACGCTCTC AATGTAGAAG GTGACGCTCT GGGGGCAGGA CTCTCCAAA 2040
 ATTAGTGA CCGTACGAG TCGAGAAGCA CAGAGCCTGA GTTGATACAA GTGAAGAGTG 2100
 AGCTGCCCCG GGATCCCGTG CCAGTCCCCA CTGAGGAAGG AAACCCCTC CTAAACACT 2160
 ATCGGGGGCC CGCAGGGGAT GCCACGGTGC CTCTGAGAA GGAATCAGTC ATGTAAACCC 2220
 CGGGAGGGAC CTTCCTGCC CTGCTGGGGG TGCTCTTTGG AACTGGATT ATGAGGAATG 2280
 GATAAATGGA TGAGCTAGGG CTCTGGGGGT CTGCTGCAC ACTCTGGGA GCCAGGGGCC 2340
 CCAGCACCTC CAGGACAGG AGATCTGGGA TGCTGGCTG CTGGAGTACA TGTGTTCACA 2400
 AGGGTTACTC CTCAAAACCC CAGTTCTCA CTCATGTCCC CAACTCAAGG CTAGAAAACA 2460
 GCAAGATGGA GAAATAATGT TCTGCTGCGT CCCCACCGTG ACCTGCCTGG CTCCCTCTG 2520
 CTCAGGGAGC AGGTACAGG TCACCATGGG GAATCTAGC CCCCCTGGG GGGATGTTAC 2580
 AACACCATGC TGGTATTTT GCGCGCTGTA GTTGTGGGGG GATGTGTGTG TGCACGTGTG 2640
 TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TTCTGTGACC TCCTGTCCCC ATGGTACGTC 2700
 CCACCTGTC CCAGATGCC CTATTCCCTC CACAATAACA GAAACACTCC CAGGGACTCT 2760
 GGGGAGAGGC TGAGGACAAA TACCTGCTGT CACTCCAGAG GACATTTTTT TTAGCAATAA 2820
 AATTGAGTGT CACTATTTA AAAAAAAAAA AAAAAA

SEQ ID NO:118 PFJ4 Protein sequence:
 Protein Accession #: NP_005019.1

1 11 21 31 41 51
 | | | | |
 MVADPPRDSK GLAAAEPTAN GGLALASIED QGAAAGGYCG SRDQVRRCLR ANLLVLLTVV 60
 AVVAGVALGL GVSAGGALA LGPERLSAFV FPGELLRLRL RMILPLVVC SLIGGAASLD 120
 PGALGRLGAW ALLFLVVTIL LASALGVGLA LALQPGAASA AINASVGAAG SAENAPSKEV 180
 LDSFLDLARN IFPSNLVSA FRSYSTTYEE RNITGTRVKV PVQVEGGMN ILGLVVFATV 240
 FGVALRLKLP EGELLIRFFN SFNEATMVLV SWIMWYAPVG IMFLVAGKIV EMEDVGLLEA 300
 RLKGYLCCCL LGHAHGLLV LPLYFLFTR KNPYRFLWGI VTPLATAFGT SSSSATLPLM 360
 MKCVENNGV AKHSRFLP IGATVNMDGA ALFQCVAAVF IAQLSQSLD FVKIITILVT 420
 ATASSVGAAG IPAGGVLTILA ILEAVNLPV DHISLILAVD WLVDRSCTVL NVEGDALGAG 480
 LLQNYVDRTE SRSTELIQL VKSELPLDPL PVPTEEGNPL LKHRYRGPAGD ATVASEKESV 540
 M

55
 SEQ ID NO:119 PFJ3 DNA SEQUENCE
 Nucleic Acid Accession #: NM_006708
 Coding sequence: 88-642 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CTAGTTAAGG CGGCACAGGG CCGAGGCGTA GTGTGGGTGA CTCCTCCGTT CTTGGGTCC 60
 CGTCGTCTGT GATACTGCAG TTAGCCATG GCAGAACCGC AGCCCCGCTC CGGCGGCTC 120
 ACGGACGAGG CCGCCCTCAG TTGCTGTCC GACGCGGACC CCACTACCAA GGATTTTCTA 180
 TTGCAGCAGA CCAATGCTACG AGTGAAGGAT CCTAAGAAGT CACTGGATT TTATACTAGA 240
 GTTCTTGAA TGACGCTAAT CCAAAATGT GATTTTCCA TTATGAAGTT TTAATCTTAC 300
 TTCTTGGCTT ATGAGGATAA AAATGACATC CCTAAAGAAA AAGATGAAAA AATAGCCTGG 360
 GCGCTCTCCA GAAAGAGTAC ACTTGAGCTG ACACACAATT GGGGCACTGA AGATGATGCG 420
 ACCCAGAGTT ACCACAATGG CAATTCAGAC CCTCGAGGAT TCGGTCTAT TGGAATTGCT 480
 GTTCTGATG TATACAGTGC TTGTAAGAGG TTGAAGAAC TGGGAGTCAA ATTGTGAAG 540
 AAACCTGATG ATGGTAAAT GAAAGGCCCTG GCATTTATTC AAGATCCTGA TGGCTACTGG 600
 ATTGAAATTT TGAATCTCAA CAAAATGGCA ACCTTAATGT AGTGTCTGTA GAATTCCTCT 660
 TTGAGATTTC AGAAGAAAGG AAACAATGTG ATTCAAGATA TTACATACC AGAAGCATCT 720
 AGGACTGATG GATCACTGTC CCGATTCAAA TTATTCTTCA GTCCATTTC CCTTCCTATT 780
 TCAGCTGTTT CTTTTCACCT AACTGTTTCA TCATTCTGGT TTCAAGCAG TGCTTTATCT 840
 CATGTCCTTG AATATAGTTG TGTAACCTTA TTTTATAGT AATAATTAGA ACAGTTCCCT 900
 TCAGAGGCTG CATTTGCCTT CTCTGCCAC CTAATATTA CTTCCTTCA AATCTGCCTT 960
 TGAATCATCA TTTTAAAAA AAAATTAACA TGTTTTGTG GTAGTTATCT TCTGGGGTTT 1020
 CAATTCCTCA GAAACAACCT TTTTCAAC GGAAGGAAA GAACACTAGT GTTCTTTCAG 1080
 TAAAGTACAA AGTGTATT TTACAAAAGA GTAGGTACTC TTGAGAGCAA TTCAATCAT 1140

GCTGACAAGG ATACTGATAG AAAAAGTGAT TTCTTCTTAT TATAAAGTAC ATTTAAAGTT 1200
 CAAGGACTAA CCTTATTTAT TTGGGAAAAGG GGAGGAGGAA GGAAATGATA TGGTACCCAG 1260
 ACCTGGGCT AGGCTGCAAC TTTATCTCAT TTAATACTCC CAGCTGTCAT GTGAGAAAGA 1320
 AAGCAGGCTA GGCATGTGAA ATCACTTTCA TGGATTATTA ATGGATTAA GAGGGCATCA 1380
 ATCAGCTCAA CTCAAGATTT CATAATCATI TTAGTATTT AGATGTGTC TCAAAGTTGT 1440
 AGTACCTCAC AATACCTCCA CTGGTTTCCT GTTGTA AAAA CCTTCAGTGA GTTTGACCAT 1500
 TGTGCTCTTG GCTCTTGGGC TGGAGTACCG TGGTGAGGGA GTAAACACTA GAAGTCTTTA 1560
 GTACAAAAC TGTCTAGGGA CACCTGGTGA TTCTACACA AGTGATGTT ATATTCTCA 1620
 TAAAGAGTCT TCCCTATCCC AAGGTCTTCA TGATGCCAGT AGCCATATAT GATAAATTAT 1680
 GTTCAGTGAT AACTTAGTTA TCAGAAATCA GTCAGTGGT CTTCGCCGCC ATGATTACACA 1740
 TTTGATGAGT TTTTAAAAAT CAAAGTGATT TTGAAATCT CTAATGGCTC AGAAAAATAA 1800
 AACATCCAGT TTGTGATGA CTATATTAG ATTTCTCTAG ACTCTAGTGG AAGACCTTTG 1860
 GAAAGGCCAT GCCAACCGTG CTGTACTGC TAGAAGCACT TTATGTTTCC TTTTGGGTG 1920
 AAATGGATTT ATGTGAGTGC TTTAAACAAA TAGCAATACT TATAGACTGA AATAAAATGA 1980
 AACTTCAAT AAG

SEQ ID NO:120 PFJ3 Protein sequence:

Protein Accession #: NP_006699.1

1 11 21 31 41 51
 MAEPQPPSGG LTDEAALSCC SDADPSTKDF LLQOTMLRVK DPKKSLDFYT RVLGMTLIQK 60
 CDFPIMKFSL YFLAYEDKND IPKEKDEKIA WALSRKATLE LTHNWGTEDD ATQSYHNGNS 120
 DPRGRGHIGI AVPDVYSACK RFEELGVKFV KKPDDGKMKG LAFIQDPDGY WIEILNPKNM 180
 ATLTM

SEQ ID NO:121 PFJ2 DNA SEQUENCE

Nucleic Acid Accession #: NM_002867

Coding sequence: 70-729 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCGACGCCAG GTCTGCCCGT CCCGCCGACC GTCCGGGAGC GAACCCGTCG TCCCGCATG 60
 GAGTCCGCGA TGGCTTCAGT GACAGATGGT AAACATGGAG TCAAAGATGC CTCTGACCAG 120
 AATTTGACT ACATGTTTAA ACTGCTTATC ATTGGCAACA GCAGTGTGG CAAGACCTCC 180
 TTCTCTTGC GCTATGCTGA TGACACGTTT ACCCCAGCCT TCGTTAGCAC CGTGGGCATC 240
 GACTTCAAGG TGAAGACAGT CTACCGTCAC GAGAAGCGGG TGAACCTGCA GATCTGGGAC 300
 ACAGCTGGGC AGGAGCGGTA CCGGACCATC ACAACAGCCT ATTACCGTGG GGCCATGGGC 360
 TTCATTCTGA TGTATGACAT CACCAATGAA GAGTCCTTCA ATGCTGTCCA AGACTGGGCT 420
 ACTCAGATCA AGACCTACTC CTGGGACAAT GCACAAGTTA TTCTGGTGGG GAACAAGTGT 480
 GACATGGAGG AAGAGAGGGT TGTTCCTACT GAGAAGGGCC AGCTCCTTGC AGAGCAGCTT 540
 GGGTTTGATT TCATTGAAGC CAGTGCAAGG GAGAACATCA GTGTAAGGCA GGCCTTTGAG 600
 CGCCTGGTGG ATGCCAATTG TGACAAGATG TCTGATTGCG TGGACACAGA CCCGTCGATG 660
 CTGGGCTCCT CCAAGAACAC GCGTCTCTCG GACACCCAC CGCTGCTGCA GCAGAACTGC 720
 TCATGCTAGC AAGGCCACCT TTCTGACCT CCCCTCATG TGCCCCCACA CCCAAGTCTG 780
 CTCTCCCTG TTACACACTG TCCGCTCT

SEQ ID NO:122 PFJ2 Protein sequence:

Protein Accession #: NP_002858.1

1 11 21 31 41 51
 MASVTDGKHG VKDASDONFD YMEKLLIGN SSVGKTSFLL RYADDTFPA FVSTVGIDFK 60
 VKTVRHEKR VKLQIWDTAG QERYRIITTA YYRGAMGFIL MYDITNEESF NAVQDWATQI 120
 KTYSWDNAQV ILVGNKCDME EERVVPTEKG QLLAEQLGFD FFEASAKENI SVRQAFERLV 180
 DAICDKMSDS LDTDPMSLGS SKNTRLSDTP PLLQQNCSC

SEQ ID NO:123 PFJ1 DNA SEQUENCE

Nucleic Acid Accession #: NM_001844

Coding sequence: 158-4621 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ACGCAGAGCG CTGCTGGGCT GCCGGGTCTC CCGCTTCCTC CTCCTGCTCC AAGGGCCTCC 60
 TGCAATGAGGG CGCGGTAGAG ACCCGGACCC GCGCCGTGCT CTGCGCGCTC 120
 CGCCCGGGCC CGGCTCAGCC AGGCCCGCG GTGAGCCATG ATTCGCTCG GGGCTCCCA 180
 GTCGCTGGTG CTGCTGACGC TGCTCGTCGC CGCTGCTCTT CGGTGTCAGG GCCAGGATG 240
 CCAGGAGGCT GGCAGCTGTG TGCAGGATGG GCAGAGGTAT AATGATAAGG ATGTGTGGAA 300
 CGCGGAGCCC TGCCGATCT GTGTCTGTGA CACTGGGACT GTCCTCTGCG ACGACATAAT 360
 CTGTGAAGAC GTGAAAGACT GCCTCAGCCC TGAGATCCCC TTCGGAGAGT GCTGCCCCAT 420
 CTGCCCACT GACCTGCCA CTGCCAGTGG GCAACCAGGA CCAAGGGGAC AGAAAGGAGA 480
 ACCTGGAGAC ATCAAGGATA TTGTAGGACC CAAAGGACCT CCTGGGCTC AGGACCTGC 540

AGGGGAACAA GGACCCAGAG GGGATCGTGG TGACAAAGGT GAAAAAGGTG CCCCTGGACC 600
 TCGTGGCAGA GATGGAGAAC CTGGGACCCC TGGAATCTCT GGCCCCCCTG GTCCTCCCGG 660
 CCCCCTGGT CCCCCTGGT TTGGTGGAAA CTTTGTCTCC CAGATGGCTG GAGGATTGTA 720
 TGAAAAAGGCT GGTGGCGCCC AGTTGGGAGT AATGCAAGGA CCAATGGGCC CCAATGGGACC 780
 TCGAGGACCT CCAGGCCCTG CAGGTGCTCC TGGGCTCAA GGATTCAAAG GCAATCCTGG 840
 TGAACCTGGT GAACCTGGTG TCTCTGGTCC CATGGGTCCC CGTGGTCTCT CTGGTCCCCC 900
 TGGAAAGCCT GGTGATGATG GTGAAGCTGG AAAAAGCTGGA AAAGCTGGTG AAAGGGGTCC 960
 GCCTGGTCTC CAGGTGCTC GTGGTTTCCC AGGAACCCCA GGCCTTCTCG GTGTCAAAGG 1020
 TCACAGAGGT TATCCAGGCC TGGACGGTGC TAAGGGAGAG GCGGGTGCTC CTGGTGTGAA 1080
 GGGTGAGAGT GGTTCGCCGG GTGAGAACGG ATCTCCGGGC CCAATGGGTC CTCGTGGCCT 1140
 GCTGGTGAA AGAGGACGGA CTGGCCCTGC TGGCGTCCG GGTGCCCGAG GCAACGATGG 1200
 TCAGCCAGGC CCCGAGGTC CTCCGGGTCC TGTGGTCTC GCTGGTGGTC CTGGCTTCCC 1260
 TGGTGTCTCT GGAGCCAAGG GTGAAGCCGG CCCCACTGGT GCCGTGGTC CTGAAGGTGC 1320
 TCAAGGTCTC CGCGGTGAAC CTGGTACTCC TGGGTCCCT GGGCTGCTG GTGCCTCCGG 1380
 TAACCTGGA ACAGATGGAA TTCTGGAGC CAAAGGATCT GCTGGTGCTC CTGGCATTGC 1440
 TGGTGTCTCT GGCTTCTCTG GGCCACGGGG TCCTCTGGC CCTCAAGGTG CAATGGTCC 1500
 TCTGGGCCCC AAAGGTGAGA CGGGTGAACC TGGTATTGCT GGCTTCAAAG GTGAACAAGG 1560
 CCCCAGGGA GAACCTGGCC CTGTGGGCC CCAGGGAGCC CTGGACCCG CTGGTGAAGA 1620
 AGGCAAGAGA GTGGCCGTG GAGAGCCTGG TGGCGTTGGG CCAATGGGTC CCCCTGGAGA 1680
 AAGAGGTGCT CCCGAAACC GCGGTTTCCC AGGTCAAGAT GGTCTGGCAG GTCCCAAGGG 1740
 AGCCCCGGA GAGCAGGGG CCAGTGGTCT TGTGGCCCC AAGGGAGCCA ACGGTGACCC 1800
 TGGCGTCTC GGAGAACCTG GCCTTCTCTG AGCCCGGGT CTCCTGGCC GCCCTGGTGA 1860
 TGTGTCTCT CAAGGCAAG TTGGCCCTTC TGGAGCCCC GGTGAAGATG GTCGTCTGG 1920
 ACCTCCAGT CCTCAGGGG CTCGTGGGCA GCCTGGTGC ATGGGTTTCC CTGGCCCCAA 1980
 AGGTGCCAAC GGTGAGCCTG GCAAAAGCTG TGAGAAGGGA CTGCCTGGTG CTCTGGTCT 2040
 GAGGGGTCTT CCTGGCAAG ATGGTGAGAC AGGTGCTGCA GGACCCCTG GCCCTGCTGG 2100
 ACCTGCTGGT GAACGAGCG AGCAGGGTGC TCCTGGGCCA TCTGGGTTC AGGGACTTCC 2160
 TGGCCCTCTC GGTCCCCAG GTGAAGGTGG AAAACCAAGT GACCAGGGTG TTCCCGGTGA 2220
 AGCTGAGCC CTGCGCTCG TGGTCCAG GGGTGAACGA GGTTCCTCAG GTGAACGTGG 2280
 CTCTCCCGGT GCCCAGGGCC TCCAGGGTCC CCGTGGCCTC CCCGCACTC CTGGCACTGA 2340
 TGGTCCAAA GGTGCATCTG GCCCAGCAGG CCCCCTGGC GCACAGGGCC CTCCAGGTCT 2400
 TCAGGGAATG CCTGGCGAGA GGGGAGCAGC TGGTATCGT GGGCCCAAAG GCGACAGGGG 2460
 TGACGTTGGT GAGAAAGGCC CTGAGGGAGC CCCTGGAAAG GATGGTGGAC GAGGCTGAC 2520
 AGGTCCCAAT GGCCCCCTG GCCCAGCTGG TGCTAACGGC GAGAAGGGAG AAGTTGGACC 2580
 TCCTGGTCTC GAGGGAAGTG CTGGTCTCG TGGCGTCCG GGTGAACGTG GAGAGACTGG 2640
 CCCCCCGGA CCAGCGGGAT TTGCTGGGCC TCCTGGTCTC GATGGCCAGC CTGGGGCCAA 2700
 GGTGTGAGCA GATGAGGCCG GCCAGAAAG CGATGCTGGT GCCCTGGTC CTAGGGGCC 2760
 CTCTGGAGCA CCTGGGCCTC AGGGTCTAC TGGAGTGAAT GGTCTTAAAG GAGCCCGAGG 2820
 TGCCCAAGGC CCCCCGGGAG CCACTGGATT CCCTGGAGCT GCTGGCCGC TTGGACCCCC 2880
 AGGTCCAAT GGCAACCTG GACCCCTGG TCCCTGGT CCTTCTGGA AAGATGGTCC 2940
 CAAAGGTGCT CGAGGAGACA GCGGCCCCC TGGCCGAGT GGTGAACCCG GCCTCCAAGG 3000
 TCCTGCTGGA CCCCCTGGC AGAAGGGAGA GCCTGGAGAT GACGTCTCT CTGGTGCCGA 3060
 AGGTCCACCA CACCGTGGCT GTCTGGCTGG TCAGAGAGGC ATCGTGGTC TGCCTGGGCA 3120
 AGTGTGTGAG AGAGGATTCC CTGGCTTGGC TGGCCCATCG GGTGAGCCCC GCAAGCAGGG 3180
 TGCTCTGGA GCATCTGAAG ACAGAGGTCC TCCTGGCCCC GTGGGTCTC CTGGCTGAC 3240
 GGTCTCTGCA GGTGAACCCG GACGAGAGGG AAGCCCCGGT GCTGATGGCC CCCCCTGGCAG 3300
 AGATGGCGCT GCTGGAGTCA AGGTGATCG TGGTGAGACT GGTGCTGTT GAGCTCTGG 3360
 AGCCCCGGG CCCCCTGGCT CCCCCTGGCC CGCTGGTCCA ACTGGCAAGC AAGGAGACAG 3420
 AGGAGAAGCT GGTGCACAAG GCCCATGGG ACCCTCAGGA CCACTGGAG CCCGGGAAT 3480
 CCAGGGTCTC CAAGGCCCA GAGGTGACAA AGGAGAGGCT GGAGAGCCTG GCGAGAGAGG 3540
 CCGTAAGGGA CACCGTGGCT TCACTGGTCT GCAAGGTCTG CCGGCCCTC CTGGTCTCTC 3600
 TGGAGACCAA GGTGCTTCTG GTCTGTCTGG TCCTTCTGGC CTAAGAGTCT CTCTGGCCC 3660
 CGTCCGTGCC TCTGGCAAAG ATGGTGCTAA TGGAATCCCT GGCCCCATTG GGCCTCCTGG 3720
 TCCCCTGGGA CGATCAGGGC AAACCCGGTCC TGCTGGTCTC CTGGAATC CTGGGCCCCC 3780
 TGGTCTCCA GGTCCCCCTG GCCTGGCAT CGACATGTCC GCCTTGTCTG GCTTAGGCCC 3840
 GAGAGAGAAG GGGCCCCGACC CCCTGCAGTA CATGCGGGCC GACCAGGCAG CCGGTGGCCT 3900
 GAGACAGCAT GACGCCGAGG TGGATGCCAC ACTCAAGTCC CTCAACAACC AGATTGAGAG 3960
 CATCCGAGC CCCGAGGGCT CCCGCAAGAA CCCTGCTCGC ACCTGCAGAG ACCTGAAACT 4020
 CTGCCACCCT GAGTGGAAGA GTGGAGACTA CTGGATTGAC CCAACCAAG GCTGCACCTT 4080
 GGACGCCATG AAGGTTTCTC GCAACATGGA GACTGGCGAG ACTTGCCTCT ACCCCAATCC 4140
 AGCAACGTT CCAAGAAGA ACTGGTGGAG CAGCAAGAGC AAGGAGAAGA AACACATCTG 4200
 GTTGGAGAA ACCATCAATG GTGGCTTCCA TTTCAGTAT GGAGATGACA ATCTGGCTCC 4260
 CAACACTGCC AACGTCCAGA TGACCTTCTC ACGCTGCTG TCCACGGAAG GCTCCAGAA 4320
 CATCACTAC CACTGCAAGA ACAGCATTGC CTATCTGGAC GAAGCAGCTG GCAACCTCAA 4380
 GAAGGCCCTG CTATCCAGG GCTCCAATGA CGTGAGATC CGGGCAGAGG GCAATAGCAG 4440
 GTTCAGTAC ACTGCCCTGA AGGATGGCTG CACGAAACAT ACCGGTAAGT GGGGCAAGAC 4500
 TGTATCGAG TACCGGTAC AGAAGACCTC ACGCTCCCC ATCATGACA TTGACCCAT 4560
 GGACATAGGA GGGCCCCGAGC AGGAATTCCG TGTGGACATA GGGCCGGTCT GTTCTTGTGA 4620
 AAAACCTGAA CCGAAGACA ACACAATCCG TTGCAACCC AAGGACCCA AGTACTTCC 4680
 AATCTCAGTC ACTTAGGAC TCTGCATGTA ATGGCTGACC TGACCTGATG TCCATTATC 4740
 CCACCTCTCT ACAGTTCGGA CTTTTCTCCC CTCTTTTCT AAGAGACCTG AACTGGGCAG 4800
 ACTGCAAAAT AAAATCTCGG TGTCTATT ATTTATGTC TTCTGTAAG ACCTTCGGGT 4860
 CAAGGCAGAG GCAGGAACT AACTGGTGTG AGTCAAATGC CCCCTGAGTG ACTGCCCCA 4920
 GCCCAGGCCA GAAGACCTCC CTTCAGGTGC CGGGCGCAGG AACTGTGTGT GTCTACACA 4980
 ATGGTGTAT TCTGTGTAAC ACACCTCTGT ATTTTAAAC ACATCAATG ATATTAAAAA 5040
 TGAAGAAGAT ATTGAAAGT

SEQ ID NO:124 PFJ1Protein sequence:

Protein Accession #: NP_001835.2

1 11 21 31 41 51
 5 MRLGAPQSL VLLTLLVA AV LRCQGQDVQE AGSCVQDQQR YNDKDVWKPE PCRICVCDTG 60
 TVLCDDICE DVKDCLSPEI PFGECCPICP TDLATASGQP GPKGQKGEPE DIKDIVGPKG 120
 PPGPQGPAGE QGPRGDRGDK GEKGAPGPRG RDGEPGTPGN PGPPGPPGPP GPPGLGNGFA 180
 AQMAGGFDEK AGGAQLGVQM GPMGPMGPRG PPGPAGAPGP QGFQGNPGEP GEPVSGPMG 240
 10 PRGPPGPPGK PGDDGEAGKP GKAGERGPPG PQGARGFPPT PGLPGVKGHR GYPGLDGAKE 300
 EAGAPGVKGE SGSPGENGSP GPMGPRGLPG ERGRTGPAGA AGARGNDGQP GPAGPPGPVG 360
 PAGGPGFFGA PGAKGEAGPT GARGPEGAQG PRGEPGTPGS PGPAGASGNP GTDGIPGAKG 420
 SAGAPGIAGA PGFPGRGPP GPQATGTPLG PKGQTGEPGI AGFKGEQGPKE GEPGAPGPQG 480
 APGPAGEEGK RGARGEPGVV GPIGPPGERG APGNRGFPQG DGLAGPKGAP GERGPSGLAG 540
 15 PKGANGDPGR PGEPGLPGAR GLTGPRPDAG PQKGVPVSGA PGEDGRFPFP GPQGARGQPG 600
 VMGFPKGKA NGEFGKAGEK GLPGAPGLRG LPGKDGETGA AGPPGAPGA GERGEQGAPE 660
 PSFGQGLPG PGPPGEGGKP GDQGVVGEAG APGLVGPGE RGFPGERGSP GAQGLQGPRG 720
 LKGTPTGDTGP KGASGPAGPP GAQGPPLQG MPGERGAAGI AGPKGDRGDV GEKGPEGAPG 780
 KDGGRLGTGP IGPPPGPAGAN GEKGEVGPFG PAGESAGARGA PGERGETGPP GPAGFAGPPG 840
 20 ADGQPGAKGE QGEAGQKGA GAPGPQGPPS APGPQGPTGV TPGKGARGAQ GPPGATGFP 900
 AAGRVPGPS NGNPFPPPP GPSGKDGPKG ARGDSGPGR AGEPLQGPA GPPGKGEPE 960
 DDGSPGAGFP PGPGLAGQR GIVGLPGQRG ERGFPGLPG SGEFGKQGP GASGDRGPPG 1020
 PVGPPGLTGP AGEPRGEGSP GADGPPGRDG AAGVKGDRGE TGAVGAPGAP GPPGSPGAP 1080
 25 PTGKQDRGE AGAQPMGPS GPAGARGIQG PQGPRGDKGE AGEFGERGLK GHRGFTGLQG 1140
 LPPGPPGSD QGASGPAGPS GPRGPPGPGV PSKDGANGI PGIPGPPGR GRSGETGPA 1200
 PPNPFPGPG PGPPGPGIDM SAFAGLGP RE KGPDLQYMR ADQAAGGLRQ HDAEVDATLK 1260
 SLNNQIESIR SPESRKNPA RTCDLKLCH PEWKSQDYWI DPNQGGCTLDA MKVFCNMETG 1320
 30 ETCVYPNPN VPKKNWSSK SKEKKHIWFG ETINGGFHFS YGDDNLAPNT ANVQMTFLRL 1380
 LSTEGSQNIT YHCKNSIAYL DEAGNLKKA LLIQGSNDVE IRAEGNSRFT YTALKDGCTK 1440
 HTGKWGKTVI EYRSQKTSRL PIDIAPMDI GGPEQEFQVD IGPVCF

SEQ ID NO:125 PFH9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005084

Coding sequence: 162-1487 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 GCTGGTCCGA GGCTCGCAGT GCTGTGCGCG AGAAGCAGTC GGGTTTGGAG CGCTTGGGTC 60
 GCGTTGGTGC GCGGTGGAAC GCGCCCAAGG ACCCCAGTTC CCGCGAGCAG CTCCGCGCCG 120
 CGCCTGAGAG CTAAGCTGA AACTGCTGCT CAGCTCCCAA GATGGTGCCA CCCAAATTGC 180
 ATGTGCTTTT CTGCTCTGCG GGCTGCTGG CTGTGGTTTA TCCTTTTGAC TGGCAATACA 240
 TAAATCCTGT TGCCCATATG AAATCATCAG CATGGGTCAA CAAATACAA GTACTGATGG 300
 45 CTGCTGCAAG CTTTGGCCAA ACTAAATCC CCCGGGAAA TGGGCCTTAT TCCGTTGGTT 360
 GTACAGACTT AATGTTTGT CACACTAATA AGGGCACCTT CTTCGTTTA TATTATCCAT 420
 CCCAAGATAA TGATCGCCTT GACACCCTT GGATCCCAA TAAAGAATAT TTTGGGGTCC 480
 TTAGCAAATT TCTTGAACA CACTGGCTTA TGGGCAACAT TTTGAGGTTA CTCCTTGGTT 540
 CAATGCAAA CCGTGCAGAA TGAATTCCT CTCTGAGGCC TGGTGAAAAA TATCCACTTG 600
 50 TTGTTTTTTC TCATGGTCTT GGGGCATICA GGACACTTTC TCTGCTATT GGCATTGACC 660
 TGGCATCTCA TGGGTTTATA GTTGCTGCTG TAGAACACAG AGATAGATCT GCATCTGCAA 720
 CTTACTATTT CAAGGACCAA TCTGCTGAG AAATAGGGGA CAAGTCTTGG CTCTACCTTA 780
 GAACCTGAA ACAAGAGGAG GAGACACATA TACGAAATGA GCAGGTACGG CAAAGAGCAA 840
 AAGAAATGTT CCAAGCTCTC AGTCTGATT TTAGCATTTA TCATGGAAG CCAAGTGAAGA 900
 55 ATGCATTAGA TTTAAAGTTT GATATGGAAC AACTGAAGGA CTCTATTGAT AGGGAAAAAA 960
 TAGCAGTAAT TGGACATTCT TTTGGTGGAG CAACGGTTAT TCAGACTCTT AGTGAAGATC 1020
 AGAGATTGAG ATGTGGTATT GCCCTGGATG CATGGATGTT TCCACTGGGT GATGAAGTAT 1080
 ATTCCAGAA TCTCAGCCC CTCTTTTITA TCAACTCTGA ATATTCCAA TATCCTGCTA 1140
 60 ATATCATAAA AATGAAAAAA TGCTACTCAC CTGATAAAGA AAGAAAGATG ATTACAATCA 1200
 GGGGTTCAGT CCACCAGAA TTTGCTGACT TCACCTTTGC AACTGGCAAA ATAATTGGAC 1260
 ACATGCTCAA ATTAAGGGA GACATAGATT CAAATGTAGC TATTGATCTT AGCAACAAA 1320
 CTTTATTAGC ATCTTACAA AAGCATTIAG GACTTCATA AGATTITGAT CAGTGGGACT 1380
 65 GCTTGATTGA AGGAGATGAT GAGAATCTTA TTCCAGGGAC CAACATTAAC ACAACCAATC 1440
 AACACATCAT GTTACAGAAC TCTTCAGGAA TAGAGAAATA CAATTAGGAT TAAATAGGT 1500
 TTTT

SEQ ID NO:126 PFH9 Protein sequence:

Protein Accession #: NP_005075.1

1 11 21 31 41 51
 70 MYPKHLVLF CLCGCLAVVY PFDWQYINPV AHMKSSAWVN KIQVLMMAAS FLQTKIPRGN 60
 GPYSVGCTDL MFDHTNKGTF LRLYPSQDN DRLDTLWIPN KEYFWGLSKF LGTHWLMGNI 120
 75 LRLFGMTT PANWNSPLRP GEKYPLVVS HGLGAFRTLY SAIGDLASH GFIVAIVEHR 180
 DRASATYYF KDQSAEIGD KSWLYLRTLK QEEETHIRNE QVRQRAKES QALSLILDID 240
 HGKPKNALD LKFDMEQLK SIDREKIAVI GHSFGGATVI QTLSEDQFRF CGIALDAWMF 300
 PLGDEVYSRI PQLFFINSE YFYQYANIK MKKCYSPDKE RKMITIRGSV HQNFADTFIA 360
 TGKIGHMLK LKGDIDSNVA IDLSNKASLA FLQKHLGLHK DFDQWDCLIE GDDENLIPGT 420
 NINTNQHM LQNSSGIEKY N

SEQ ID NO:127 PFH8 DNA SEQUENCE

5

Nucleic Acid Accession #: NM_015900

Coding sequence: 32-1402 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 CACGAGCGGC ACGAGGATTT CCAGCTCAGC GATGCCCCCA GGTCCTGGG AGAGCTGCTT 60
 CTGGGTGGGG GGCCTCATTT TGTGGCTCAG CGTTGGAAGT TCAGGGGATG CACCTCCTAC 120
 CCCACAGCCA AAGTGCCTGT ACTTCCAGAG CGCCAACCTT TTTGAAGGCA CCGATCTCAA 180
 AGTCCAGTTT CTCCTCTTTG TCCCTTCGAA TCCTAGCTGT GGGCAGCTAG TAGAAGGAAG 240
 CAGTGACCTC CAAAACCTCT GGTTC AATGC CACTCTGGGA ACCAACTAA TTATCCATGG 300
 15 ATTCAGGGTT TTAGGAACAA AGCCTTCCTG GATTGACACA TTTATTAGAA CCCTTCTGCG 360
 TGCAACGAAT GCTAATGTGA TTGCGTGGG CTGGATTAT GGGTCTACAG GAGTCTACTT 420
 CTCAGCTGTG AAAAATGTGA TTAAGTTGAG CCTCGAGATC TCCCTTTCC TCAATAAACT 480
 CCTGGTGCTG GGTGTGTCGG AATCCTCAAT CCACATCAAT GGTGTTAGCC TGGGGGCCCA 540
 20 CGTTGGGGGC ATGGTGGGAC AGCTCTTCGG AGGCCAGCTG GGACAGATCA CAGGCTTGGG 600
 CCCCCTGGG CCTGAGTACA CCAGGGCCAG TGTGGAAGAG CGCTTGGATG CTGGAGATGC 660
 CCTCTTCGTG GAAGCCATCC ACACAGACAC CGACAATTG GGTATTTCGGA TTCCCGTTGG 720
 ACATGTGGAC TACTTCGTCA ACGGAGGCCA AGACCAACCT GGCTGCCCA CCTTCTTTTA 780
 CGCAGGTTAT AGTTATCTGA TCTGTGATCA CATGAGGGCT GTGCACCTCT ACATCAGCGC 840
 CCTGGAGAAT TCCTGTCCAC TGATGGCCTT TCCCTGTGCC AGCTACAAGG CCTTCCTTGC 900
 25 TGGACGCTGT CTGGATTGCT TTAACCTTT TCTGCTTTCC TGCCCAAGGA TAGGACTGGT 960
 GGAACAAGGT GGTGTCAAGA TAGAGCCGCT CCCCAGGAA GTGAAAGTCT ACCTCCTGAC 1020
 TACTTCCAGT GCTCCGACT GCATGCATCA CAGCCTCGTG GAGTTTCACT TGAAGGAAC 1080
 GAGAAACAAG GACACCAACA TCGAGGTTAC CTTCCTTAGC AGTAACATCA CCTCTTCATC 1140
 TAAGATCACC ATACCTAAGC AGCAACGCTA TGGGAAAGGA ATCATAGCCC ATGCCACCCC 1200
 30 ACAATGCCAG ATAAACCAAG TGAATTCAA GTTTCAGTCT TCCAACCGAG TTTGGAAAAA 1260
 AGACCGGACT ACCATTATTG GGAAGTCTG CACTGCCCTT TTGCTGTCA ATGACAGAGA 1320
 AAAGATGGTC TGCTTACCTG AACCAGTGAA CTTACAAGCA AGTGTGACTG TTTCTGTGA 1380
 CCTGAAGATA GCCTGTGTGT AGTTTAACCT GGGCAGGACA CATCTCCCTG CATTTTITTT 1440
 TTTTITTTTT GAGAGAGAGG TGTGATGAGG GATGTGTGTG TGCAGCTTAT TGTAGACCAT 1500
 35 TACTACTAAG GAGAAAAGCA AAGCTCTTTC TTATTTTCTC CATAATCAGC TACCCTGGAG 1560
 GGGAGGGAGA ACTCATTTTA CAGAACTTGG TTTCTTTGC CGATCTTATG TACATACCCA 1620
 TTTTAGCTTT CCATGTCATA CTAACTGCA CTTGCTTTAT CTCCTTGGGC ATTCGTACTT 1680
 AGGATTCAAT AGAAACATGT ACAGGGTAAA CAATTTTITA AAAATAAAAC TTCATGGAGT 1740
 40 AAAAAAAAAA AAAAAAAAAA

SEQ ID NO:128 PFH8 Protein sequence:

Protein Accession #: NP_056984.1

45 1 11 21 31 41 51

MPPGPWESCF WVVGGLLWLS VGSSGDAPPT PPKCADFQS ANLFEGTDLK VQFLLFVPSN 60
 PSCGQLVEGS SDLQNSGFNA TLGTLKLIHG FRVLGTFPSW IDTFIRTLR ATNANVIAVD 120
 WYGSTGVVYF SAVKNVIKLS LEISLFLNKL LVLGVSESSI HIIGVSLGAH VGGMVGQLFG 180
 50 GQLGQITFLD PAGPEYTRAS VEERLDAGDA LFVEAIHDT DNLGIRIPVG HVDYFVNGGQ 240
 DQPGCTTFYF AGYSYLICDH MRAVHLYISA LENSCLMAF PCASYKFLA GRCLDCFNPF 300
 LLSCPRIGLV EQGGVKIEPL PKEVKVYLLT TSSAPYCMHH SLVEFHLKEL RNKDTNIEVT 360
 FLSSNITSSS KITIPKQQRV GKGIHAHATP QCQINQVKFK FQSSNRVWKK DRTTIIGKFC 420
 55 TALLPVNDRE KMVCLPEPVN LQASVTVSCD LKIACV

SEQ ID NO:129 PFH7 DNA SEQUENCE

60

Nucleic Acid Accession #: NM_014384

Coding sequence: 89-1336 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

65 CGTTGCCGGG TCGCAGGTCC CGCCAGTGGC AGCGCAACGG AGGTCGAAGG CGTTCAGACT 60
 CTTAGCTGAA CGCGGAGCTG CGGCGGCTAT GCTGTGGAGC GGCTGCCGGC GTTTCGGGGC 120
 GCGCCTCGGC TGCTGCGCCG GCGGTCTCCG GGTCTCGTC CAGACCGGCC ACCGGAGCTT 180
 GACCTCCTGC ATCGACCTTT CCATGGGACT TAATGAAGAG CAGAAAGAAT TTCAAAAAGT 240
 GGCCTTTGAC TTTGCTGCCC GAGAGATGGC TCCAAATATG GCAGAGTGGG ACCAGAAGGA 300
 70 GCTGTTCCCA TCGATATGTA TCGGGAAGGC AGCCAGCTA GGCTTCGGAG GGGTCTACAT 360
 ACAAACAGAT GTGGGCGGGT CTGGGCTGTC ACCTCTTGAT ACCTCTGTCA TTTTGAAGC 420
 CTTGGCTACA GGCTGCACCA GCACCACAGC CTATATAAGC ATCCACAACA TGTGTGCCTG 480
 GATGATTGAT AGCTTCGGAA ATGAGGAACA GAGGCACAAA TTTTGCCAC CGCTCTGTAC 540
 CATGAGAAGG TTTGCTTCTT ACTGCCTCAC TGAACCAGGA AGTGGGAGTG ATGTGCCTC 600
 75 TCTTCTGACC TCGCTAAGA AACAGGGAGA TCATTACATC CTCAATGGCT CCAAGGCCTT 660
 CATCAGTGGT GCTGGTGAGT CAGACATCTA TGTGGTCATG TGCCGAACAG GAGGACCAGG 720
 CCCCAGGGGC ATCTCATGCA TAGTTGTGA GAAGGGGACC CCTGGCCTCA GCTTTGGCAA 780
 GAAGGAGAAA AAGGTGGGGT GGAACCTCCA GCCAACACGA GCTGTGATCT TCGAAGACTG 840
 TGCTGTCCCT GTGGCCAACA GAATTGGGAG CGAGGGGCAG GGCTTCCTCA TTGCGGTGAG 900

5 AGGACTGAAC GGAGGGAGGA TCAATATTGC TTCCTGCTCC CTGGGGGGCTG CCCACGCCTC 960
 TGTCATCCTC ACCCGAGACC ACCTCAATGT CCGGAAGCAG TTTGGAGAGC CTCTGGCCAG 1020
 TAACCACTAC TTGCAATTCA CACTGGCTGA TATGGCAACA AGGCTGGTGG CCGCGCGGCT 1080
 GATGGTCCGC AATGCAGCAG TGGCTCTGCA GGAGGAGAGG AAGGATGCAG TGGCCTTGTC 1140
 10 CTCCATGGCC AAGCTCTTTG CTACAGATGA ATGCTTTGCC ATCTGCAACC AGGCCTTGCA 1200
 GATGCACGGG GGCTACGGCT ACCTGAAGGA TTACGCTGTT CAGCAGTACG TCGGGGACTC 1260
 CAGGGTCCAC CAGATTCTAG AAGGTAGCAA TGAAGTGATG AGGATACTGA TCTCTAGAAG 1320
 CTGCTTCAG GAGTAGAACC CACACTGTT CTGGCTGGT GTTCAGTGCG ACTGCAGTCA 1380
 GTGTTGAGTG GTGCCATGTG GGCCGCTCTA TTCCAAAGGA ATCATGGATT AGACCCAAGG 1440
 GCTGAGCTCC TCTAGGGCAG GACCTGCACC CTGTGTGTTG GCACCAGCAT CGGGTCTTTG 1500
 15 ACTGGGGCAG AATCCCCAGT GGAACCGGAA GAGCTGGACT GATGAGAAAC ATCAGAAGAA 1560
 CACATACTAC CTGTCTTCC TAATGCCAGA AGGGTGACCA GTGAAGATTC ACCGTCAAA 1620
 CATGAAAGTC CTCTCTTGA TCCACTTTAT CTTGATTAGT CTGCATTTTA CTAGTTCACT 1680
 GGATCCCTCC TCTAGGGGCC TGGGGACTTT CACTGATGCT CTTCCTGATT CTAGAGCAAA 1740
 GGTGTGGGAA GGGGAAATGG AGGAATGCCC TCCTGTCTGT GTCTGTTCTCT GTGCCACAGC 1800
 TACAGATGCA GAAGTTTCT CTGGATAGCA CACCTCTGAA TGTAATCAT GATAAAATGG 1860
 ATATTGGAA ACTTACTCCT AAGCTGTGAT GTAGGGTGTA TTCTACTTC TGGACTGCCT 1920
 CAATATCAAG GGCTGAGACT TTTGAATGTT GAATATTCGT TGGGTTCAT GTTAAGACGC 1980
 20 CTGTGGTCCA FGAGTGTCT TCAGTGTTC TGTTCCTGAT AAACACITTG AATATTTTTT 2040
 TGTGTTTTTG TTCTCTTTC TGAAGCTGTT CCTCCTTTA AATATTTTA ATCACATTGA 2100
 TAAAACTAT CCTTCATCCA CCTCTGGTTC TACTATAGTT GATTTTTATT TTAATGTTT 2160
 AATTGATTT GATTAAACAC TTAAGTGGAT TTTGGAATAA TAAACCTC TCACCAATTTG 2220
 GCTTTTAAAA AAAAAAAA

25

SEQ ID NO:130 PFH7 Protein sequence:
 Protein Accession #: NP_055199.1

30

1 11 21 31 41 51
 | | | | |
 MLWSGCRRF ARLGLPGL RVLVQTGHR LTSCIDPSMG LNEEQKEFK VAFDFAAREM 60
 APNMAEWDQK ELFPVDVMRK AAQLGFGGVY IQTDVGGSL SRLDTSVFE ALATGCTSTT 120
 35 AYISIHNMCA WMDSFGNEE QRHKFCPLC TMEKFASYCL TEPGSGSDAA SLLTSAKKQG 180
 DHYILNGSKA FISGAGESDI YVVMCRITGGP GPKGISCIVV EKGTPGLSFG KKEKKVGNWS 240
 QPTRAVIDED CAVPVANRIG SEGQGLIAV RGLNGGRINI ASCSLGAHA SVILTRDHLN 300
 VRKQFGEPLA SNQYLQFILA DMATRLVAAR LMYRNAVAL QEERKDAVAL CSMAKLFATD 360
 ECFACNQAL QMHGGYGLK DYAVQQYVRD SRVHQILEGS NEVMRILISR SLLQE

40

SEQ ID NO:131 PFH6 DNA SEQUENCE

Nucleic Acid Accession #: NM_013989
 Coding sequence: 707-1105 (underlined sequences correspond to start and stop codons)

45

1 11 21 31 41 51
 | | | | |
 GCCTGCAGAG AGAGGCACCTT TGCACCACAG ACAGATAGCA AGAAGGGAAA GACAGAGAGT 60
 50 GAGAAAAAAG AGGAGTCAGT CGCTCCTGGG GAAGGGAGAG AGTGAGACTG GGAGAAAAGAG 120
 AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAAC TACCTTAAA 180
 GCACATTTAA AAAAAAATAA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240
 CATAGAGACA ATGAAAGGCT AAAGAAAATT TAAAAATCTC TGCCACAGTC TCATAGGTGC 300
 TTGGAATGTA AAGTAGAACT GCCTGTCTTT AACGGACTCT GACAGAGGTA ACTGGATTAG 360
 55 GGACGAGTAC GCCAGCTTTT TTTTCTTTT TTTTCTTTT TTTAACATCT TAAATCCTGA 420
 AAAAAAATAA AAAAAAATAA AAAAGGCAGC AGCTCCGAAT TGAATGAATT GATGGGCACA 480
 CTCCAACCTGC TGGGCTGGAG AGACTGGACT TAGTCTTGCC ATTTCTGCTT CTTTGAAAGA 540
 GGAGACAACT TGGGCTTCTT TTTAATTTAG TTTTCTTCC CTTCTCCCC CAACCCCAA 600
 CCTTCCCCCT TACCTCCCCC ACCCCCTTTA TCACCACCCC CCTTTTAAAT AAGAGGGTGA 660
 60 AGGGGAACCA GAGCGCACAA GGGAACCTGAC TCAGGAGGCA GAGAAGATGG GCATCCTCAG 720
 CGTAGACTTG CTGATCACAC TGCAAAATCT GCCAGTTTTT TTCTCCAACCT GCCTCTTCTT 780
 GGCTCTCTAT GACTCGGTCA TTCTGCTCAA GCACGTGGTG CTGCTGTTGA GCCGCTCCAA 840
 GTCCACTCGC GGAGAGTGGC GGCAGCATGCT GACCTCAGAG GGAAGTGGCT GCGTCTGGAA 900
 GAGCTTCTCT CTGATGCTCT ACAAACAGGT GAAATGGGT GAGGATGCC CCAATTCAG 960
 65 TGTGTTGATG GTCTCCAGTA CAGAAGGAGG TGACAACAGT GGCAATGGTA CCCAGGAGAA 1020
 GATAGCTGAG GGAGCCACAT GCCACCTTCT TGACTTTGCC AGCCCTGAGC GCCCACTAGT 1080
 GGTCAACTTT GGCTCAGCCA CTGACCTCTC TTTCACGAGC CAGCTGCCAG CCTTCCGCAA 1140
 ACTGGTGGAA GAGTCTTCTT CAGTGGCTGA CTCTCTGCTG GTCTACATTG ATGAGGCTCA 1200
 TCCATCAGAT GGCTGGGCGA TACCGGGGGA CTCCTCTTTG TCCTTTGAGG TGAAGAAGCA 1260
 CCAGAACCAG GAAGATCGAT GTGCAGCAGC CCAGCAGCTT CTGGAGCGTT TCTCTTGCC 1320
 70 GCCCAGTGC CGAGTTGTGG CTGACCGCAT GGACAATAAC GCCAACATAG CTTACGGGGT 1380
 AGCCTTTGAA CGTGTGTGCA TTGTGCAGAG ACAGAAAATT GCTTATCTGG GAGGAAAGGG 1440
 CCCCTTCTCC TACAACCTTC AAGAAGTCCG GCATTGGCTG GAGAAGAATT TCAGCAAGAG 1500
 ATGAAAGAAA ACTAGATTAG CTGGTTAAAG GTATGATTAT AAGAGAGCTT ATTGTTTTAA 1560
 AAAGTTATAT AAAGGCAAGG AAATTAAGAA CTGAATCCAT ATTTCAACAG AGCCCTATTG 1620
 75 GCTTACTGAA AGACAGGAGT TTATCTATCG GAAGAACATG AATCTCTAAC AGCTCCATAC 1680
 TTCTTCACT ACTCAAATGG CATTGGGCTG AGTAAGTAAC CATATCACT CTCTCTTAG 1740
 TAAAAAGCCC TATGTGAAAA GATCCCAAGA TGGAGAGGAA GAAACGCTAA TTCAGCATGT 1800
 GTTCATTCTG CATTGAGAGG GAAGTGATAC ATCTGATGCA TGCTTTGAGA CCAGAAGAAA 1860
 AGACTTACCT GAATAATTAC TACATTAGGG AAGCTACTGT CTACGTTAAG ATAAAGGGA 1920

TTGCCCTTGGC TCTATTTGGC ATGGATGGAG CCCAGTTGGA AAATTCCTCAA ATATTACAAC 1980
 AAGTCCTTGA ACCCAGGCCA TGTGGTTAGA CGTIGGTGTT AAGGTITAGC CTIATGTTAG 2040
 AGTCATTTCCT GATGTTCAG CTCTAGCCA TGTAGTGCTC TCAGTCTTCA TACCCAGAA 2100
 5 ATTATTTGGA TATTTGTAGA TACCGAGAAT GATCCCTCAG TCTGAGAGGT TAGAATGATC 2160
 ATCTGTAATC TGAGGGTTAA TTCTAGGCA GGTGGAGAGA GTGGTAAAAA AGAAATGAAA 2220
 TTGACAAGCT AGGAAAGAGG AGGCAGAAAAG ATTTGGAAAA TTCACAGAGT TTCACCTTA 2280
 AGCTGTAGAG AGTGGGTCAC ATTTGTTAGC CACGGAAACA TAGAAACATA CACAAGGCCA 2340
 GAAAAAGAG AAGGAGCTCA ACTAAAAGTG GCATAGAGAA TACACATATA AAAACAATAT 2400
 10 ATTTGTCATA TGCTCCTAGA GAGGAGAAAAG GGGTGATTGA AAGAAAAAAA AATACTTAAA 2460
 TATTTGTAAT TGTGAGGGGT TTCTTTTGA AATAATTACT TTGAACCAT GTATGTGGTA 2520
 TGTATATTTT CAGTGGGTTA ATTATACCCC ATGATACCTA TTAAGGAAA ACCAGTGGGT 2580
 CTGGTGGTGC TGGTCTTTTC CTCCCCATTC CTACAATTC TATGTGGCCC AAGTCATTCC 2640
 TAATCTTGGT CTCTATAGCA GTGTCTCTC TGAATGCTGA GCTGAAGAAA TTATACGTAC 2700
 15 ATACACACAT ACATACATAC ATACAAATAT ATGTATATAT ATTCTCAGCT GCTGCGGGAG 2760
 GTAGGTACCA TGGCCATTCA GCACAGCCTT GATTTCCTCC CAAAGTAGGT GAGCTATAGT 2820
 GAAGAATAGG TGCAACAAA CAAGCTTACT TCCATTGCAA AATAGAAGAA GAGGAAGTTA 2880
 GAGATAACT TGTCAACTA TTTGGAGGC TTGTATATA GGCAACCCCC GGTATATCAT 2940
 GGAAATTTCA TTGACATTG AATTGGGACT TGGATCTTCC CTGGTCCCC TTAGCTGAGG 3000
 20 TTAGTAATC TAAAGTCCCT ATAGTATAIG ATTATAATGC TATTTTAAAA AATATATATA 3060
 TAAAAATATT TTTCCTTTT AAAATAGACA CTATAGTTT ACCCATAAGT AATATTTAAA 3120
 GATTATAGCT CCAAAAAGAA TGGACCAACC ACTTTCGTAT CATAATTCTT TTITGGTAAA 3180
 TATGAGACTA TTATGAAATC ATAGTATATG ATGTATTTA AAGGTACAAT CAAAGGATCT 3240
 TTTGTCCATT CCATTAATAA CTGAATAAAA AATAAATAA ATGGATAGAA AAAAATAAAA 3300
 25 GTTGAATAA CATCTTAAA CTAGTTGCTT GAAATGAGAA AAGAGTGAGA ACTAGGTGTG 3360
 CAAGAACCAA ACGTATTTTA TTITATTTT TAAATGGGAG CAACATATCA GTCGTGTCAC 3420
 CAGCTGGTAT ATTTGTGAAA TATIAAGCT CCAATGGGAC TGATTTTTC TGGCAACATC 3480
 AGCTTTCTAA TGTCTTAAA TCTATAAAA CCACCCACA AGAAACAAAG CAAATTTTCA 3540
 TATCTAATGA GTTGCTGGA AATCATATTG AGAATAATTA TTTCAGATTC CTCAGTTGTT 3600
 30 AACTTCTACA TCAAGGGCT TATCTCTGCC CCCATTGATT TTAACTCTA AAATGGGTGTG 3660
 AGATTACTG TGAACCCCTA AAGCAGTAAA ATAAAAACC TGGTGCAGC ACATTACAC 3720
 TGTGTCTCT AAAATTCCTT TTITCTCT ATGTACGATA AAGTAACAGT ATGCAGATA 3780
 AGCCGGTGGG GGGATGAGAT TAGGCTGAGG CAGTGCTAGT CACTGGGGG AAAAGGATGA 3840
 TGGAAAAATC ACCAGTTGT GCTATATTT TAAAGAAGGA GGTCTTTAT GTGTGCAGAC 3900
 35 AATTCCTCCT GAGGTTAGCC CAATGGAGAA ATGAAGCAGA GGAAGGAAAC ATAGAAAGAC 3960
 ATGGGCTATC AGGGAGGAA ATGTTCAATA GAACATGCAA GAATTTCTGG AAGAAAGGCT 4020
 GTGGAAGGGC CAATGGAGAA AATGAATGGA CAAAGCTCAG GAATCCCTAC GCTATGTAGA 4080
 ATGTTCTTGG TGTATCAGG GTTAAGCCCT GTAATTATGT AACCTATTTA TCGCAACATG 4140
 AATTTTATG ATTTCTTGTG ATGTATCTT TTATGAAAT AACAGAAGT CATTATTTTG 4200
 40 AGGTAGAGGA AATCAATGC TTTATCTGAT ATGCTGAGAA ATTATTAGAT TGCCAATACT 4260
 CATGTGCGTT TCATGTGTTT TATAAGGTTT GTTCCTTTGA AGAATTGTAG TTCTTAGTCC 4320
 CACAGGAAAA TGTGTATCTA TTATATATC ATAGTATAAA TCTATGATAT ATTTATATCA 4380
 TATATAAAG TCTGAGTTCT CTTCCTTAGT CCCTAATCAT GTTCTCCCA TAGGCTGTGT 4440
 TTACATGAG CTATCGGTTT AGCCTTTTAA GCTTCATTAG CTGTCTATT ATTGAAATAG 4500
 45 TTTCCAAGAA ATTTAGATA TTATCATAAC ATCTGGGTCT ACTCAAAAC TATTGTTTG 4560
 AAAGACTTAT GTCTGGACC TATCAAAAAC TGACTTTATT TATTGCTTAG TGAATAACT 4620
 AGTGGGATCA ACGTGAATT TCTGAATGG GCATGAATGG AGATGCCCGC ACAGTAATGT 4680
 AGAAATGTTT CATACAGCTA TAAAAATGTA ACTGACCTCC TTAGAGGCGA ATTAGTAACT 4740
 GTTCCTACTT TGTATAGTA AGTGACAGTC ACTTAACTTA CATGACTTTC TTTTTCACA 4800
 50 TIGGGTCTCT GGTCTGTGT CTACCTCA TTTATAGCAC GTCTCCTTGA TTTTGGTAG 4860
 TATCAACTTC CAGTGATCT GTTCAGTTAA GTTCTCTCC CGTTAACCGA GAAGTGCTTA 4920
 TTCTCTATC ACGTGGGAA GAATAGCCTA TTGTCTTTA TTTGCTTGA GTGTATTTA 4980
 CTATTTGGGC TCTGAAATAA AAATTATGAA ATATGGTGAG GTCACATGTT GGTGCTGCCT 5040
 TGCTGCATAA AATCTTAGGA GGGCAGGTTA GGAGACAGTT ATGTATGGCC TTTCGGGAAA 5100
 55 ATCAAAAGGG TGGGATTACA AGGTGTCTC TCAGGCATGC CCTATGGGC CCTATGTGGA 5160
 AGCAAGAAGA ATGACTGAT TTACAGGACT TCTCTTATG TCAATCTTAA GAGGATGGAT 5220
 GAATCTGGAC ATTTGTTCCA CCGACCTCT GACTGATGGT TTGAAAAATA ACTTTAATTA 5280
 GGATCATATG ACCATTGAAA AAGGAAAAAT GTAGACTCTG ACTTCGCTCC CACTGAAGGA 5340
 TTAATGAAAA CCTTACTAG CATTTAGAGC TTTTCAGAAC ATCCCCACTG TCATGTGTCT 5400
 60 CAGCAGTGGG GACTGCAAGT AAGGCTTTA ATTTAGGAG GTTTTTTTTT TTTTTTTTT 5460
 TTCCCTTAAA TGGTATGGCC AAAAGTCAGA GTTAAATAT ATATAGTTAG ATTCCAACCT 5520
 CCTCCTTCA TCTAAAAATA GAATCCAAAC CCATCTTCA TATATGCTC CAGAATGGGG 5580
 CTTAAGTACC AATCTCTGCT TGTCAATGGG CACAATCTTG GTCATGCTC GAGGCTCTCT 5640
 AAGAAAAGAG AGGATCTAGG ATGGGAGAGC TAGAAAGTTG CTAAGTGGGA AGAACAAGGC 5700
 65 CCTGAGGGGT TGGTCTACCA ATCTGGGAAG ATTTGAAAAA AAATCTCTCG CAACTGAAGG 5760
 AAGGCTGAAG GCTGCTGCAA GTCATTGAGT GACTTTAGGA TGAGCAAAAAC ATTGGGCCAC 5820
 TTCCTAATGC CCTATGTGTA TAGTACCAGA AGCAAGGTCT CAGACTTAAC AGACCCAGCT 5880
 CTGTTCCAA GTGAGTTGTA ACCAATAGAA AGCAAAACATG TGCAGATATC CAAACAAGAC 5940
 TGCTCATGCA AGTCGGGGCT GGCTACCCGT CTTAGGCAGC AACAGCAGAG CTCAGGGGAG 6000
 70 CTTATTCAAT ATTTACTGAG ACTTCGAAGA CCCAGCAGAT GTTTAATGAA GTCACATTTT 6060
 TGGCTCAAAC CCTCCACTTC TCCCCTCCC CTCAAAAAGC CAACAGGTAA ACACATAAAT 6120
 GAAAGAAACC CACAGAGGGG GATGGGAAAT AAAGAAAAAT CTCTCAAGAC TTCTCCAGGC 6180
 CCATGTCACT GGTTCAGGTG GTTTTATGT GTATTAGGAT TGGGGGATGT GAAGAAAAATA 6240
 GTATCCAGTA TTTTATAACC AAAGCAATTA AATGATATTG GGGTAGGGAA TGTGGCCAG 6300
 TTTTGTITAG TTTTGCCATC ACATGTGTC CAGAGCTCA CCTAGCCCCA AGTAATCGGG 6360
 75 CGCCCCAAG GTGAGTACAG AGATGTGCCA GAGTTGACCC AGTGTGCGGA TGATAACTAC 6420
 TGACGAAAGA GTCATCGACC TCAGTTAGTG GTTGGATGTA GTCACATTAG TTTGCTCTC 6480
 CCCATCTTTG TCTCCCTGGC AAGGAGAATA TGGGGGACAT GATGCTAAGA GCCTGGGTA 6540
 AATGTGGTGA GAATGCACGC GTGCATATGC TACACATATG TGCTTCTCAG TTGCAGAAAA 6600
 TGAAGTCTT TGGGAGATTA TCAGTAGAAA GAGTGTATC ATATTGGTGC TGAGTGTAT 6660

GTGTGCTTAT ACAATTGTCTT CTTGTATTTT AATAAACTTT GAATAAAAGA ATAAAAAAA 6720
 AAAAAAAAAA AAAAA

5 **SEQ ID NO:132 PFH6 Protein sequence:**
 Protein Accession #: NP_054844.1

1 11 21 31 41 51
 10 MGILSVDLLI TLQLPVFFS NCLFLALYDS VILLKHHVLL LSRKSTRGE WRRMLTSEGL 60
 RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDNSGN GTQEKIAEGA TCHLLDFASP 120
 ERPLVVNFGS ATXPPFTSQL PAFRKLVEEF SSVADFLVY IDEAHPSDWG AIPGDSLSF 180
 EVKKHQHQED RCAAQQLLE RFLSPQCRV VADRMNNAN IAYGVAERFV CIVQRQKIAY 240
 15 LGGKGPFYSN LQEVHRHLEK NFSKRXXKTR LAG

SEQ ID NO:133 PFH5 DNA SEQUENCE

20 Nucleic Acid Accession #: NM_001141
 Coding sequence: 72-2102 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 25 CAGGCGTGTC CCAGGGGGAG CCCCGCTCTG CAGCCCTGTG CGCCGTAGAG AGCTGGACTT 60
 AGGCTGGCAG CATGGCCGAG TTCAGGGTCA GGGGTGCCAC CGGAGAAGCC TTCGGGGCTG 120
 GCACATGGGA CAAAGTGCTC GTACGATCG TGGGGACCCG GGGAGAGAGC CCCCCACTGC 180
 CCCTGGACAA TCTCGGCAAG GAGTTCATCT CGGGCGCTGA GGAGGACTTC CAGGTGACGC 240
 TCCCGGAGGA CGTAGGCCGA GTGCTGCTGC TGGCGGTGCA CAAGGCGCCC CCAGTGCTGC 300
 30 CCCTGCTGGG GCCCTGGCC CCGGATGCCT GGTTCGTCCG CTGGTCCAG CTGACACCGC 360
 CGCGGGGCGG CCACCTCTCT TCCCCCTGCT ACCAGTGGCT GGAGGGGGCG GGGACCCCTG 420
 TGCTGCAGGA GGGTACAGCC AAGGTGTCCT GGGCAGACCA CCACCTGTG CTCCAGCAAC 480
 AGCGCCAGGA GGAGCTTCA GCGCGGCAGG AGATGTACCA GTGAAGGCT TACAACCCAG 540
 35 GTTGGCCTCA CTGCTGGAT GAAAAGACAG TGAAGACTT GGAGCTCAAT ATCAATACT 600
 CCACAGCCAA GAATGCCAAC TTTATCTAC AAGCTGGCTC TGTTTTGCA GAGATGAAAA 660
 TCAAGGGGTT GCTGGACCGC AAGGGGCTCT GGAGGAGTCT GAATGAGATG AAAAGGATCT 720
 TCAACTTCCG GAGGACCCCA GCAGCTGAGC ACGCATTGA GCACTGGCAG GAGGATGCCT 780
 TCTTCGCTC CAGTTCCTG AATGGTCTCA ACCCTGTCTT GATCCGCCGC TGCTACTACC 840
 TCCCAAAGAA CTTCCTCGTC ACTGATGCCA TGGTGGCTC ATTGTGGGT CCTGGGACCA 900
 40 GCTTGCAGGC TGAGCTAGAG AAGGGCTCCC TGTCTTGGT GGATCACGGC ATCTCTCTG 960
 GCATCCAGAC CAATGTCAAT AATGGGAAGC CGCAGTCTC TGGCGCCCCA ATGACCCCTG 1020
 TATACAGAG CCCAGGCTGC GGGCCGCTGC TGCCTCTCG CATCCAGTC AGCCAGACCC 1080
 CCGGCCCAAA CAGCCCCATC TTCCTGCCA CTGATGACAA GTGGGACTGG TTGCTGCCA 1140
 AGACCTGGGT GCGCAATGCC GAGTCTCTCT TCATGAGGC CCTACGCCAC CTGCTGCACT 1200
 45 CACATCTGCT GCCTGAGGTC TTCACCTGG CTACCTGCG TCAGTGCCT CACTGCCACC 1260
 CTCTCTCAA GCTGCTGATC CCGCACACC GATACACCT GCACATCAAC AACTCGCCC 1320
 GGGAGCTGCT TATCGTGCCA GGGCAGGTGG TGGACAGGTC CACAGGCATC GGCATTGAAG 1380
 GCTTCTCTGA GTTGATACAG AGGAACATGA AGCAGCTGAA CTATCTCTC CTGTGCTGC 1440
 50 CTGAGGATAT CCGGACCCGA GGAGTTGAAG ACATCCAGG CTACTACTAC CGTGATGATG 1500
 GGATGCAGAT TTGGGGTGCA GTGGAACGCT TTGTCTCTGA AATCATCGGT ATCTACTACC 1560
 CAAGTGATGA GTCTGTCCAA GATGACAGAG AGCTCCAGGC CTGGGTGAGA GAGATCTTCT 1620
 CCAAGGGCTT CCTAAACGAG GAGAGCTCAG GTATCCCTTC CTACTGGAG ACCCGGGAAG 1680
 CCCTGTGCA GTATGTCAAC ATGGTGATAT TCACCTGCTC AGCCAAGCAT GCGGCTGTCA 1740
 55 GTGCAGGGA GTTTGACTCC TGTGCTTGA TGCCCAACCT GCCACCCAGC ATGCAGCTGC 1800
 CACCACCCAC CTCCAAAGGC CTGGCAACAT GCGAGGGCTT CATAGCCACC CTCCCACCTG 1860
 TCAATGCCAC ATGTGATGTC ATCCTTGCTC TCTGTTGCT GAGCAAGGAG CTTGGAGACC 1920
 AAAGGCCCTT GGGCACCTAT CCGGATGAGC ACTTCACAGA GGAGGCCCTT CCGCGGAGCA 1980
 TCGCCACCTT CCAGAGCCGC CTGGCCAGGA TCTCGAGGGG CATCCAGGAG CGGAACCGGG 2040
 60 GCCTGGTGCT GCCCTACACC TACCTAGACC CTCCCTCAT CGAGAACAGC GTCTCCATCT 2100
 AATCCCAAG GGAACACAGG CCCAGATGAC ATCCCTTGA CCACATCGCT CTAGGATAAC 2160
 TGGCACCCAG AGAAAAGGAC TCCTCAGAAA AAACAGGCCC CCATGTGCCT CTCTGGGAC 2220
 AACCAGACTC TGTAACCTAC CCCCACCACC ATACACACAC AAAAAACAG AAACAAATC 2280
 AAAACAGAGA AAGCAGAAAA TCTACCAAGA ACAGAGTCTC AGGACAGAAC CACTGAGTCT 2340
 65 TTTGGAGGCT CCAAGCCTCA AAGTGCCCGC AGAGCCACCC TTGAGGGTTT TGCTAGTTGG 2400
 TTTTGTTTT CGTTTACAGC CGTGGGGGA AGCATAAT CCGCCCCAG GGCCCACTAG 2460
 CATCCACTGA TTGGACCTTA TGGTCACCA ACTCAAGGAC AGCCACCAAG AAGTGGCTGC 2520
 CAAAGAGACT GGGCGCAGTG GCTCATGCC ATAATCCAG CACTTTGGGA GATGGAGGCG 2580
 70 GGAAATCAT TTGAGGTCAG AAGTCAAGG CCAGCCTGGA CGACATAGCG AGACTCCACC 2640
 TCTACCAAAA AATAAAAAAT AAAAAACAAA AAAAAAAAAA AAAAA

75 **SEQ ID NO:134 PFH5 Protein sequence:**
 Protein Accession #: NP_001132.1

1 11 21 31 41 51
 MAEFRVRVST GEAFGAGTWD KVSIVGTR GESPLPLDN LGKEFTAGAE EDFQVILPED 60
 VGRVLLLRVH KAPVPLLLG FLAPDAWFCR WFQLTTPRGG HLLFCYQWL EGAGTLVLQE 120
 GTAKVSWADH HPVLQQRQE ELQARQEMYQ WKAYNPGWPH CLDEKTVEDL ELNIKYSTAK 180

NANFYLQAGS AFAEMKIKGL LDRKGLWRSI NEMKRIFNFR RTPAAEHAFH HWQEDAFFAS 240
 QFLNGLNPVL IRRCHYLPKN FVPTDAMVAS LLPGTSLQA ELEKGSFLV DHGILSGIQT 300
 NVINGKPQFS AAPMTILLYQS PGCGLPLPLA IQLSQTGPN SPIFLPTDDK WDWLLAKTWV 360
 RNAEFSFHEA LTHLLSHLL PEVFTLATLR QLPCHPLFK LLIPHTRYTL HINTLARELL 420
 IVPQVVDVRS TGIGIEGFSH LIQRNMKQLN YSLLCLPEDI RTRGVEDIPG YYYRDDGMQI 480
 WGAVERFVSE IGIYYPDSH SVQDDRELQA WVREIFSKGF LNQESSGIPS SLETREALVQ 540
 YVTMVIPTCS AKHAAVSAGQ FDSCAWMPNL PPSMQLPPPT SKGLATCEGFIATLPPVNAT 600
 CDVILALWLL SKEPGDQRLP GTYPDEHFTS EAPRRSIATF QSRLAQISRG IQERNRGLVL 660
 PYYLDPPLI ENSYSI

SEQ ID NO:135 PFH4 DNA SEQUENCE

Nucleic Acid Accession #: NM_002742

Coding sequence: 236-2974 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GAATTCCTTC TCTCCTCCTC CTCGCCCTTC TCCTCGCCCT CTCCTCCTC CTCGCCCTCC 60
 CCTCCCGATC CTCATCCCCT TGCCCTCCCC CAGCCCCAGG ACTTTTCCGG AAAGTTTTTA 120
 TTTTCCGTCT GGGCTCTCGG AGAAAGAAGC TCCTGGCTCA GCGCTGCAA AACTTTCCTG 180
 CTGCCGCGCC GCCAGCCCCC GCCCTCCGCT GCCCGGCCCT GCGCCCCGCC GAGCGATGAG 240
 CGCCCTCCG GTCTGCGGC CGCCAGTCC GCTGCTGCC GTGCGCGCGG CAGCTGCCGC 300
 AGCGCGCGCC GCACGTGGTC CAGGGTCCG GCCCGGCCCG GCGCCGTCTT TGGCTCCTGT 360
 CGCGGCCCG GTGCGGGGCA TCTCGTTCCA TCTGCAGATC GGCCTGAGCC GTGAGCCGCT 420
 GCTGCTGCTG CAGGACTCGT CCGGGGACTA CAGCTGGCG CAGTCCCG AGATGGCTTG 480
 CTCATTGTC AGTCAGAAAT TCCCTGAATG TGGTTCTAC GGAATGTATG ATAAGATCCT 540
 GCTTTTTCGC CATGACCTTA CCTCTGAAA CATCCTTCAG CTGGTGAAAG CGGCCAGTGA 600
 TATCCAGGAA GCGGATCTTA TTGAAGTGGT CTGTACAGT TCCGCCACT TTGAAGACTT 660
 TCAGATTCGT CCCACGCTC TCTTGTTC TTCATACAGA GCTCCAGCTT TCTGTGATCA 720
 CTGTGGAGAA ATGCTGTGGG GGTCTGTACG TCAAGGTCTT AAATGTGAAG GGTGTGGTCT 780
 GAATTACCAT AAGAGATGTG CATTTAAAA ATCCCAACAAT TGCAGCGGTG TGAGGCGGAG 840
 AAGGCTCTCA AACGTTTCCC TCACTGGGGT CAGCACCATC CGCACATCAT CTGCTGAACT 900
 CTCTACAAGT GCCCCTGATG AGCCCCCTCT GCAAAAATCA CCATCAGAGT CGTTTATTGG 960
 TCGAGAGAAG AGGTCAAAT CTCAATCATA CATTGGACGA CCAATTCACC TTGACAAGAT 1020
 TTTGATGTCT AAAGTAAAG TGCCGCACAC ATTTGTCATC CACTCTACA CCCGCCCCAC 1080
 AGTGTGCCAG TACTGCAAGA AGCTTCTGAA GGGGCTTTTC AGGCAAGGCT TGCAGTGCAA 1140
 AGATTGCAGA TTCAACTGCC ATAAACGTTG TGCACGAAA GTACCAACA ACTGCCITGG 1200
 CGAAGTGACC ATTAATGGAG ATTGCTTAG CCCTGGGGCA GAGTCTGATG TGGTCAATGA 1260
 AGAAGGGAGT ATGACAATG ATAGTAAAG GAACAGTGGG CTCATGGATG ATATGGAAGA 1320
 AGCAATGGTC CAAGATGAG AGATGGCAAT GGCAGAGTGC CAGAACGACA GTGGCGAGAT 1380
 GCAAGATCCA GACCCAGACC ACGAGGACGC CAACAGAAC ATCAGTCCAT CAACAAGCAA 1440
 CAATATCCCA CTACATGAGG TAGTGAGTC TGTCAAACAC ACGAAGAGGA AAAGCAGCAC 1500
 AGTCATGAAA GAAGGATGGA TGGTCCACTA CACCAGCAAG GACACGCTGC GGAACCGGCA 1560
 CTATTGGAGA TTGGATGACA AATGTATTAC CCTCTTCAG AATGACACAG GAAGCAGGTA 1620
 CTACAAGGAA ATTCCTTTAT CTGAAATTTT GTCTCTGAAA CCAGTAAAAA CTTCAGCTTT 1680
 AATTCCTAAT GGGGCCAATC CTCATGTGTT CGAAATCACT ACGGCAAAATG TAGTGTATTA 1740
 TGTGGGAGAA AATGTGGTCA ATCCTTCCAG CCATCACCA AATAACAGTG TTCTACCCAG 1800
 TGGCGTTGGT GCAGATGTGG CCAGGATGTG GGAGATAGCC ATCCAGCATG CCCTTATGCC 1860
 CGTCATTCCT AAGGCTCCT CCGTGGGTAC AGGAACCAAC TTGCACAGAG ATATCTCTGT 1920
 GAGTATTTCA GTATCAAAT GCCAGATTCA AGAAATGTG GACATCAGCA CAGTATATCA 1980
 GATTTTCTCT GATGAAGTAC TGGGTCTGG ACAGTTTGGG ATTGTTTATG GAGGAAAAA 2040
 TCGTAAACA GGAAGAGATG TAGCTATTAA AATCATTGAC AAATTACGAT TTCCAACAAA 2100
 ACAAGAAAGC CAGCTTCGTA ATGAGGTGAC AATCTACAG AACCTTCATC ACCTGGTGT 2160
 TGTAAATTG GAGTGTATG TTGAGACGCC TGAAGAGTG TTTGTTGTTA TGGAAAAACT 2220
 CCATGGAGAC ATGCTGGAAG TGATCTTGT CAGTGAAAAG GGCAGGTTGC CAGAGCACAT 2280
 AACGAAGTTT TTAATTAATC AGATACTCGT GGCTTGGCG CACCTTCATT TAAAAATAT 2340
 CGTTCACGTG GACCTCAAC CAGAAAATGT GTTGCTAGCC TCAGCTGATC CTTTCTTCA 2400
 GGTGAAACTT TGTGATTTTG GTTTGCCCC GATCATTGA GAGAAGTCTT TCCGGAGGTC 2460
 AGTGGTGGGT ACCCCCGCTT ACCTGGCTCC TGAGGTCCTA AGGAACAAGG GCTACAATCG 2520
 CTCTCTAGAC ATGTGTCTG TTGGGGTCAT CATCTATGTA AGCCTAAGCG GCACATTCCC 2580
 ATTTAATGAA GATGAAGACA TACACGACCA AATTCAGAAT GCAGCTTTC TGTATCCACC 2640
 AAATCCCTGG AAGGAAATAT CTCATGAAGC CATTGATCT ATCAACAATT TGCTGCAAGT 2700
 AAAAAAGAGA AAGCGCTACA GTGTGGATA GACCTTGAGC CACCCTTGGC TACAGGACTA 2760
 TCAGACCTGG TTAGATTGCG GAGAGCTGGA ATGCAAAATC GGGGAGCGCT ACATCACCCA 2820
 TGAAAGTGT ATCTGAGGT GGGAGAAGTA TGCAGGCGAG CAGCGGCTGC AGTACCCAC 2880
 ACACCTGATC GAATCCAAGT CTAGCCACAG TGACACTCCT GAGACTGAAG AAACAGAAAT 2940
 GAAAGCCCTC GGTGAGCGTG TCAGCATCCT CTGAGTTCCA TCTCTATAA TCTGTCAAAA 3000
 CACTGTGAAA CTAATAATA CATACGGTCA GGTTTAACAT TTGCCCTTGA GAACCTGCCAT 3060
 TATTTTCTGT CAGATGAGAA CAAAGCTGTT AAAGTGTAG CACTGTTGAT GTATCTGAGT 3120
 TGCCAAGACA AATCAACAGA AGCATTGTGA TTTTGTGTGA CCAACTGTGT TGTATTAACA 3180
 AAAGTTCCCT GAAACACGAA ACTGTATTAT GTGAATGATT CATGTTATAT TTAATGCATT 3240
 AAACCTGTCT CCATGTGCC TTTGCAAAAT AGTGTTTTC TACTGGAGC TTCATTTTGG 3300
 TAAGAGACAG AATGTATCTG TGAAGTAGTT CTGTTGGTG TGTCCATTG GTGTTGTCAT 3360
 TGTAAACAAA CTCTTGAGAA GTCGATTATT TCCAGTGTTC TATGAACAAC TCCAAACCC 3420
 ATGTGGGAAA AAAATGAATG AGGAGGGTAG GGAATAAAAT CCTAAGACAC AAATGCATGA 3480
 ACAAGTTTCA TGAATCTT TGCTGCTGCT GTGTGCTCA GTATATTTAA 3540
 ACTCAAGACA ATGCACCTAG CTGTGCAAGA CCTAGTGTCT TTAAGCCTAA ATGCCTTGA 3600
 AATGTAAACT GCCATATATA ACAGATACAT TTCCCTCTTT CTATAATAC TCTGTGTAC 3660

TATGGAAAAT CAGCTGCTCA GCAACCTTTC ACCTTTGTGT ATTTTCAAT AATAAAAAAT 3720
ATTCTGTGCA AAAAAAAAAA AA

5 SEQ ID NO:136 PFH4 Protein sequence:
Protein Accession #: NP_002733.1

10 1 11 21 31 41 51
MSAPPVLRPP SP LLPVAAAA AAAAAALVPG SGPGAPFLA PVAAPVGGIS FHLQIGLSRE 60
PVLLQDSSG DYSLAHVREM ACSIVDQKFP ECGFYGM YDK ILLFRHDP TS ENILQLVKAA 120
SDIQEGDLIE VVLSRSATFE DFQIRPHALF VHSYRAPAF C DHC GEM LWGL VRQGLKCEGC 180
15 GLNYHKRC AF KIPNNCSGVR RRRLSNVSLT GVSTIRTS SA ELST SAPDEP LLQKSPSESF 240
IGREKRSNSQ SYIGRPIHLD KILMSKVKVP HTFVHSYTR PTVCQYCKKL LKGLFRQGLQ 300
CKDCRFNCHK RCAFKNVNNC LGEVTINGDL LSPGAESDVV MEEGSDNDNS ERNSGLMDDM 360
EAMVQDAEM AMAECQND SG EMQDPDPDHE DANRTISP ST SNNIPLMRVV QSVKHTKRKS 420
STVMKEGWMV HYTSKDTLRK RHYWR L DSKC ITLFQNDTGS RYYKEIPLSE ILSLEPVKTS 480
20 ALIFNGANPH CFEITANVV YYVGENVVNP SSPSPNNSVL TSGVGADVAR MWELAIQH AL 540
MPVIPKGSSV GTGTNLHRDI SVSISVSNQC IQENVDISTV YQIFPDEV LG SGQFGIVYGG 600
KHKRTGRDVA IKIIDLKRF PKQESQLRNE VAILQNLHHP GVVNLECMFE TPERV FV VME 660
KLHGDMLLEMI LSSEKGR LPE HITKFLITQI LVALRHLHFK NIVHCDLKPE NVLLASADPF 720
PQVKLCDFGF ARIGEKSF RSVVGTPAYL APEVLRNKGY NRS LDMWSVG VHYVSLSGT 780
25 PFNEDEDIH DQIGNAAMFY PPNPWKEISH EADILNNLL QVKMRKRYSV DKTL SHPW LQ 840
DYQTWLDLRE LECKIGERYI THESDDL RWE KYAGEQRLQY PTHLINPSAS HSDTPETEET 900
EMKALGERVS IL

30 SEQ ID NO:137 PFH3 DNA SEQUENCE

Nucleic Acid Accession #: X95425
Coding sequence: 712-3825 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
AATGGTCAGT CAATACATTA TAACATAATA CACCAAATGC TAGAATAGAA GGGGAGGGGG 60
GCACACATAA TGACTCACTG CTGGAAGAAG GGTGCATCAG TGAATTAAAA AATGTCCCTC 120
CCCTCTTCAG CACTCAGCGC GCAGCTATTT CCTCTGCCA GTCTCTTGA ACTCTGGATC 180
40 TTGTCTTTG CTCGCTGCTC TCCTGTTTTT CATCTCCAC ATTTTCTCAA TCCTCTTTCT 240
TTATCCTTAG CCACCTGCT TTTTCTCTCC TTTTAAAAA AATCGGAGAT TTCGTCTTAA 300
AATGATTTGT CTTCCTTACC TTCGTCCATT TCAACACTGA AGGCTGCAAA GAACTTCACC 360
TTTCCCTAG TGGTATTTAA AAATTTCTAA TCCGTAAAAA GTCTTTTGA AAGGCAAAAGG 420
AACAGGACCC AGACCCTCTC GACACCCTTG ATCCGAGTCA GATCTGCACT AGCAACCAGA 480
45 ACTAATATTT CATTTAACCC ACCAAAAGGG GGAGGCGAGA GGAGCCAGAA GCAAACCTCA 540
TCTGTCTCAG ACGGATCCGT GGTTCCTACA TTTGGAGGAG CCGCGTGTC GAAGGCGTAG 600
GACCCCAAGG GGGGACAAGG AGGACTCCCG AGTCTCCTT CTCCGCTCTC CGAGACCGAA 660
GAGGTGGACT GAGCGCTCG GGACAGCGGC ACCGGAGGAG GCTCGGAGAA GATCGGGGGC 720
TCGGGGCCCC GGGGTGCGGG ACACCGGCGG CCCCAGCG GCGGCGGCGA CACCCCATC 780
50 ACCCCAGCGT CCTTGGCGGG CTGCTACTCT GCACCTCGAC GGCTCCCTC CTGGACGTGC 840
CTTCTCTGT GCGCGCACT CCGGACCTC CTGGCCAGCC CCAGCAACGA AGTGAATTTA 900
TTGGATTAC GCATGTGTC GGGGGACCTG GGATGGATTG CTTTTCCAAA AAATGGGTGG 960
GAAGAGATTG GTGAAGTGA TGA AATTAAT GCCCTATCC ACACATACCA AGTATGCAAA 1020
GTGATGGAAC AGAATCAAG TAACTGGCTT TTGACCAATT GGATCTCCAA TGAAGGTGCT 1080
55 TCCAGAACTC TCATAGAACT CAAATTTACC CTGCGGGACT GCAACAGCCT TCCTGGAGGA 1140
CTGGGGACCT GTAAGGAAAC CTTAATATG TATTACTTTG AGTCAGATGA TCAGAATGGG 1200
AGAAACATCA AGGAAAACCA ATACATCAAA ATTGATACCA TTGCTGCCGA TGA AAGCTTT 1260
ACAGAACTTG ATCTTGGTGA CCGTGTATG AAATGAATA CAGAGGTCAG AGATGTAGGA 1320
CTCTAAGCA AAAAGGGAAT TTATCTTGCT TTCAAGATG TTGGTGCTTG CATGTGCTCTG 1380
60 GTTCTGTGC GTGTATACTA TAAAAAATGC CCTTCTGTGG TACGACACT GGCTGTCTTC 1440
CCTGACACCA TCATCGGAGC TGATCTCTCC CAATGTCTCG AAGTGTCAAG CTCCTGTGTC 1500
AACCATCTG TGACCGATGA ACCTCCAAA ATGCACTGCA GCGCGAAGG GGAGTGGCTG 1560
GTGCCATCG GGAATATGCAT GTGCAAGGCA GGATATGAAG AGAAAAATGG CACCTGTCAA 1620
GTGTGCAGAC CTGGGTCTT CAAAGCCTCA CTCACATCC AGAGCTGCGG CAAATGTCCA 1680
65 CCTCAGATT ATACCATGA GGAAGCTTCA ACCTCTTGTG TCTGTGAAAA GGATTATTTT 1740
AGGAGAGAGT CTGATCCACC CACAATGGCA TGCACAAGAC CCCCCTCTGC TCCTCGGAAT 1800
GCCATCTCAA ATGTTAATGA AACTAGTGT CTTCTGGAAT GGATCCGCC TGCTGACACT 1860
GGTGAAGGA AAGACGTGTC ATATTATAT GCATGCAAGA AGTGCAACT CCATGCAAGT 1920
GTGTGTGAGG AGTGTGGCGG TCATGTCAAG TACCTTCCCC GGCAAGCGG CCTGAAAAAC 1980
70 ACCTCTGTGA TGATGTGGA TCTACTCGCT CACACAACT ATACCTTGA GATTGAGGCA 2040
GTGAATGGAG TGICCGACTT GAGCCAGGA GCCCGGCAGT ATGTGTCTGT AAATGTAACC 2100
ACAAATCAAG CAGCTCCATC TCCAGTCACC AATGTGAAAA AAGGGAAAAAT TGCAAAAAAC 2160
AGCATCTCTT TGTCTTGGCA AGAACCAGAT CGTCCCAATG GAATCATCCT AGAGTATGAA 2220
ATCAAGCATT TTGAAAAAGGA CCAAGAGACC AGCTACACGA TTATCAAATC TAAAGAGACA 2280
75 ACTATTACTG CAGAGGGCTT GAAACAGCT TCAGTTATG TCTTCCAAAT TCGAGCACGT 2340
ACAGCAGCAG CGATGGTGT CTTCAGTCA AGATTGAGT TTGAAACCAC CCCAGTGT 2400
GCAGCATCCA GCGATCAAG CCAGATTCTT GTAATTGCTG TGCTGTGAC AGTAGGAGTC 2460
ATTTGTGTTG CAGTGTGTTAT CGGCGTCTC CTCAGTGGA GTTGCTGCGA ATGTGGCTGT 2520
GGGAGGGCTT CTCCCTGTG CGCTGTGCC CATCCAATCC TAATATGGCG GTGTGGCTAC 2580
AGCAAAGCAA ACAAAGATCC AGAAGAGGAA AAGATGCATT TTCATAATGG GCACATTAAA 2640

CTGCCAGGAG TAAGAACTTA CATTGATCCA CATACCTATG AGGATCCCAA TCAAGCTGTC 2700
 CACGAATTGG CCAAGGAGAT AGAAGCATCA TGTATCACC AITGAGAGAGT TATTGGAGCA 2760
 GGTGAATTGG GTGAAGTTTG TAGTGGACGT TTGAACTAC CAGGAAAAAG AGAATTACCT 2820
 GTGGCTATCA AAACCCCTAA AGTAGGCTAT ACTGAAAAGC AACGCAGAGA TTTCTAGGT 2880
 5 GAAGCAAGTA TCATGGGACA GTTTGATCAT CCTAACATCA TCCATTTAGA AGGTGTGGTG 2940
 ACCAAAAGTA AACCAAGTAT GATCGTGACA GAGTATATGG AGAATGGCTC TTTAGATACA 3000
 TTTTGAAGA AAAACGATGG GCAGTTCAC TGTATTGAGT TGTGTCGAT GCTGAGAGGT 3060
 ATCTCTGAC GAATGAAGTA CCTTCTGAC ATGGGCTATG TGCATAGAGA TCTGTCTGCC 3120
 10 AGAAACATCT TAATCAACAG TAACCTTGTG TGCAAAAGTG CTGACTTTGG ACTTTCCCG 3180
 GTACTGGAAG ATGATCCCGA GGCAGCCTAC ACCACAAGGG GAGGAAAAAT TCCAATCAGA 3240
 TGGACTGCC CAGAAGCAAT AGCTTTCCGA AAGTTTACT CTGCCAGTGA TGTCTGGAGT 3300
 TATGGAATAG TAATGTGGGA AGTTGTGTCT TATGGAGAGA GACCTACTG GAGATGACC 3360
 AATCAAGATG TGATTAAGC GGTAGAGGAA GGCTATCGTC TGCCAAGCCC CATGGATTGT 3420
 15 CCTGCTGCTC TCTATCAGTT AATGCTGGAT TGCTGGCAGA AAGAGCGAAA TAGCAGGCC 3480
 AAGTTTGATG AAATAGTCAA CATGTTGGAC AAGCTGATAC GTAACCCAAG TAGTCTGAAG 3540
 ACGCTGGTGA ATGCATCTG CAGAGTATCT AATTATTGG CAGAACATAG CCACTAGGA 3600
 TCTGGGGCTC ACAGATCAGT AGGTGAATGG CTAGAGGCAA TCAAGATGGG CCGGTATACA 3660
 GAGATTTTCA TGGAAAAATG ATACAGTTCA ATGGACGCTG TGGCTCAGGT GACCTGGAG 3720
 GATTGGAGC GGCTTGGAGT GACTCTTGTG GGTACCCAGA AGAAGATCAT GAACAGCCTT 3780
 20 CAAGAAATGA AGGTGCAGCT GGTAAACGGA ATGGTGCCAT TGTAACCTCA TGTAATGTC 3840
 GCTTCTTCAA GTGAATGATT CTGCACTTTG TAAACAGCAC TGAGATTAT TTTAACAAAA 3900
 AAA

25

SEQ ID NO:138 PFH3 Protein sequence:
 Protein Accession #: CAA64700.1

30

35

40

45

50

1 11 21 31 41 51
 MRSGPRGAG HRRPPSGGG TPITPASLAG CYAPRRAPL WTCLLCAAL RTLLASPSNE 60
 VNLLDSRTVM GDLGWIAFPK NGWEEIGEVD ENYAPIHTYQ VCKVMEQNQN NWLLTSWISN 120
 EGASRIEFL KFTLRDCNSL PGGLGTCKET FNMYYFESDD QNGRNIKENQ YIKIDTIAAD 180
 ESFTDLGD RVMKLNTEVR DVGPLSKKG YLAFQDVGAC IALVSVRVYY KKCPVVRHL 240
 AVFPDITGA DSSQLLEVS SCVNHSVTDE PPKMHCSAEG EWLVPIGKCM CKAGVEEKNG 300
 TCQVCRPOFF KASPHIQSCG KCPHSHSYTHE EASTSCVCEK DYFRRESDEP TMACTRPSSA 360
 PRNAISNVNE TSVFLEWIPP ADTGGRKDV YIACKKCNS HAGVCEECGG HVRYLPRQSG 420
 40 LKNTSVMMVD LLAHTNYTFE IEAVNGVSDL SPGARQYVSV NVTINQAAPS PVTNVKKGKI 480
 AKNSLSWQ EPDRPNGLL EYEIKHFEKD QETSYTIKS KETTITAEG LKPAASVYVFI 540
 RARTAAGYGV FSRREFEFT PVFAASSDQS QIPVAVSVT VGVILLAVVI GVLLSGSCCE 600
 CGCGRASSLC AVAHPIILWR CGYSKAKQDP EEKMHFHNG HIKLPVVRTY IDPHYEDPN 660
 QAVHEFAKEI EASCITIERV IGAGEFGEVC SGRLKLPGRK ELPVAIKTLK VGYTEKQRRD 720
 45 FLGEASIMGQ FDHPNIHLE GVVTKSKPVM IVTEYMENGSLDTFLKKNNG QFTVIQLVGM 780
 LRGISAGMKY LSDMGYVHRD LAARNILNS NLVCKVSDFG LSRVLEDDPE AAYTTRGGKI 840
 PIRWTAPEAI AFRKFTSASD VWSYGIVMWE VVSYGERPYW EMTNQDVIKA VEEGYRLPSP 900
 MDCPAALYQL MLDCWQKERN SRPKFDEIVN MLDKLRNPS SLKTLVNASC RVSNLLAEHS 960
 PLGSGAYRSV GEWLEAKMG RYTEIFMENG YSSMDAVAQV TLEDLRLRGV ILVGHQKIM 1020
 50 NSLQEMKVQL VNGMVPL

55

SEQ ID NO:139 PFH2 DNA SEQUENCE

Nucleic Acid Accession #: NM_016029
 Coding sequence: 78-1097 (underlined sequences correspond to start and stop codons)

60

65

70

75

1 11 21 31 41 51
 CTGCGATCCC GCAGGGCAGC GACGCGACT TGGTGGGGC CGTCTTCTTC CCCCGAGCT 60
 GGGCGTGGC GGCCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120
 TGCTCTGCT CTGGTGCAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
 TATGGCCGA GTGGCAGGA CGACGCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240
 TGACTGGAGC CTCGAGTGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACCTAGGAG 300
 65 TTTCTTGT GCTGTGAGC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAG AGAAGATGCC 360
 TAGAGAATCG CAATTAAAA GAAAAAGATA TACTTGTTTT GCCCTTGAC CTGACCGACA 420
 CTGGTTCCG TGAAGCGCT ACCAAAGCTG TTCTCCAGGA GTTGGTGA ATGACATTC 480
 TGGTCAACAA TGGTGAATG TCCAGCGTT CTCTGTGAT GGATACCAAG TTGGATGCT 540
 ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTG CTGACAAAA TGTGTTCTGC 600
 70 CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660
 TATCTGTACC TCTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTITTTT 720
 ATGGCCTTG AACAGAAGCT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTGCCAG 780
 GACCTGTGCA ATCAATATT GTGGAGAATT CCTAGCTGG AGAAGTACA AAGACTATAG 840
 GCAATAATGG AGACCACTC CACAAGATGA CAACCACTG TGTGTGCGG CTGATGTTAA 900
 75 TCAGCATGGC CAATGATTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
 CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020
 AAAGGATTGA GAACCTTAAAG AGTGGTGTGG ATGCAGACTC TTCTTATTT AAAATCTTTA 1080
 AGACAAAACA TGACTGAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
 AAACATGAAA ACAGCAATCT TCTATGCTT CTGAATAATC AAAGACTAAT TTGATTTTT 1200

ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
AGATTGCCAT GAATCTTGCA AA

5

SEQ ID NO:140 PFH2 Protein sequence:
Protein Accession #: NP_057113.1

10

15

1 11 21 31 41 51
| | | | |
MNWELLWLL VLCALLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60
GIGBEAYQL SKLGVSLVLS ARR VHELERV KRRCLENGNI KEKDILVLPL DLTDTGSHEA 120
ATKAVLQEFQ RIDILVNNGG MSQRLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER 180
KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGPVQSN 240
IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLLVTVLWQY 300
MPTWAWWITN KMGGKRIENF KSGVDADSSY FKIFKTKHD

20

SEQ ID NO:141 PFH1 DNA SEQUENCE

Nucleic Acid Accession #: NM_021614
Coding sequence: 1-1740 (underlined sequences correspond to start and stop codons)

25

30

35

40

45

50

55

1 11 21 31 41 51
| | | | |
ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCGCG TCAGCAACTT GAGCGCGTCC 60
CGCCGGAACC TGCACGAGAT GGACTCAGAG GCGCAGCCCC TGCAGCCCCC CGCGTCTGTC 120
GGAGGAGGTG GCGGCGCGTC CTCCTCGTCT GCAGCCGCTG CCGCCGCCGC CGCTGTTTCG 180
TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACACTCCAA CAACCTGGCG 240
CTCTATGGAA CCGGCGGCGG AGGCAGCACT GGAGGAGGCG GCGGCGGTGG CGGGAGCGGG 300
CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAAGAAA ACCAGAACAT CGGCTACAAG 360
CTGGGCCACC GCGCGGCCCT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC 420
TTCGGCATGT TCGGCATCGT GGTGATGGTC ATCGAGACCG AGCTGTCTGT GGGCGCCTAC 480
GACAAAGGCGT CGTGATATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC 540
CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAAATAC AGTTGTTTAT GGTGGACAAT 600
GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGAA 660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGAATTATA CATTACATG GACGGCCCCG 720
CTTGCCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780
CCAAATGTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840
ACTGATGCCT CTTCTAGAGG CATTGGAGCA CTTAATAAGA TAACTTCAA TACACGTTTT 900
GTTATGAAGA CTTTAAATGAC TATATGCCCA GGAAGTGTAC TCTTGGTTTT TAGTATCTCA 960
TTATGGATAA TTGCCGCATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT 1020
GTTACTAGCA ACTTCTCTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT 1080
TATGGTGACA TGGTACCTAA CACATACTGT GGAAGAGGAG TCTGCTTACT TACTGGAATT 1140
ATGGGTGCTG GTTGACAGC CCGTGGTGGT GCTGTAGTGG CAAGGAAGCT AGAAGTTACC 1200
AAAGCAGAAA AACAGGTGCA CAATTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260
AATGCAGCTG CCAATGTACT CAGGGAAGAA TGGCTAATTT AAAAAAATAC AAAGCTAGTG 1320
AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTTCAT 1380
CAATTAAGAA GTGTAAGAAA GGAGCAGAGG AAAGTGAATG ACCAAGCAAA CACTTTGGTG 1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT 1500
GAAGACTTCG AGAAGAGGAT TGTACCCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC 1560
ATCCACGCCC TCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620
GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACTTACA ATGCTGAGCG GTCCCGGTCC 1680
TCGTCCAGGA GCGGCGGTC CTCTCCACA GCACCACCAA CTTATCAGA GAGTAGCTAG

SEQ ID NO:142 PFH1 Protein sequence:
Protein Accession #: NP_067627

60

65

70

1 11 21 31 41 51
| | | | |
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS AAAAAAAVS 60
SSAPEIVVSK PEHNNNNL LA YGTGGGGST GGGGGGGSG HGSSSGTKSS KKKNNIGYK 120
LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPI GNYTFTWTAR 240
LAFSYAPSTT TADVDIISI PMFLRLYLIA RVMLLHSLF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVFSI LWIAAWTVR ACERYHDQDQ VTSNFGAMW LISITLSIG 360
YGDMPVENTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNEM MDTQLTKRVK 420
NAAANVLRET WLIIYKNTKL VKKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480
DLAKTQNMV DMISDLNERS EDFEKRIIVL ETKLETIGS IHALPLISQ TIRQQQRDFI 540
EAQMESYDKH VTYNAERSRS SSRRRSSST APPTSSSS

75

SEQ ID NO:143 PFG9 DNA SEQUENCE

Nucleic Acid Accession #: AL110139, coding region is FGENESH predicted
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5
 10
 15
 20
 25
 30
 35

| | | | |
 ATGCGGCGCG TGCCGCTGCC CGCCCCGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC 60
 GCTCCCGCCG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
 CGCGAGTTCG GGCACCCGCC CGGCCCGGG CCCGGGAACA CCACCCGGTT TGGGTCTGGG 180
 GCGGCGGGCG GCAGCGGCAG CTCACGCTCC AACAGCAGTG GCGACGCCTT GGTGACCCGC 240
 ATTTCATCC TCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCCTTCGCC 300
 TTTACCAACC TCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTCCGG AAAGAGGTTA 360
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGA AATGGCGCCA 420
 CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
 TCCTTGCCGG CTGCAGTGA ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
 GTGCCCCAC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCCTGAT 600
 GGTGGAATCA GACCTGGTAA AACCTGTTT CCAGCCTGGT GGCATCCTGT GGAAGTIGG 660
 TCAGCTGCAA CCTGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGT 720
 GAAACCAAAA GCAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840
 TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
 CTGAATCTCA TGGAAAAGCT GGATTCTCT GCCTACGCA GAAACACCCG GGCTCCATCT 960
 GCCAGGTGCT TGCCACTGGT CTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG 1080
 AGTACCTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TGTGAAGAC 1140
 AGAGCAGTGA CTAAGTTCT CCAGGTAGC TCTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
 ACCCATCTG TCAGGTGGG TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
 AGGGTGTTC GGGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCACT 1380
 TGCCTTTGG TTTGAAGAT TCTGTGAGG CGCCATCCTC ACCTTGACCT CTCTACAAA 1440
 ATCTGTCTCC CTGCTGTGC CGTGGAAAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
 GTCCTTGGCT CATTTGAGCA GAGCCACAA AAGGCAGCTG CTGCCACGG GGAGCCTGTC 1560
 AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACATGTCCT CTGGCTGGGG GATCACACAT 1620
 GCGAACCTGC AGACAAATCC AGATACCAA GGCCAGGAAG GCCACGTGA GGATGTCACT 1680
 CACCTGGAG GAGACTTGA TGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTCCAG 1740
 GATGCGAGAT GCCAGAAGT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
 TGTGAGAGG TCACAGGTT CCATCACTTC TCCAGCCATT CCAAGTCTG GTCCTTCCTT 1860
 TCCCCCGAC AGCCCTGTT TCTGTCCAGG CCCTGA

SEQ ID NO:144 PFG9 Protein sequence:

Protein Accession #: none available, FGENSEH predicted

40
 45
 50

1 11 21 31 41 51
 | | | | |
 MRAPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGP PGNTTFRGSG 60
 AAGGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTLIACLL LRVFRSGKRL 120
 KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQITLLTVP 180
 VPPFFILDID LPARCGRFD GGRPKGTCF PAWWHPVESW SAATWGVKDW TWKPSVGGV 240
 ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VITMELLPP FGHFPKVPPT STPHGFRQLQ 300
 LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLPN PWWHFSATGS PIKTLTYQIM 360
 STLGLDVFEG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHL RLLRECPPLS 420
 THPVLARSD ARQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILL RHPHLDLFYK 480
 ICLPCCAVEH LREAKRSVT VLASFQSPQ KAAAHAHEPV KRGPFGQLTR HTCPGWGITH 540
 ANLQIPTDQ QGEGPREDDV HPGGDLGVA NFYLEEEGFQ DGRGCKMVLN SEEGPPSLTG 600
 CERLTGSHHF SSHSKWSFL SPRQPLFSR P

SEQ ID NO:145 PFG6 DNA SEQUENCE

55 Nucleic Acid Accession #: NM_013427

Coding sequence: 875-3799 (underlined sequences correspond to start and stop codons)

60
 65
 70
 75

1 11 21 31 41 51
 | | | | |
 GGCTGGGCTG CGAATAGCGT GTTCTCTCC GGCGGAACAC ACACACCCGG CCTTGGGGCT 60
 GTCTCCTGAA GCTCCCTCCT CCACGGAGAG CGCTGAGCGC CGCCGGGAAT TCCATCCAC 120
 CGTGGGCACG CAGTCTTTGG AGGTCCCGGG CGCAGCACGC TCGGTGTCCC CACTGCGAG 180
 CAAGACAGAG ACCCGCGCGG AACCTTGAGC TTGGAACAAC CCTTGAGCCT CTGCACTCGG 240
 AAGAGTGGGC GCAGCAGCCC AGCGGAGGCC AGCGCGCAA CCTCGGGCGC CGGGGCAAGG 300
 AGAGAGTGCA GGGAGGCGCA GCTCAGGCGC CCGGCTCAGG AGCGGGAGGA AGTTCGCG 360
 GCGCGGGAG CCGGTGGGAC GCGCCTGGG CGCACGCCCA GGCAGCCTTC TCCCTGGCCC 420
 TCGGGACTGT CCTCGGGCGG CAAGGAGGAG CTGCTGGAG TCTTAGAGGC CATCCAGAGC 480
 CAGCGAGCAG GAGCGCTGCG TCTCCGCCCT CAGCTAGGAA GGGGGAGTGG CGCTGGCAGG 540
 CTGGAGCTGG GAACCCAGCG AGCGCCTGAC CTTCTCCTC CTCTTCTGA CCTCTTCGC 600
 GTCTTGGGCT CCGGAGGAAG GTTCTAGCGG CTGCAAGAGG TCCCAAGACC CATTTCCTA 660
 GAAGGCTGGT GATGGATCTG CTGCTCTGCG CGCCGCGGG GCACTTGAG CGCACCGCGG 720
 GCGGTGAGG TGGGCTTTGC TCTCCACCGC CTTGGGCAA CCCTGGGCGA GCCCGCTG 780
 GCACCTTTGC CTGAGTCCCT TTCGGTTCCC GACCCAAAGC CACCAGCGTC CAGGGAGGGA 840
 GGAGGAGGTG GTCTCAAGGT GCAGCCCGC CGAGATGTCC GCGCAGAGCC TGCTCCACAG 900
 CGTCTTCTCC TGTTCTCGC CCGCTTCAAG TAGCGCGGCC TCGGCCAAGG GCTTCTCAA 960
 GAGGAAGCTG CGCCAGACCC GCAGCCTGGA CCGGCGCCTG ATCGGCGGCT GCGGGAGCGA 1020
 CGAGGCGGGC GCGGAGGGA GTGCGCGGG AGCCACGGCG GCGCGCTCT ACTCCCCATC 1080
 ACTCCAGACC GAGAGTCTCG GCCTCGCTT GCGTCTCTT TCCCGGGGTC CGCCCCCAG 1140
 GGCCACCAGG CTACCGCCTC CTGGACCTCT TTGCTCTGCC TTCTCCACAC CCAGACCCCC 1200

GCAGGAGAAG TCACCATCCG GCAGCTTTCA CTTTACTAT GAGGTTCCCG TGGGTCGCGG 1260
 CGGCCTCAAG AAGAGCATGG CCTGGGACCT GCCTTCTGTC CTGGCGGGGC CAGCCAGTAG 1320
 CCGAAGCGCT TCCAGCATCC TCTGTTTCATC CGGGGGAGGC CCCAATGGCA TCTTCGCTTC 1380
 TCCTAGGAGG TGGCTCCAGC AGAGGAAGTT CCAGTCCCCA CCCGACAGTC GCGGGCACCC 1440
 5 CTACGTCGTG TGGAAATCCG AGGGTGATTT CACCTGGAAC AGCATGTTCAG GCCGCAGTGT 1500
 GCGGCTGAGG TCAGTCCCA TCCAGAGTCT CTCAGAGCTG GAGAGGGCCC GGCTGCAGGA 1560
 AGTGCCTTTT TATCAGTTGC AACAGGACTG TGACCTGAGC TGTCAGATCA CCATTCCCAA 1620
 AGATGGACAA AAGAGAAAAG AATCTTTAAG AAAGAAACTG GATTCACTAG GAAAGGAGAA 1680
 10 AAACAAGAC AAAGAATTCA TCCCACAGGC ATTTGGAATG CCCTTATCCC AAGTCATTGC 1740
 GAATGACAGG GCCTATAAAC TCAAGCAGGA CTTCAGAGG GACGAGCAGA AAGATGCATC 1800
 TGACTTTGTG CTTCCCTCC TCCCATTGG AAATAAAAAG CAAAACAAAG AACTCTCAAG 1860
 CAGTAATCA TCTCTCAGCT CAACCTCAGA AACACCGAAT GAGTCAACGT CCCCACACAC 1920
 CCCGGAACCG TCCCTCGGG CTAGGAGGAG GGGTGCCATG TCAGTGGATT CTATCACCGA 1980
 15 TCTTGATGAC AATCAGTCTC GACTACTAGA AGCTTTACAA CTTTCTTGC CTGCTGAGGC 2040
 TCAAAGTAA AAGGAAAAAG CCAGAGATAA GAAACTCAGT CTGAATCCTA TTTACAGACA 2100
 GGTCCCTAGG CTGCTGGACA GCTGCTGTCA GCACCTAGAA AAACATGGCC TCCAGACAGT 2160
 GGGGATATTC CGAGTTGGAA GCTCAAAAAA GAGAGTGAGA CAATTACGTG AGGAATTGTA 2220
 CCGTGGGATT CATGTCTCTC TGGAGGAGGA GCACAGTGT CATGATGTGG CAGCCTTGCT 2280
 20 GAAAGAGTTC GTAGGGGACA TGCCAGACCC CTTCTCACC AGGAGCTGT ACACAGCTTT 2340
 CATCAACACT CTCTTGTGG AGCCGGAGGA ACAGCTGGGC ACCTTGACG TCCTCATATA 2400
 CCTTCTACT CCTGCAACT GCGACACCC CCACCGCCTG CTACAGTTC TCTCATCGT 2460
 GGCCAGGCAT GCCGATGACA ACATCAGCAA AGATGGGCAA GAGTCACTG GGAATAAAAT 2520
 GACATCTCTA AACTTAGCCA CCATATTGG ACCCAACCTG CTGCACAAGC AGAAGTCATC 2580
 25 AGACAAAGAA TTCTCAGTTC AGAGTTCAGC CGGGCTGAG GAGAGCACGG CCATCATCGC 2640
 TGTGTGCAA AAGATGATTG AAAATTATGA AGCCCTGTTC ATGGTTCCCG CAGATCTCCA 2700
 GAACGAAGTG CTGATCAGCC TGTTAGAGAC CGATCCIGAT GTCGTGACT ATTTACTCAG 2760
 AAGAAAGGCT TCCCAATCAT CAAGCCCTGA CATGCTGCAG TCGGAAGTTT CCTTTCCGT 2820
 GGGAGGGAGG CATTCACTA CAGACTCCAA CAAGGCCCTC AGCGGAGACA TCTCCCTTA 2880
 30 TGACAAAC TCCCTAGTGC TGCTGAGCG CTCCCTGCTG GCTATGCAAG AGGACGCGCG 2940
 CCCGGGGGCG TCGGAGAAGC TTTACAGAGT GCCAGGGCAG TTTATGCTGG TGGGCCACTT 3000
 GTCGTCGICA AAGTCAAGGG AAAGTCTCC TGGACCAAGG CTGGGAAAG ATCTGTCAGA 3060
 GGAGCCTTTC GATATCTGGG GAACCTGGCA TTCAACATTA AAAAGCGGAT CCAAGACCC 3120
 AGGAATGACA GGTTCCTCTG GAGACATTT TGAAGCAGC TCCCTAAGAG CGGGGCCCTG 3180
 35 CTCCCTTCT CAAGGGAACC TGTCGCCAAA TTGGCTCGG TGGCAGGGGA GCCCGCAGA 3240
 GCTGGACAGC GACACGCAGG GGGCTCGGAG GACTCAGGCC GCAGCCCCCG CGACGGAGGG 3300
 CAGGGCCAC CCTGCGGTGT CGCGCGCTG CAGCACGCCC CAGTCCAGG TGGCAGGGAA 3360
 AGCCGAGCG CCCACGGCA GGTGCGAGCA GTACTTGACC CTGAGCGGCG CCCACGACCT 3420
 CAGCGAGAGT GAGCTGGATG TGGCCGGGCT GCAGAGCCGG GCCACACCTC AGTGCCAAAG 3480
 40 ACCCATGGG AGTGGGAGG ATGACAAGCG GCCCCCGCT CCATACCCGG GCCCAGGGAA 3540
 GCCCGCGGA GCGGCGAGCT GGATCCAGG GCCCCCGGA GGCCTGGAGA CACCCACGGA 3600
 CCAGGAGGCG CAAGCAGCCG AGCGAGAGCA GCAGGTACG CAGAAAAAC TGAGCAGCGC 3660
 CAACTCCCTG CCAGCGGGCG AGCAGGACAG TCCGCGCTG GGGGACGCTG GCTGGCTCGA 3720
 CTGGCAGAGA GAGCGCTGGC AGATCTGGGA GCTCCTGTG ACCGACAACC CCGATGCCCT 3780
 GCGCGAGAGC CTGCTGAGG CCCGACCCA GCCGAGCCCC CCTGCCCCG AGCCCCCGC 3840
 45 CCTCAGCCC AGGGGGGACC GTGGGTGGTG GCCACTGGCA CACTTAGTGT TCTCTTTCA 3900
 CACTTCTCAA AAGTGACACA AGAGAAATCC AGTTCACCTA CAGAGGTAGA GCACTACGC 3960
 CCCCCTATT GAGAATAAGG TTCCATTGCG TAGCCAGCCT TAGGAAAAAC AAACAGAAC 4020
 CAAACAGAT GGCAATGTCC AATCTAAAAA CGTCCCTCTT GGCTCTATA TATAAGATAC 4080
 50 AACTCTGTCT TGTATAGCC TAACCGTATT TATGTGCTT CGGTTTTGAC TATTGTGTAT 4140
 TCTGTAACAG ATTATGTATA ATCATATATG ATATATTCAC AAAGAGAAAA CAAAAGGAAC 4200
 TTTAAAAA AAAATCACTT CACTTATATT AAGCAATGAG ATATACTAAA CAATGAGATT 4260
 CTATAGAATG TTCTAGAATG TGCACAAGCG GGTTCCTGT CTTTGGCAT AGCTTTATAA 4320
 CTGGGATAA CCCTTCTCT GATACCAAA ACTAACAAGA GGAAGCAGAA TATGAGAAGC 4380
 55 CATATTTTA CATAGGAGTC AGATACAAAA AGAAAAATCA CTGAATGCTT TTAGATATTG 4440
 AATACGTTTT CAGGAAAAATG CTAATCTGA TAGATTACGA AATATATTT TAGAACTTGT 4500
 TTAGAAAGGA TTCAGTTAAC CAAACAAGAA AAAGGCAGTG CCTCACAAAG AAATTAAGAA 4560
 GTTGTCCGTC CCACGTTACA TCAAAATCAG TTTTATATAG GCCATATATA ATATATATTT 4620
 ATAATGTATA ATTTTATGT ATTTTTCAAA ACTACAACT GGAATCCAAC TATAAAGTGT 4680
 60 TTAAGAATCT ACACAGAATA TTCAAATTAT AGAACATGTT TTTCCCTTT GCCCATAAT 4740
 CAGTATTTGC CAAATTACAT GCAATTCCTT AAAAACTAAA TCACATTGGT AAAAGGCCCTA 4800
 CAGCTTTGTA TTAACATTGT GCCAAAGGCT GAGGAAATGT TTTCTTTCGA ATTTTATGT 4860
 GTATTGTAAA ATGTTCTACC GTACTTTAGT AGTTTGAAGT TTCAAGTGC ATAACATATT 4920
 TTGACCAGCA GAAGGCGATA CGCTTCAGTA TTTTATGCAA TTTTTCICA CTTCGAAGGG 4980
 65 AAAGTGATTT ATAAAAAAG ATTTTITTTT TTTAAACAT GCTACTCTTA ATTTTCATGT 5040
 TGGTGATGAA ATCCCAAGTG GTGTTTCTTA AGGTTCATAT TTGTGCCATG ATGAATAAAA 5100
 AGTTAAGCAA AAAAAAAAAA AAAAAAAAAA AAA

70 SEQ ID NO:146 PF66 Protein sequence:
 Protein Accession #: NP_038286.1

1 11 21 31 41 51
 75 MQAQLLSV FSCSSPASSS AASAKGFSCR KLRQTRSLDP ALIGGCGSDE AGAEGSARGA 60
 TAGRLYSPSL PAESLGPRLA SSSRGPPRA TRLPPLGPLC SSFSTPTQ EKSPSGSFHF 120
 DYEVLPRGG LKKSMAWDLP SVLAGPASSR SASSILCSSG GGPNGIFASP RRWLQQRKFQ 180
 SPDSRGHPY VVWKSEGGFT WNSMSGRSVR LRSVPIQSL ELERARLQEV PFYQLQDDCD 240
 LSCQITPKD GQKRKKSRLK KLSLGKEKN KDKEFIQAF GMPLSQVIAN DRA YKLKQDL 300
 QRDEQDASD FVASLLPFGN KRQNKELSSS NSSLSTSET PNESTSPNTP EPAPRRRRR 360

AMSVDSITDL DDNQSRLEA LQLSLPAEAQ SKKEKARDKK LSLNPIYRQV PRLVDSCCQH 420
 LEKHGLQTVG IFRVGSSKKR VRQLREEFDR GIDVSLIEEE SVHDVAALLK EFLRDMPDPL 480
 LTRELYTAFI NTLLEPEEQ LGTLQLLIYL LPFCNCDTLH RLLQFLSIVA RHADDNISKD 540
 GQEVGTGNKMT SLNLATIFGP NLLHKQKSSD KEFSVQSSAR AEESTAIIV VQKMIENYEA 600
 LFMVPPDLQN EVLISLETD PDVVDYLLRR KASQSSSPDM LQSEVSFSVG GRHSSDTSNK 660
 ASSGDISPYD NNSPVLRSR LAMQEDAAP GGSEKLYRVP GQFMLVGHLS SSKSRESSPG 720
 PRLGKDLSEE PFDIWTGWH S TLKSGSKDPG MTGSSGDIFE SSSLRAGPCS LSQGNLSPNW 780
 PRWQGSFAEL DSDTQGARRT QAAAPATEGR AHPAVSRACS TPHVQVAGKA ERPTARSEQY 840
 LTLGSAHDL S ESELDVAGLQ SRATPQCQRP HSGSRDDKRP PPYPGPGKP AAAAAWIQGP 900
 PEGVETPTDQ GGQAAEREQV VTQKLLSSAN SLPAGEQDSP RLGDAGWLWD QRERWQIWEL 960
 LSTDNPDALP ETLV

15 SEQ ID NO:147 PFG4 DNA SEQUENCE

Nucleic Acid Accession #: NM_002202

Coding sequence: 240-1289 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 CCCCCGAGCC GCGCCGAGTC TGCCGCCGCC GCAGCGCCTC CGCTCCGCCA ACTCCGCCGG 60
 CTFAAATTGG ACTCCTAGAT CCGCGAGGGC GCGGCGCAGC CGAGCAGCGG CTCTTTCAGC 120
 ATTGGCAACC CCAGGGGCCA ATATTCCCA CTTAGCCACA GCTCCAGCAT CCTCTCTGTG 180
 25 GCGTGTTCAC CAACTGTACA ACCACCATT CACTGTGGAC ATTACTCCTT CTACAGATA 240
 TGGGAGACAT GGGAGATCCA CCAAAAAAAAA AACGTCTGAT TTCCTATGT GTTGGTTGCG 300
 GCAATCAGAT TCACGATCAG TATATTCTGA GGGTTTCTCC GGATTGGAA TGGCATGCGG 360
 CATGTTTGAA ATGTGCGGAG TGTAATCAGT ATTTGGACGA GAGCTGTACA TGCTTTGTTA 420
 GGGATGGGAA AACCTACTGT AAAAGAGATT ATATCAGGTT GTACGGGATC AAATGCGCCA 480
 30 AGTGACGAT CCGCTTCAGC AAGAACGACT TCGTGATGCG TGCCCGCTCC AAGGTGTATC 540
 ACATCGAGTG TTTCGCTGT GTGGCCTGCA GCGGCCAGCT CATCCCTGGG GACGAATTG 600
 CGCTTCGGGA GGACGGTCTC TTCTGCCGAG CAGACCACGA TGTGGTGGAG AGGGCCAGTC 660
 TAGGCGGTGG CGACCGCTC AGTCCCCTGC ATCCAGCGCG GCCACTGCAA ATGGCAGCGG 720
 AGCCCATCTC CGCCAGGCAG CCAGCCCTGC GCGCCACGT CCACAAGCAG CCGGAGAAGA 780
 35 CCACCCGCGT GCGGACTGTG CTGAACGAGA AGCAGCTGCA CACCTTGGCG ACCTGCTACG 840
 CCGCAAAACC GCGGCCAGAT GCGCTCATGA AGGAGCAACT GGTAGAGATG ACGGGCCTCA 900
 GTCCCGTGT GATCCGGTCT TGGTTTCAAA ACAAGCGGTG CAAGGACAAG AAGCGAAGCA 960
 TCATGATGAA GCAATCCAG CAGCAGCAGC CCAATGACAA AACTAATATC CAGGGGATGA 1020
 CAGGAATCC CATGGTGGCT GCCAGTCCAG AGAGACACGA CGGTGGCTTA CAGGTAACC 1080
 40 CAGTGGAAGT ACAAAAGTAC CAGCCACCTT GGAAAGTACT GAGCGACTTC GCCTTGAGA 1140
 GTGACATAGA TCAGCTGTCT TTTCAGCAAC TGTGCAATTT TTCAGAAGGA GGACCGGGCT 1200
 CTAATTCAC TGCCAGTGAA GTAGCATCAA TGTCTCTCA ACTTCCAGAT ACACCTAACA 1260
 GCATGGTAGC CAGTCTATT GAGGCAATGAG GAACATTAT TCTGTATTT TTTTCCCTGT 1320
 TGGAGAAAGT GGGAAATTAT AATGTGCAAC TCTGAAACAA AAGTATTAA CGACCCAGTC 1380
 45 AATGAAAACT GAATCAAGAA ATGAATGCTC CATGAAATGC ACGAAGTCTG TTTTAATGAC 1440
 AAGGTGATAT GGTAGCAACA CTGTGAAGAC AATCATGGGA TTTTACTAGA ATTAACAAC 1500
 AAACAAACG CAAAACCCAG TATATGCTAT TCAATGATCT TAGAAGTACT GAAAAAATA 1560
 GACGTTTTTA AAACGTAGAG GATTATATT CAAGGATCTC AAAGAAAGCA TTTTCATTTC 1620
 50 ACTGCACATC TAGAGAAAAA CAAAATAGA AAATTTTCTA GTCCATCCTA ATCTGAATGG 1680
 TGCTGTTTCT ATATTGGTCA TTGCTTGCC AAACAGGAGC TCCAGCAAAA GCGCAGGAAG 1740
 AGAGACTGGC CTCCTTGGCT GAAAGAGTCC TTTAGGAAG GTGGAGCTGC ATTGGTTTGA 1800
 TATGTTTAAA GTTGACTTTA ACAAGGGGTT AATTGAAATC CTGGGTCTCT TGGCCTGTCC 1860
 TGTAGCTGGT TTATTTTTTA CTTTGGCCCC TCCCCACTTT TTTTGAATC CATCCTTTAT 1920
 CAAGAAGTCT GAAGCGACTA TAAAGGTTTT TGAATTCAGA TTTAAAAACC AACTTATAAA 1980
 55 GCATTGCAAC AAGGTTACCT CTATTTTGCC ACAAGCGTCT CGGGATTGTG TTGACTTGT 2040
 GTCTGTCCAA GAACTTTTCC CCCAAAGATG TGTATAGTTA TTGGTTAAAA TGACTGTTT 2100
 CTCTCTCTAT GGAATAAAAA AGGAAAAAAA AAAGGAAACT TTTTGTGTT GCCTTGCAT 2160
 TGCAAAAAAT ATAAAGTAAT TTATTATTTA TTGTCGGAAG ACTTGCCACT TTTCATGTCA 2220
 60 TTGACATTT TTGTTTGTCT GAAGTGAAAA AAAAGATAA AGGTGTGACG GTGTCCTTTG 2280
 AATTATATGT CTAATCTAT GTGTTTGTCT TTTTCTTAA ATATTATGTG AAATCAAAGC 2340
 GCCATATGTA GAATTATATC TTCAGGACTA TTTCTAAT AAACATTGG CATAGAT

65 SEQ ID NO:148 PFG4 Protein sequence:

Protein Accession #: NP_002193.1

70 1 11 21 31 41 51
 MGDPPKKRRL ISLCVGGGNQ IHDQYLRSV PDLEWHAACL KCAECNQYLD ESCTCFVRDG 60
 KTYCKRDYIR LYGIKCAKCS IGFSKNDFVM RARSKVYHIE CFRVACSRQ LIPGDEFALR 120
 EDGLFCRADH DVVERASLGA GDPLSLHPA RPLQMAAEPI SARQPALRPH VHKQPEKTR 180
 VRTVLNEKQL HTLRTCYAAN PRPDALMKEQ LVEMTGLSPR VIRVWFQNKR CKDKKRSIMM 240
 75 KQLQKQPPND KTNIQGMGTG PMVAASPERH DGGLQANPVE VQSYQPWKV LSDFALQSDI 300
 DQFAFQQLVN FSEGGPGSNS TGSEVASMSS QLPDTNMSV ASPIEA

SEQ ID NO:149 PFG2 DNA SEQUENCE

Nucleic Acid Accession #: NM_001172

Coding sequence: 39-1103 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
 | | | | |
 GCGGAGCTCT GCCTTGGAGA TTCTCAGTGC TGCGGATCAT GTCCCTAAGG GGCAGCCTCT 60
 CGCGTCTCCT CCAGACGCGA GTGCATTCCA TCCTGAAGAA ATCCGTCCAC TCCGTGGCTG 120
 10 TGATAGGAGC CCCGTTCTCA CAAGGGCAGA AAAGAAAAGG AGTGGAGCAT GGTCCCGCTG 180
 CCATAAGAGA AGCTGGCTTG ATGAAAAGGC TCTCCAGTTT GGGCTGCCAC CTAAAAGACT 240
 TTGGAGATTG GAGTTTACT CCAGTCCCA AAGATGATCT CTACAACAAC CTGATAGTGA 300
 ATCCACGCTC AGTGGGCTCT GCCAACCAAG AACTGGCTGA GGTGGTTAGC AGAGCTGTGT 360
 CAGATGGCTA CAGCTGTGTC AACTGGGAG GAGACCACAG CCTGGCAATC GGTACCATTA 420
 GTGGCCATGC CCGACACTGC CCAGACCTTT GTGTTGCTG GGTGATGCC CATGCTGACA 480
 15 TCAACACACC CCTTACCATT TCATCAGGAA ATCTCCATGG ACAGCCAGTT TCATTCTCC 540
 TCAGAGAACT ACAGGATAAG GTACCACAAC TCCCAGGATT TTCCTGGATC AAACCTTGTA 600
 TCTCTCTGCG AAGTATTGTG TATATTGGTC TGAGAGACGT GGACCTCCTT GAACATTTTA 660
 TTTTAAAGAA CTATGATATC CAGTATTTT CCATGAGAGA TATTGATCGA CTGGTATCC 720
 AGAAGGTGAT GAAACGAACA TTTGATCTGC TGATTGGCAA GAGACAAAGA CCAATCCATT 780
 20 TGAGTTTGA TATTGATGCA TTGACCCTA CACTGGCTCC AGCCACAGGA ACTCCTGTG 840
 TCGGGGACT AACCTATCGA GAAGGCATGT ATATTGCTGA GGAAATACAC AATACAGGGT 900
 TGCTATCAGC ACTGGATCTT GTTGAAGTCA ATCCTCAGTT GGCCACCTCA GAGGAAGAGG 960
 CGAAGACTAC AGTAACTCTG GCAGTAGATG TGATTGCTTC AAGCTTTGGT CAGACAAGAG 1020
 AAGGAGGGCA TATTGCTAT GACCAACTTC CTACTCCAG TTCACCAGAT GAATCAGAAA 1080
 25 ATCAAGCAGC TGTGAGAAAT TAGGAGACAC TGTGCACTGA CATGTTTCAC AACAGGCATT 1140
 CCAGAATTAT GAGGCATTGA GGGGATAGAT GAATACTAAA TGGTTGTCTG GGTCAATACT 1200
 GCCTTAATGA GAACATTTC ACATTCTCAC AATTGTAAAG TTTCCCTCT ATTTTGGTGA 1260
 CCAATACTAC TGTAATGTA TTTGGTTTT TGCAGTTCAC AGGGTATTAA TATGTACAG 1320
 TACTATGTAA AITTAAGAA GTCATAAACA GCATTATTA CCTTGGTATA TCATACTGGT 1380
 30 CTGTGCTG TGTTCCCTC ACATTTAAGT GGTTTTCAT CTTCCTCCC TCCTCCACA 1440
 GCCTGGCTAT ACAGTGATC CTGAACTGT CAGCCACAG CAGCAATATG CTATTCTAT 1500
 CCACATCCCT ACATCATGC ATTCAAGG TCAAAGTCTT GGTCCACAAA CCCTTCCTA 1560
 TAGAAGTTCA ATGGCTCGCA AAGAATTGT AGTAAACCAG GCCTCCACAG ATGGCGAGCT 1620
 CCAGTAAGAT GATAATGGAA AGCAGCAGCT TGTGGTTGT CACTCTACAA AGAGAAGCAA 1680
 35 AGTGGGAGT AGTCAGAAAT TTGGATAACC TTCTTCTAA ACATTGGGG GTTAGACCTG 1740
 GGACCACGGC TGGATACTCT GAGGCTGTAT GTTGTATCAG ACAGCCACTT AGCAGGAAGT 1800
 ACTCATAAGG TTCTTAGCT GTCATTAGG GATAACACTG TCTACCTCAG AGAAATGTTA 1860
 AACTGAGACA ATAAACCCA AAGCAT

SEQ ID NO:150 PFG2 Protein sequence:

Protein Accession #: NP_001163.1

45 1 11 21 31 41 51
 | | | | |
 MSLRGSLSRL LQTRVHSILK KSVHSAVIG APFSQGQKRK GVEHGPAAIR EAGLMKRLSS 60
 LGCHLKDFGD LSFITVPKDD LYNNLIVNPR SVGLANQELA EVVSRAVSDG YSCVILGGDH 120
 SLAIGTISGH ARHCPDLGVV WYDAHADINT PLTSSGNLH GQPVSELLRE LQDKVPQLPG 180
 50 FSWIKPCESS ASIVYIGLRD VDPPEHFILK NYDIQYFSMR DIDRLGIQKV MERTFDLLIG 240
 KRQRPHLSF DIDAFDPTLA PATGTPVVG LTYREGMYIA EEIHNTGLLS ALDLVEVNPQ 300
 LATSEEEKAT TANLAVDVIA SSFGQTRREG HIVYDQLPTP SSPDESENQA RVRI

SEQ ID NO:151 PFG1 DNA SEQUENCE

Nucleic Acid Accession #: NM_017906

Coding sequence: 80-1255 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 AATTATATAT TTTTACTCTA TGTTTCTCTA CATGTTTTT TCTTTCCGT GCTGGCGGAA 60
 GAGGCACGTG CGTGTCTGAA TGGAGCTGGT CGCTGGTTGC TACGAGCAGG TCCTCTTTGG 120
 GTTCGCTGTA CACCCGGAGC CCAAGGCTTG CGGCGACCAC GAGCAATGGA CTCTTGTGGC 180
 65 TGACTTCACT CACCATGCTC AACTGCCTC CTGTGACGA GTAGCTGTAA ATAGTCGTTT 240
 TGTGGTCACT GGGAGCAAAG ATGAAACAAT TCACATTTAT GACATGAAAA AGAAGATTGA 300
 GCATGGGGCT CTAGTGATC ACAGTGGTAC AATAACTTGC CTGAAAATCT ATGGCAACAG 360
 GCATTTAATC AGTGGAGCGG AAGATGGACT CATCTGTATC TGGGATGCAA AGAAATGGGA 420
 ATGCTGAAG TCAATTAAG CTCACAAAGG ACAGGTGACC TTCTTTCTA TTCACCCATC 480
 TGGCAAGTTG GCCCTGTGCG TTGGTACAGA TAAACTTTA AGAAGTGGGA ATCTTGTAGA 540
 70 AGGAAGATCA GCATTCTATA AAAATATAAA ACAAAATGCT CACATAGTAG AATGGTCCCC 600
 AAGAGGAGAG CAGTATGTAG TTATCATACA GAATAAAATA GACAICTATC AGCTTGACAC 660
 TGCATCCATT AGTGGACCA TCACAAATGA AAAGAGAATT TCCTCTGTTA AATTTCTTTC 720
 AGAGTCTGTC CTGTGCACTG CTGGAGATGA AGAAGTTATA AGGTTTTTTG ACTGTGATTG 780
 ACTAGTGTGC CTCTGCGAAT TTAAGCTCA TGAAGACAGG GTAAAGGACA TGTTCAAGTT 840
 75 TGAATTCGA GAGCATCATG TTATTGTTT AGCATCGAGT GATGGTTTCA TCAAAATGTG 900
 GAAGCTTAAG CAGGATAAGA AAGTTCCCC ATCTTACTC TGTGAAATAA ACATAATGC 960
 CAGGCTGACG TGTCTGGAG TGTGGCTAGA CAAAGTGGCA GACATGAAAA GCCTTCCTCC 1020
 AGCTGCAGAG CTTCTCTCTG TAAGTAAAGA ACAGTCCAAA ATTGGCAAAA AGGAGCCTGG 1080
 TGACACAGTG CACAAAGAAG AAAAGCGGTC AAAACCTAAC ACAAGAAAC GCGGTTTAAC 1140

AGGTGACAGT AAGAAAGCAA CAAAAGAAAG TGGCCTGATA TCAACCAAGA AGAGGAAAAT 1200
 GGTAGAAATG TTGGAAAAAG AGAGGAAAAA GAAGAAAAATA AAAACAATGC AGTGAATCAC 1260
 AGATGTCTCC TGAAGAAGCT CTTTATAGATG AAATCATCTT ACTCAAAATGT ACCTTAATTT 1320
 TTTTTTTTCC CTGAGTAAAA GCAAGAAATTT TCTTCCTTTG GAAAAAATAT ATATATTAAA 1380
 AAACCACTTT TAGATGGTTT TTTTAAAAA AAAAAAAAAA ACTGGTAAAA TTACTTTTGG 1440
 CAGACAGTGT TTTATGAATT ATGTATCATG TTGATATATA ATATGTTAAT GTGTCATGTA 1500
 ATTTTACTT TGTACAAAGC AAATAAAGAT CTTTCTCAAA AAAAAAAAAA AAAA

SEQ ID NO:152 PFG1 Protein sequence:
 Protein Accession #: NP_060376.1

1 11 21 31 41 51
 MELVAGCYEQ VLFGFAVHPE PKACGDHEQW TLVADFTHHA HTASLSAVAV NSRFVVTGSK 60
 DETIHYDMK KIEHGALVH HSGTITCLKF YGNRHLISGA EDGLICIWDA KKWECLKSIK 120
 AHKGQVTFLL IHPSGKLALS VGTDKTLRTW NLVEGRSAFI KNKQNAHIV EWSRGEQYV 180
 VIQNKIDII QLDASISGT ITNEKRISVV KFLSESVLAV AGDEEVIRFF DCDLSVCLCE 240
 FKAHENRVKD MFSFEIPEHH VIVSASSDGF IKMWKLKQDK KVPSSLCEINTNARLTCLG 300
 VWLDKVDAMK SLPPAAEPP VSKEQSKIGK KEPGDTVHKE EKRSKPNTKK RGLTGDSKKA 360
 TKESGLISTK KRKMVEMLEK KRKKKKIKTM Q

SEQ ID NO:153 PFD6 DNA SEQUENCE

Nucleic Acid Accession #: NM_014668
 Coding sequence: 110-2953

(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GATGTCTTGG ACATGCTCTG GCTGGCTAAT CTCCATGTTG TAGCCGACTG AAAATACGGT 60
 GGCCAAAGTG ATGGTGTGCT TATTTCAGT CTAAAGAAAT TTCTTTTGA TGTGGCAGAA 120
 AATCGAGGAT GTGGAGTGGA GACCCAGAC TTACTTGGAG CTGGAGGGTC TGCCCTGCAT 180
 CCTGATCTTC AGTGGGATGG ACCCGCATGG GGAGTCTTGG CCGAGGTCTT TGAGGTACTG 240
 TGACCTGCGA TTGATAAAT CCTCTGCTT GGTGAGAACA GCCTGGAGC AGGAGCTGGG 300
 CCTGGCTGCC TACTTTGTGA GCAACGAGGT TCCCTTGGAG AAGGGGGCTA GGAACGAGGC 360
 CTGGAGAGT GATGCTGAGA AGCTGAGCAG CACAGACAAC GAGGATGAGG AGCTGGGGAC 420
 AGAAGGCTCT ACCTCGGAGA AGAGAAGCCC CATGAAAAGG GAGAGGTCCC GCTCCACGA 480
 CTCAGCATCC TCATCCCTCT CCTCCAAGGC TTCCGGTTCA GCGCTCGGTG GCGAGTCCCT 540
 GGCTCAGCCC ACAGCACTCC CCCAGGGAGA GCATGCCAGG TCGCCCCAGC CCCGTGGCCC 600
 CGCAGAGGAG GGCAGAGCCC CTGGTGAGAA ACAGAGGCCG CGGGCAAGTC AGGGGCCACC 660
 CTCGGCCATC AGCAGGCACA GTCCCGGGCC GACGCCCCAG CCCGACTGTA GCCTCAGGAC 720
 CGGCCAGAGG AGCGTCCAGG TGTCGGTCAC CTCGTCTGTC TCCAGCTGT CCTCTCTC 780
 GGGCTCATCC TCCTATCCG TGGCGCCCGC TGCCGGCAGC TGGGTCTGTC AGGCCTCCCA 840
 GTGCTCTTGA ACCAAGGCCT GCGGCCAGCC ACCCATTTGC TTCTTGCCCA AGCTCGTGTA 900
 CGACATGGTT GTGTCCAATG ACAGCAGTGG CTGCGCAAG GCCGCTCCC TCCTGCCCTC 960
 CCCCTCGGTC ATGTGGGCCA GCTCTTTCCG CCCCTGCTC AGCAAGACCA TGACATCCAC 1020
 CGAGCAGTCC CTCTACTACC GGCAGTGGAC GGTGCCCCCG CCCAGCCACA TGGACTACGG 1080
 CAACCGGGCC GAGGGCCGCG TGGACGGCTT CCACCCCGC AGGCTGTCTG TCAGCGGGCC 1140
 CCCTCAGATC GGGAGACAG GTGCCTACCT GCAGTCTCTC AGTGTCTGT CCAGGATGCT 1200
 TGTTGGGCTC ACAGAAGTGG ATGTCTATGA CGAGGAGGAG ATCAATATCA ACCTCAGAGA 1260
 AGAATCTGAC TGGCATTATC TCCAGCTTAG CGACCCCTGG CCAGACCTGG AGCTGTTCAA 1320
 GAAGTTGCC TTTGACTACA TCATTACGA CCCGAAGTAT GAAGATGCCA GCCTGATTTG 1380
 TTCGCACTAT CAGGGTATAA AGAGTGAAGA CAGAGGGATG TCCCGGAAGC CGGAGGACCT 1440
 TTATGTGCGG CGTCAGACGG CACGGATGAG ACTGTCCAAG TACGAGCGT ACAACACTTA 1500
 CCACCACTGT GAGCAGTGCC ACCAGTACAT GGGCTTCCAC CCCGCTACC AGCTGTATGA 1560
 GTCCACCCTG CACGCCCTTG CCTTCTCTTA CTCCATGCTA GGAGAGGAGA TCCAGCTGCA 1620
 CTTCATCATC CCCAAGTCCA AGGAGCACCA CTTTGTCTTC AGCCAACCTG GAGGCCAGCT 1680
 GGAGAGCATG CGACTCCACC TCGTGACAGA CAAGAGCCAT GAATATATAA AAAGTCCGAC 1740
 ATTCACTCCA ACCACCGGCC GTCACGAACA TGGGCTCTTT AATCTGTACC ACGCAATGGA 1800
 CGGTGCCAGC CATTGTGACG TGCTGGTGT CAAGGAATAC GAGATGGCAA TTTATAAGAA 1860
 ATATTGGCCC AACCACATCA TGCTGGTGT CCCCAGTATC TTCAACAGTG CTGGAGTTGG 1920
 TGCTGCTCAT TTCTCATCA AGGAGCTGTC CTACCATAACT CTGGAGCTCG AGCGGAACCG 1980
 GCAGGAGGAG CTGGGAATCA AGCCGACAGA CATCTGGCCT TTCAATTGTA TCTCTGATGA 2040
 CTCTGCGTG ATGTGGAACG TGTTGGATGT CAACTCTGCT GGGGAGAGAA GCAGGGAGTT 2100
 CTCCTGGTGC GAAAGGAACG TGCTTTTGA GCACATCATG CAGCACATCG AGCGGGCCCC 2160
 CGACATCATG CACTACCGCC TGCTGGGCT GCGGAAGTGG TCCAGCAAGA CCCGGGCCAG 2220
 CGAGGTGCAA GAGCCCTTCT CCCGCTGCCA CGTGCAACAAC TTCATCATCC TGAACGTGGA 2280
 CCTGACCCAG AACGTGCACT ACAACCAGAA CCGTTTCTG TGTGACGATG TAGACITCAA 2340
 CTTGCGGGTG CACAGCGCCG GCCTCTGCT CTGCGGGTTC AACCGCTTCA CGGTGATGAA 2400
 GAAGCAGATG GTGTGGGGG GCCACAGGTC CTTCACATC ACATCCAAGG TGTCTGATAA 2460
 CTCTGCCGCG GTCTGCCGG CCCAGTACAT CTGTGCCCG GACAGCAAGC ACACGTTCT 2520
 CGCAGCGCCC GCCAGCTCC TGCTGGAGAA GTCTCTGAG CACCACAGCC ACCTCTTCT 2580
 CCCGCTGTCC CTGAAGAACC ATGACCACCC AGTGCTGTCT GTGCACTGT ACCTGAACCT 2640
 GGGATCTCAG ATTTCTGTTT GCTATGTGAG CTCCAGGCC CACTCTTAA ACATCAGCTG 2700
 CTCGGAATG CTGTTCAGTG GGTCTGTGCT GTACCTCTGT GACTCTTTTG TGGAGCTAG 2760
 CTTTTTGA AAAGTTTCA TTCTGAAAGG TCGGACGTTG TGTGTATCT GTCAAGACCG 2820
 GAGCTCACTG CGCCAGACGG TCGTCCGCT GGAGCTGAG GACGAGTGGC AGTTCCGGCT 2880

GCGCGATGAG TTCCAGACCG CCAATGCCAG GGAAGACCGG CCGCTCTTTT TTCTGACGGG 2940
 ACGACACATC TGAAGGAAGAC AGCGGCGAGT TTTCTGAAGA GATGAGTGTCT CAGAGCCCTC 3000
 ATGCTGTTGA GGCTAAAGGG AGGCCTGGAA CGGTGGGGCG TTGACTGGA ATGGACCCCA 3060
 GGGACTGTCC AGGTGCAGCC CCTCTAGTA CACATGGGCC CCCGAGGCCG TGGTCTGGG 3120
 5 AGCCAGGAAG ACTCCGAGT GGGTGAGAAT GAAAACCTGA GACTCCCAAG TTCTGGGCCA 3180
 GCCCATTGCT CTGGGCTGTT TTAAGGCCA TTTCACGAGG AACAAAGATT TACTTCTGT 3240
 CCTGCCATTC GTGTGCTTCC ATGGACAAAC CTGATTTTTT TCTCTTAGTT CTAAAGAATC 3300
 TTGGGTATT TTGTAGCGGT GCCAGTATTT CAGTAGATGG GATTTCAGCC AAGTAGGTT 3360
 10 CCCTGTAACC TCCTACAAAG CAATATTCCA AAGGAACATT TTAAGTAA AGGCTGGAGA 3420
 CAAGAAAAAA TAAGTAGATC GTTTAATAA CAATTATTTA ATTGCCTATA AGTTTGCTGT 3480
 TTCAGAGGCT AGCCCAAGG CATCAAAATTT AATAAAGTTA AACAAATTGA TTTACTTCAG 3540
 AGCAAAATAG ATCCTATTAA AATAATATAG GGTAAATACC CTACCTCTTA GAAAGGGCAA 3600
 AAATGCAAG AAGCTTCTT TAAACTAAA AGGGTTTTT GGGGGGGGAG TTGGCGGGGA 3660
 15 GGAAATAAGG CTAACAGAGG TTGACCTAAA ATTAGCCTTA CAAAGGAGAA AGGACCACAT 3720
 TGCTTACTTG AAACAGACAA TGAACAAC CAAAGTGATA TATAAATAG TTGATGAGAA 3780
 CTAGACTTAT GACTGTAGTT TACTAGAGTT TAGTTTTT CAG TTGCTGAAGT AGTCAATTT 3840
 CTCTACTAA TGTGTGTT CACAGGGAAG AATCTCACTT GACTAGAGAG GAGGTGGGA 3900
 CAGAAGAGAG AAGGAGGAG GGAGATGTAT TTCTTAGGGC TCACCCCTTC ACAGACTGAC 3960
 AGAATGGTTT TGTTTTGT TTGTGTGTT TTGAGATGGA CTCTAGCTCT 4020
 20 GTCACCCAGG CTGAGTGA GTGGTGGAT CTGGCTCAC TGCAAGCTCC GCCTCCCGG 4080
 TTCTACCAT CTCTCTGCT CAGCTCCG AGTAGCTGG ACTACAGCG CCCACCACCA 4140
 CGCCCGGCTA ATTTTTTGT TTTTGTAGT GAGACGGGT TTCACCATGT TAGCCAGGAT 4200
 GGTCTCGATC TCTGACCTC GTGATCCGCC CGCTCGGCC TCCCAAAGT CTGGGATTAC 4260
 AGCGGTGAGC CACCGTGCT GCCCAGAAT GGTTTTAAA GCCACAGTTG AGAGGCCACC 4320
 25 CATGCCCCG CGCTGGACA GTGATCATCT TGTTCATCT GTTCAGTCT TTCTGTGTG 4380
 ATTGGAATTA TTCATCCCT TTGAAAGATG AGAAGGTGA GATGCAAAGA GTCTACCTTT 4440
 CCAAGTTCTC ACTGCTGGA AGAGCTAGAA GCACAGTTCA AGTTCTGGC TTCTGGACTC 4500
 TGCAGTCCAG GTCTCCCTTC TCCCACTTC CTACCTCAA TGCCACACTG TTTTGAAGT 4560
 GGCCCAAC TTGAAGGAA AGTTAAAGA CAGTTCAATT TAATCATCAG AATGCATTCT 4620
 30 TTTTTTTT CGAGACGGAG TTCCTCTT GCTGCCAGG CTGGAGTGCA ATGGTGAAT 4680
 GATCTCGGCT CACTGCAACC TCTGCTCT GGTGTCAAGT GATCTCCAG CCTCAGCTC 4740
 CCGAGTAGCT GGGATTATGG GCGCCACCA CCATGCCAG CTAATTTT TATTTTTTT 4800
 TTTTAGTAGA GATGGGGTT CGCCAGGTTG GCCAGGCTGG TCTGTGAAC TCCTGGCCTC 4860
 AGGTGATCTG CCCACCTCAT CCTCAAAAAG TGCTGGGATT ACAGGCATGA GCCACTGCGC 4920
 35 CTGGCTCAG AATGCATTCT TACACATCTA TCCTAGACAT TTATAAGCAC TCAATGGAT 4980
 AACAAATCAA GAATAAATGA TTGAAAGA TGATGCCGAA GAGTTGATGT CAATCTTTT 5040
 TTCTTAAGAA AAAAAGTCCG CGAGTATTA ATATTAGAT CAATGTTT AAAATGATTA 5100
 CTTTGTATAT CTCATTATTC CTATTTTGA ATAAAACTG ACCTCTTTA ATCATATACT 5160
 40 TGCTTTTGT AAATAGCAGC TTTGTGTCA TTCTCCAC TTTATTAGTT AATTAAAT 5220
 GGAAAAAACC CTCAACTAA TATCTTGTG TGTCCAGTC TTATAATAA AACTTATAAT 5280
 GCATG

45 SEQ ID NO:154 PFD6 Protein sequence:
 Protein Accession #: NP_055483.1

1 11 21 31 41 51
 MWQKIEDVIEW RPQTYLELEG LPCILIFSGM DPHGESLPRS LRYCDLRLLN SSCLVRTALE 60
 50 QELGLAAFYF SNEVPLEKGA RNEALESDAE KLSSTDNEDE ELGTEGSTSE KRSPMKRERS 120
 RSHDSASSSL SSKASGASLG GESSAQPTAL PQGEHARSPO PRGPAEEGRA PGEKQRPAS 180
 QGPPSAISRH SPGPTPOPC SLRTGQRSVQ VSVTSSCSQL SSSGSSSSS VAPAAGTWVL 240
 55 QASQCSLTKA CRQPPVFLP KLVDYDMVST DSSGLPKAAS LLPSPVMWA SSFRPLSKT 300
 MSTEQSLYY RQWTVPRPSH MDYGNRAEGR VDGHFPRRL LSPPQIGKT GAYLQFLSVL 360
 SRMLVRLTEV DVYDEEINI NLRESDWHY LQLSDPWPDL ELFKLPFDY IHDPKYEDA 420
 SLICSHYQGI KSEDRGMSRK PEDLYVRRQT ARMRLSKYAA YNTYHHCQC HQYMGFHPRY 480
 60 QLYESTLHAF AFSYSMLGEE IQLHFIPKS KEHFFVFSQP GGQLESMLRP LVTDKSHYI 540
 KSPTFTPTTG RHEHGLFNLY HAMDGASHLH VLVVKEYEMA IYKKYWPNHI MLVLPISFNS 600
 AGVGAHFLLI KELSYPHLEL ERNRQEELGI KPQDIWPFIV ISDDSCVMWN VVDVNSAGER 660
 SREFSWERN VSLKHIMQHI EAPDIMHYA LLGLRKWSSK TRASEVQEPF SRCHVHNFI 720
 LNVDLTQNVQ YNQNRFLCDD VDFNLRVHSA GLLLCRFNRF SVMKKQIVVG GHRSFHITSK 780
 VSDNSAAVVP AQYICAPDSK HTFLAAPAQL LLEKFLQHHS HLFFPLSLKN HDHPVLSVDC 840
 65 YLNLGSQISV CYVSSRPHEL NISCDLLFS GLLLYLCDSF VGASFLKKFH FLKGATLCVI 900
 CQDRSSLRQT VVRLELEDEW QFRLRDEFQT ANAREDRPLF FLTGRHI

70 SEQ ID NO:155 PFC6 DNA SEQUENCE
 Nucleic Acid Accession #: NM_000522
 Coding sequence: 1-1167 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 ATGACAGCCT CCGTGCTCT CCACCCCGC TGGATCGAGC CCACCGTCAT GTTCTCTAC 60
 GACAACGCG CGGCCTGGT GGCCGACGAG CTCAACAAGA ACATGGAAGG GGCGGCGCG 120
 GCTGCGAGC CGGCTGCAGC GGGCGCGCT GCCGGGGCGG GGGCGGGGGG CTTCCTCCAC 180
 CCGGCGGCTG CGGCGGACAG GGGCAACTTC TCGGTGGCGG CCGCGGCGCG GCGTGGCGG 240
 GCCGCGCGG CCAACCATG CCGCAACTG ATGGCGCAC CCAGCGCCCTT GGCGCCAGGA 300
 GCCGCGTCCG CCTACAGCAG CGCCCCGGG GAGGCGCCCC CGTGGCTGCG CGCGCTGCT 360

5 CCGCGGCTG CCGCTGCAGC CGCGCCGCC GCCGCCGCT CGTCTCGGG AGTCCCGGC 420
 CCGCGGGCC CCGCGGGCC AGAGGCGCC AAGCAATGCA GCCCTGCTC GGCAGCGCG 480
 CAGAGCTCGT CGGGGCCCGC GCGCTGCC TATGGCTACT TCGGCAGCG CTACTACCG 540
 TCGCGCCGCA TGGGCGCCGCC CCCCAACGCC ATCAAGTCGT GCCCCAGCC CCCCTCGGCC 600
 GCGCGCGCC CCGCCTTCGC GGACAAGTAC ATGGATACCG CCGGCCAGC TGCCGAGGAG 660
 TTCAGTCCC GCGCTAAGGA GTTCGCTTC TACCACCAGG GCTACGCAGC CGGCCTTAC 720
 CACCACATC AGCCCATGCC TGGCTACCTG GATATGCCAG TGGTGCCGGG CCTCGGGGG 780
 CCGGCGAGT CGCGCCACGA ACCCTTGGGT CTTCCTATGG AAGGTACCA GCCCTGGGG 840
 CTGCCAACG GCTGGAACGG CCAATGTAC TGCCCCAAG AGCAGGCGCA GCCTCCACC 900
 10 CTCTGGAAGT CCACTCTGCC CGACGTGGT TCCCATCCCT CGGATGCCAG CTCCTATAG 960
 AGGGGGAGAA AGAAGCGCGT GCCTTATACC AAGGTGCAAT TAAAGAACT TGAACGGGAA 1020
 TACGCCACGA ATAAATTCAT TACTAAGGAC AAACGGAGGC GGATATCAGC CACGACGAAT 1080
 CTCTCTAGC GGCAGGTAC AATCTGGTTC CAGAACAGGA GGGTTAAAGA GAAAAAGTC 1140
 15 ATCAACAAAC TGAACACCAC TAGTTAA

SEQ ID NO:156 PFC6 Protein sequence:
 Protein Accession #: NP_000513.1

20 1 11 21 31 41 51
 | | | | |
 MTASVLLHPR WIEPTVMFLY DNGGGLVADE LKNKMEGAAA AAAAAAAAAA AGAGGGGFPH 60
 PAAAAAGGNF SVAAAAA AAAANQCRNL MAHPAPLAPG AASAYSSAPG EAPPSAAAAA 120
 25 AAAAAA AAAASSGGPG PAGPAAAEAA KQCSPCSAQA QSSGPAALP YGYFGSGYYP 180
 CARMGPPPA IKSCPPPSA AAAAFADKY MDTAGPAEE FSSRAKEFAF YHQGYAAGPY 240
 HHHQPMFPGYL DMPVVPGLGG PGESRHEPLG LPMESYQFWA LPNGWNGQMY CPKEQAQPPH 300
 LWKSTLPDVV SHPSDASSYR RGRKKRVPYTV KVQLKELERE YATNKFITKD KRRRISATIN 360
 LSRQVTIWF QNRVRKKEKV INKLKITS

SEQ ID NO:157 PFA3 DNA SEQUENCE

Nucleic Acid Accession #: AW102723
 Coding sequence: 523-2676 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 | | | | |
 CCCTTATGGC GATTGGGCGG CTGCAGAGAC CAGGACTCAG TTCCCTGCC CTAGTCTGAG 60
 CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTCAGAAG CAGGTTTCAG TTGCAGAGTT 120
 40 TTCCTACACT TTCTCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCA GCGGAGGAC 180
 ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCGGGCG TGATCTCACC 240
 ATGTGCGGAT TTGCGAGGCG CGCCTGGAG CTGCTAGAGA TCCGAAGCA CAGCCCCGAG 300
 GTGTGCGAAG CCACCAAGAG TCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCG 360
 TCTCGGCGCT GTCTGCACCC TGTCGCTGA GCTGCTGAC AGTGACAATG ACATCCCACT 420
 45 TACCACTGTC TTGAATTGA TAGTGGCTTC TGTGTGTCAG TCTCATATAA GAACTACAGC 480
 TCATCAGGAG GAGATCGCAG CAGGGTAAGA GACACCAACA CCACTGTTCTG CACGAAGCTC 540
 AAGGATCTCA AGATCACAGG AGAGTGTCTT TTCTCTTAC TGGCACCAGG TCAAGTTCTT 600
 AACGAGTCTT CAGAGGAGGC AGCAGGAAGC TCAGAGAGCT GCAAGCAAC CGTGCCCATC 660
 TGTCAAGACA TTCCTGAGAA GAACATACAA GAAAGTCTTC CTCAAAGAAA AACCAGTCGG 720
 50 AGCCGACTCT ATCTTCACAC TTTGGCAGAG AGTATTGCA AACTGATTTT CCCAGAGTTT 780
 GAACGGCTGA ATGTTGCACT TCAGAGAACA TTGGCAAAGC ACAAAATAAA AGAAAGCAGG 840
 AAATCTTTGG AAAGAGAAGA CTTTGAAAAA ACAATTGCAG AGCAAGCAGT GCAGCAGAGT 900
 CCACTGGAGT TATCAAAGAA TCTCTGGTG AAGAGGTTT TAAAAATATG TACGAGGAAG 960
 55 ATGAAAAACAT CCTTGGGGTG GTTGGAGGCA CCCTTAAAGA TTTTAAACA GCTTCAGTAC 1020
 CCTTCTGAAA CAGAGCAGCC ATTGCAAGA AGCAGGAAAA AGGGGAGCT TGAGGACGCC 1080
 TCCATTCTAT GCCTGGATAA GGAGGATGAT TTCTACATG TTTACTACTT CTTCCCTAAG 1140
 AGAACCACT CCTGATTCT TCCGGCATC ATAAAGGCAG CTGCTACGT ATTATATGAA 1200
 ACGGAAGTGG AAGTGTGCTT AATGCCTCCC TGCTCCATA ATGATTGCAG CGAGTTTGTG 1260
 60 AATCAGCCCT ACTTGTGTA CTCGCTTAC ATGAAAAGCA CCAAGCCATC CCTGTCCCC 1320
 AGCAACCCC AGTCTCGCT GGTGATTCCC ACATCGCTAT TCTGCAAGAC ATTTCATT 1380
 CATTTCATGT TTGACAAAAG TATGACAATT CTGCAATTG GCAATGGCAT CAGAAGGCTG 1440
 ATGAACAGGA GAGACTTTCA AGGAAAGCCT AATTTTGAAT ACTTTGAAAT TCTGACTCCA 1500
 AAAATCAACC AGACCTTTAG CGGGATCATG ACTATGTTGA ATATGCAGTT TGTGTACGA 1560
 65 GTGAGGAGAT GGGACAAC TCAGAGAAA TCTTCAAGGG TTATGGACCT CAAAGGCCAA 1620
 ATGATCTACA TTGTTGAATC CAGTGCAATC TTGTTTTGG GGTACCCCTG TGTGGACAGA 1680
 TTAGAAGATT TTACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATCA CAATGCACTG 1740
 AGGGATGTGG TCTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCTGAA GAAGAGGCTG 1800
 GGAAGCTGA AGGCTACCTT TGAGCAAGCC CACCAAGCCC TGGAGGAGGA GAAGAAAAAG 1860
 70 ACAGTAGACC TTCTGTGCTC CATATTCCC TGTGAGGTTG CTCAGCAGCT GTGGCAAGGG 1920
 CAAGTTGTGC AAGCCAAGAA GTTCAGTAAT GTCACCATGC TCTTCTCAGA CATCGTTGGG 1980
 TTCCTGCCA TCTGCTCCCA GTGCTACCG CTGCAGGTCA TCACCATGCT CAATGCACTG 2040
 TACACTCGCT TCGACEAGCA GTGTGGAGAG CTGGATGCTT ACAAGGTGGA GACCATTTGG 2100
 ATGCCTATTG TGTGGCTTGG GGGATTACAC AAAGAGAGTG ATACTCATGC TGTTCAGATA 2160
 GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC CCATGGAGAA 2220
 75 CTTATCAAGA TCGCAATTGG ACTGCACCTT GGATCAGTTT TTGCTGGCGT CGTGGAGTT 2280
 AAAATGCCCC GTTACTGTCT TTTTGAAAC AATGTCACT TGGCTAACAA ATTTGAGTCC 2340
 TGCAGGTAC CAGCAAAAT CAATGTACG CCAACAACCT ACAGATTACT CAAAGACTGT 2400
 CCTGTTTTCG TGTTAACCCC TCGATCAAGG GAGGAACCT CACCAACTT CCCTAGTGAA 2460
 ATCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAACTC AAAACCATGC 2520

TTCCAAAAGA AAGATGTGGA AGATGCAAGC CAATTTTTTA GGCAAAGCAT CAGGAATAGA 2580
 TTAGCAACCT ATATACCTAT TTATAAGTCT TTGGGGTTTG ACTCATTGAA GATGTGTAGA 2640
 GCCTCTGAAA GCACTTTAGG GATTGTAGAT GGCTAACAAG CAGTATTAAA ATTTCAGGAG 2700
 CCAAGTCACA AICTTTCTCC TGTTTAACAT GACAAAATGT ACTCACTICA GTACTTCAGC 2760
 TCTTCAAGAA AAAAAAAAAA ACCTTAAAAA GCTACTTTTG TGGGAGTATT TCTATTATAT 2820
 AACCAGCACT TACTACCTGT ACTCAAAATT CAGCACCTTG TACATATATC AGATAATTGT 2880
 AGTCAATTGT ACAAACCTGAT GGAGTCACCT GCAATCTCAT ATCTGGTGG AATGCCATGG 2940
 TTATTAAAGT GTGTTTGTGA TAGTTGTCTG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3000
 AAAA

SEQ ID NO:158 PFA3 Protein sequence:
 Protein Accession #: NP_000947.1

1 11 21 31 41 51
 MFCTKLKDLK ITGECFSLP APGQVPNESS EEAAGSSESC KATVPICQDI PEKNIQESLP 60
 QRKTSRSRVY LHTLAESICK LIPEFERLN VALQRTLAKH KIKESRKSLE REDFEKTIAE 120
 QAVQQSPVEL SKNLLVKRFL KYVTRKMKTS LGWLEAPLKI FKQLQYPSSET EQPLPSRKK 180
 QQLDEDASILC LDKEDDFLHV YYFFPKRTTS LILPGHKAH AHVLYETEVE VSLMPPCFHN 240
 DCSEFVNQPY LLYSVHMKST KPSLSPSKPQ SSLVPTSLF CKTFPFHMF DKDMTILQFG 300
 NGIRRLMNRR DFQGKPNFEY FEILTPKINQ TFSGIMTMLN MQFVVRVRRW DNSVKKSSRV 360
 MDLKGQMIYI VESSAILFLG SPCVDRLEDF TGRGLYLSDI PIHNALRDVV LIGBQARAQD 420
 GLKKRLGLKL ATLEQAQHAL EEEKKKTVDL LCSIFPCEVA QQLWQGVVQ AKKFSNVTML 480
 FSDIVGFTAI CSQCSPLQVI TMLNLYTRF DQCCGELDVY KVETIAMPV WLGLHKESD 540
 THAVQIALMA LKMMELSDV MSPHGEPIKM RIGLHSGSVF AGVVGVMKMP YCLFGNNVTL 600
 ANKFESCSVP RKNVSPPTY RLLKDCPGFV FTPRSREELP PNFPSIPIGI CHFLDAYQQG 660
 TNSKPCQKK DVEDASQFFR QSIRNRLATY IPIYKSLGFD SLKMCRASES TLGIVDQ

SEQ ID NO:159 PFA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_004362
 Coding sequence: 102-1934 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGCCGGCGGG ACTGGTCTGA AGAGACGCGG GGACAAAGTG GCAACGACTT GGACATCTGA 60
 GCTGTCACTG CCGAAAACAG GCCGCAAGAG AGATAATCAA TATGCATTTC CAAGCCITTT 120
 GGCTATGTTT GGGTCTTCTG TTCATCTCAA TTAATGCAGA ATTATGGAT GATGATGTTG 180
 AGACGGAAGA CTTTGAAGAA AATTCAGAAG AAATGATGT TAATGAAAGT GAACITTCCT 240
 CAGAGATTA ATATAAGACA CCTCAACCTA TAGGAGAAGT ATATTTTGA GAAACTTTTG 300
 ATAGTGAAG GTTGGCTGGA TGGGTCTTAT CAAAAGCAAA GAAAGATGAC ATGGATGAGG 360
 AAATTTCAAT ATACGATGGA AGATGGGAAA TTGAAGAGTT GAAAGAAAAC CAGGTACCTG 420
 GTGACAGAGG ACTGGTATTA AAATCTAGAG CAAAGCATCA TGCAATATCT GCTGTATTAG 480
 CAAAACCATT CATTTTGTCT GATAAACCTT TGATAGTTCA ATATGAAGTA AATTTTCAAG 540
 ATGGTATTGA TTGTGGAGGT GCATACATTA AACTCTAGC AGACACTGAT GATTGTGATT 600
 TGGAAAACCT TTAATGATAA ACATCCTATA TCATTATGTT TGGACCATG AAATGTGGAG 660
 AAGATTATAA ACITCATTTT ATCTTCAGAC ATAAACATCC CAAAACCTGA GTTTTCGAAG 720
 AGAAACATGC CAAACCTTCA GATGTAGACC TTAATAAGTT CTTTACAGC AGGAAGACTC 780
 ATCTTTATAC CCTTGTGATG AATCCAGATG ACACATTGTA GGTGTTAGTT GATCAACAG 840
 TTGTAAACAA AGGAAGCCTC CTAGAGGATG TGGTCTCTCC TATCAAACT CCCAAAGAAA 900
 TTGAAGATCC CAATGATAA AAACCTGAGG AATGGGATGA AAGAGCAAAA ATTCCTGATC 960
 CTCTGCGGT CAAACAGAA GACTGGGATG AAGTGAACC TGCCCAATAA GAAGATTCAA 1020
 GTGTGTGTTA ACCTGCTGGC TGGCTTGATG ATGAACCAAA ATTTATCCCT GATCCTAATG 1080
 CTGAAAAACC TGATGACTGG AATGAAGACA CGGATGGAGA ATGGGAGGCA CCTCAGATTG 1140
 TTAATCCAGC ATGTCCGATT GGGTGTGGTG AGTGGAAACC TCCCATGATA GATAACCCAA 1200
 AATACAAAGG AGTATGGAGA CTCCACTGG TCGATAATCC TAACATACAG GGAATCTGGA 1260
 GTCTCGAAA AATTCCTAAT CCAGATTATT TCGAAGATGA TCATCCATT CTCTGACTT 1320
 CTTCAGTGC TCTGGTTTA GAGCTTTGGT CTATGACCTC TGATATCTAC TTGATAATT 1380
 TTATTATCTG TTCGAAAAAG GAAGTAGCAG ATCACTGGGC TGCAGATGGT TGGAGATGGA 1440
 AAATAATGAT AGCAATGCT AATAAGCTG GTGTATTAAC ACAGTTAATG GCAGCTGCTG 1500
 AAGGGCACC ATGGCTTTGG TTGATTTATC TTGTGACAGC AGGAGTGCCA ATAGCATTAA 1560
 TTACTTCATT TTGTGGCCA AGAAAAAGTAA AGAAAAACA TAAAGATACA GAGTATAAAA 1620
 AAACCGACAT ATGTATACCA CAAACAAAAG GAGTACTAGA GCAAGAAGAA AAGGAAGAGA 1680
 AAGCAGCCTT GGAACCAACA ATGGACCTGG AAGAGGAAAA AAAGCAAAAT GATGGTGAAA 1740
 TGCTTGAAGA AGAAGAGGAA AGTGAACCTG AGGAAAAGAG TGAAGAAGAA ATTGAAATCA 1800
 TAGAAGGGCA AGAAGAAAGT AATCAATCAA ATAAGTCTGG GTCAGAGGAT GAGATGAAAG 1860
 AAGCAGATGA GAGCACAGA TCTGGAGATG GGCCGATAAA GTCAGTACGC AAAAGAAGAG 1920
 TACGAAAGGA CTAAGCTAGA TTGAAATATT TTAATTCCTC GAGAGGATGT TTGGCATTGT 1980
 AAAAATCAGC ATGCCAGACC TGAACTTTAA TCAGTCTGCA CATCTGTTT CTAATATCTA 2040
 GCAACATTAT ATTCTTTCAG ACATTTATTT TAGTCCTTCA TTTCGAGGA AAAAGAAGCA 2100
 ACTTGAAGT TACCTCATCT TTGAATTITG AATAAAAGTG GCACATTACA TATCGGATCT 2160
 AAGAGATTAA TACCATTAGA AGTTACACAG TTTTAGTTGT TTGGAGATAG TTTTGGTTTG 2220
 TACAGAACAA AATAATATGT AGCAGCTTCA TTGCTATTGG AAAATCAGT TATTGGAATT 2280
 TCCACTTAAA TGCTATACA ACAATATAAC TGGTAGTTCT ATAATAAAAA TGAGCATATG 2340
 TTCTGTGTG AAGAGCTAAA TGCAATAAAG TTTCTGTATG GTTGTGTGAT TCTATCAACA 2400
 ATTGAAAGTG TTGTATATGA CCCACATTTA CTAAGTTTGT GTCAAAATAT AGTTACAGTG 2460
 AGTTGTTTGC TTAATTATA GATTCCTTTA AGGACATGCC TTGTTCATAA AATCACTGGA 2520

TTATATTGCA GCATATTTTA CATTGGAATA CAAGGATAAT GGGTTTTATC AAAACAAAAT 2580
 GATGTACAGA TTTTITTTTCA AGTTTITATA GTTGCITTTAT GCCAGAGTGG TTTACCCCAT 2640
 TCACAAAATT TCTTATGCAT ACATTGCTAT TGAATAATAA ATTAAATAT TTTTCATCC 2700
 TGAAAAAAA

SEQ ID NO:160 PFA1 Protein sequence:
 Protein Accession #: NP_004353.1

1 11 21 31 41 51
 | | | | |
 MHFQAFWLCL GLLFISINAE FMDDDVETED FEENSEEIDV NESELSSEIK YKTPQPIGEV 60
 YFAETFDSEGR LAGWVLSKAK KDDMDEEISI YDGRWEIEEL KENQVPGDRG LVLKSRAXHH 120
 AISAVLAKPF IFADKPLIVQ YEVNFQDGID CGGAYIKLLA DTDDLILENF YDKTSYIMF 180
 GPDKCGEDYK LHFIFRHKHP KTGVEEEKHA KPPDVLKKF FTDRKTHLYT LVMPNDDTFE 240
 VLVDQTVVVK GSLLLEDVVP IKPPKEIEDP NDKKPEEWE RAKIPDPSAV KPEDWDESEP 300
 AQIEDSSVVK PAGWLDDEPK FIPDPNAEKP DDWNEDTGE WEAPQLNPA CRICGGEWKP 360
 PMIDNPKYKG VWRPPLVDNP NYQGIWSPRK IPNPDYFEDD HPFLITSFSA LGLELWSMTS 420
 DIYFDNFIC SEKEVADHWA ADGWRWKIMI ANANKPGVLK QLMAAAEGHP WLWLIYLVTA 480
 GVPIALITSF CWPRKVKKKH KDTEYKKTDI CIPQTKGVLE QEEKEEKAAL EKPMDLEEEK 540
 KQNDGEMLEK EEESEPEEKS EEEIEIEGQ EESNQSNKSG SEDEMKEADE STGSGDGIPIK 600
 SVRKRVRKRD

SEQ ID NO:161 PEZ9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005932
 Coding sequence: 75-2216 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GCGGAGCGCG CGCTCCAGC GAAAGCAGCA GGGCAGGGAT CTGCGTTGGA GGAAGGGACT 60
 GCTCTGGTGC TAGAATGCTG TGGCTCGGAA GGCTGGGCGG CTGGGAGCC AGAGCAGCAG 120
 CTCTGCCGCC CCGCGGGCGG GGCCGGGGAA GCCTCGAAGC CGGGATCCGG GCCCGAAGGG 180
 TCAGCACCAG CTGGTCTCCC GTGGGCGCGG CCTTCAATGT CAAGCCCCAG GGCAGCCGCT 240
 TGGACCTGTT CGGCGAGCGG GCGCGTCTTT TTGGAGTTCC TGAGCTGAGT GCCCCAGAAG 300
 GATTTTCATAT TGCACAAGAA AAAGCCTTGA GAAAGACAGA ATTGCTTGTTG GACCGTGCAT 360
 GTTCCACCCC ACCTGGGCCC CAGACCGTGC TGATCTTCA TGAGCTCTCG GATTCCCTAT 420
 GCAGAGTGGC CGACTTGGCT GATTTTGTGA AAATCGCTCA CCCTGAGCCA GCATTGAGAG 480
 AAGCTGCGGA AGAAGCTTGT AGAAGTATTG GCACCATGGT AGAGAAGTTG AACACAAATG 540
 TGGATTATA TCAAAGTTTG CAAAAATTAC TAGCTGATAA AAAACTTTGTG GATTCCCTTG 600
 ATCCAGAAAC AAGGCGAGTG GCTGAAGTGT TTATGTTTGA TTTTGAAAT AGTGGAATCC 660
 ATCTAGACAA AAAAAAGCGT AAAAGAGCAG TGGACCTCAA TGTTAAAAATC TTGGATTGTA 720
 GTAGTACATT TCTATGGGA ACCAATTTTC CCAACAAGAT TGAGAAGCAT CTCTTACCAG 780
 AACACATTCT TCGTAACITT ACATCTGCTG GGGATCATAT CATAATTGAT GGTCTCCACG 840
 CAGAAATACC AGATGACTGT GTGCGAGAAG CTGCTTATA AATTTTCTT TATCCCAATG 900
 CTGGTCAATT GAAATGTTTA GAAGAATTGC TCAGCAGCAG AGATCTTCTG GCAAAGTTGG 960
 TGGGGTATTG CACGTTTCT CACAGGCTC TCCAAGGAAC GATAGCTAAA AATCCAGAGA 1020
 CTGTCATGCA GTTCCTTGAA AAATATCTG ACAAACCTTC TGAAAGAACT CTGAAAGATT 1080
 TTGAGATGAT ACGAGGGATG AAAATGAAAC TGAATGCTCA AAATCCGAA GTAATGCCCT 1140
 GGGACCCCC TTACTACAGT GGTGTGATTC GTGCAGAAAG GTATAATATT GAGCCAGGCC 1200
 TATATTGCCC TGTATTCTCT CTGGAGCAT GCATGGAAGG CCTGAATATT TTGCTTAACA 1260
 GACTGTGGG GATTTTCTTA TATGCAGAGC AGCCTGCAAA AGGAGAGGTG TGGAGCGAAG 1320
 ATGTCCGAAA ACTGGCTGTT GTTCATGAAT CTGAAGGATT GTTGGGTAC ATTACTGTG 1380
 ATTTTTTICA GCGAGCAGAC AAACCACATC AGGATTGCCA TTCACTATC CGTGGAGGCA 1440
 GACTAAAGGA AGATGGAGAC TATCAACTCC CACTTGTAGT TCTTATGCTG AATCTTCCCC 1500
 GTTCTCAAG GAGTTCTCCA ACTTTGCTAA CTCTGGCAT GATGGAAAAT CTTTCCATG 1560
 AAATGGGACA TGCCATGCAT TCAATGCTAG GACGTACTCG TTACCAACAC GTCAGTGGGA 1620
 CCAGGTGCCC TACTGATTTT GCTGAGGTTT CTCTATTCT GATGGAGTAC TTTGCAATG 1680
 ATTATCGAGT AGTTAAACAA TTTGCCAGAC ATTATCAGAC TGGACAGCCA CTGCCAAAAA 1740
 ATATGGTGTG TCGTCTTGT GAATCTAAAA AGGTTTGTGC TGCAGCTGAT ATGCAACTTC 1800
 AGGTCTTTTA TGCCACTCTG GATCAATCT ACCATGGGAA GCATCCCTG AGGAATTCAA 1860
 CCACAGACAT TCTCAAGGAA ACACAAGAGA AATCTATGG CCTACCATAT GTTCCAAATA 1920
 CTGCTGGCA GCTGCGATTG AGCCACCTCG TGGGGTATGG TGCTAGATAT TACTTCTACC 1980
 TCATGTCCAG AGCGGTGCGC TCCATGGTTT GGAAGGAGTG TTTCTACAG GATCCTTTCA 2040
 ACAGGGCTGC CGGGGAGCGC TATCGCAGGG AGATGCTGGC CCACGGTGGG GGCAGGGAGC 2100
 CCATGCTCAT GGTGGAAGGT ATGCTTCAGA AGTGCTCTTC TGTGATGAC TTCGTAAGTG 2160
 CCTCGTTTC CGACTTTGAT CTGGACTTCG AAACCTTCT CATGGATTCT GAATAAAAA 2220
 AACACTCTAC ACCTCTAATC AAGGTCATGT AGTAATGACT TTGTATATAA TGCTACAGCT 2280
 GTGAGAGCTT GTTCTGATT GTTTCATTGT TCGTCTCTGT AATCTGAAA AACTTTAAAC 2340
 TGGTAGAACT TGAATAAAT AATTGTTTT AATTAATAA AAAAAAAAAA AA

SEQ ID NO:162 PEZ9 Protein sequence:
 Protein Accession #: NP_005923.1

1 11 21 31 41 51
 | | | | |
 MLCVGRGLGL GARAAALPPR RAGRGSLAEG IRARRVSTSW SPVGAAFNVK PQGSRLDLFG 60
 ERARLFGVPE LSAPEGFHIA QEKALRKTEL LVDRACTPP GPQTVLIFDE LSDSLCRVAD 120

5 LADFKVIAHP EPAFREAAEE ACRSIGTMVE KLNTNVDLYQ SLQKLLADKK LVDSLDPETR 180
 RVAELFMDFE EISGHLDDQ KKRRAVDLNV KILDLSTFL MGTNFPNKIE KHLLEPHIR 240
 NFTSAGDHII IDGLHAESPDLVREAAKYI FLYPNAGQLK CLEELSSRD LLAKLVGYST 300
 FSHRALQGTI AKNPETVMQF LEKLSDKLSE RILKDFEMIR GMKMKLNAQN SEVMPWDPPY 360
 YSGVIRAERY NIEPSLYCPF FSLGACMEGL NILLNRLGI SLYAEQPAKG EVWSEDVRKL 420
 AVVHESEGLL GYIYCDFFQR ADKPHQDCHF TIRGGRLKED GDYQLPLVVL MLNLPSSRS 480
 SPTLLTPGMM ENLFHEMGHA MHSMGLGRTRY QHVTGTRCPT DFAEVPISLM BYFANDYRVV 540
 10 NQFARHYQTG QPLPKNMVSR LCESKKVC AA ADMQLQVFYA TLDQIYHGKH PLRNSTTDIL 600
 KETQEKFYGL PYVPNTAWQL RFSHLVGYGA RYYSYLSMRA VASMVWKECF LQDPFNRAAG 660
 ERYRREMLAH GGGREFMLMV EGMLQKCPVS DDFVSALVSD LDLDLFETFLM DSE

SEQ ID NO:163 PEZ8 DNA SEQUENCE

15 Nucleic Acid Accession #: AF103907
 Coding sequence: none (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 ACAGAAGAAA TAGCAAGTGC CGAGAAGCTG GCATCAGAAA AACAGAGGGG AGATTGTGT 60
 GGCTGCAGCC GAGGGAGACC AGGAAGATCT GCATGGTGGG AAGGACCTGA TGATACAGAG 120
 GAATTACAAC ACATATACTT AGTGTTCCTA TGAACACCAA GATAAATAAG TGAAGAGCTA 180
 25 GTCCGCTGTG GTGACACAGG GCTGGATCAC CATCGACGCG ACTTCTGAG 240
 TACTCAGTGC AGCAAGAAA GACTACAGAC ATCTCAATGG CAGGGGTGAG AAATAAGAAA 300
 GGCTGCTGAC TTACCATCTT GAGGCCACAC ATCTGCTGAA ATGGAGATAA TTAACATCAC 360
 TAGAAACAGC AAGATGACAA TATAATGTCT AAGTAGTGAC ATGTTTTCG ACATTTCAG 420
 CCCCTTTAAA TATCCACACA CACAGGAAGC ACAAAGGAA GCACAGAGAT CCTCGGAGAG 480
 AATGCCCGGC CGCCATCTTG GGTGATCGAT GAGCCTCGCC CTGTGCTGG TCCCGCTTGT 540
 GAGGGAAGGA CATTAGAAAA TGAATTGATG TGTTCCTTAA AGGATGGGCA GGAAAAACAGA 600
 30 TCCTGTGTGT GATATTTATT TGAACGGGAT TACAGATTTG AAATGAAGTC ACAAAGTGAG 660
 CATTACCAAT GAGAGGAAAA CAGACGAGAA AATCTTGATG GCTTACAAG ACATGCAACA 720
 AACAAAATGG AATACTGTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCACGGG 780
 GCAGAGGGTC AGGATCTCTG CCCTGCTGCC TAACTGTGC GTTCATAACC AAATCATTTC 840
 ATATTTCTAA CCCTCAAAAC AAAGCTGTGT TAATATCTGA TCTCTACGGT TCCTCTGGG 900
 35 CCAACATTC TCCATATATC CAGCCACACT CATTTTAAT ATTAGTTC CAGATCTGTA 960
 CTGTGACCTT TCTACACTGT AGAATAACAT TACTCATTTT GTTCAAGAC CCTTCGTGTT 1020
 GCTGCCAAT ATGATAGCTA CTGTTTTTCC TAAGGAGTGT TCTGGCCAG GGGATCTGTG 1080
 AACAGGCTGG GAAGCATCTC AAGATCTTTC CAGGGTTATA CTACTAGCA CACAGCATGA 1140
 TCATTACGGA GTGAATTATC TAATCAACAT CATCCTCAGT GTCTTGGCC ATACTGAAAT 1200
 40 TCATTTCCTA CTTTTGTGCC CATCTCAAG ACCTCAAAAT GTCATTCCAT TAATATCACA 1260
 GGATTAACCT TTTTTTTTAA CCTGGAAGAA TTCAATGTGA CATGCAGCTA TGGGAATTTA 1320
 ATTACATATT TTGTTTTTCA GTGCAAGAT GACTAAGTCC TTTATCCCTC CCCTTTGTTT 1380
 GATTTTTTTT CAGTATAAAA GTTAAATGTC TTAGCCTTGT ACTGAGGCTG TATACAGCAC 1440
 AGCCTCTCCC CATCCCTCCA GCCTTATCTG TCATCACCAT CAACCCCTCC CATACCACCT 1500
 45 AAACAAAATC TAACCTGTAA TTCTTGAAC ATGTCAGGAC ATACATTATT CCTTCTGCCT 1560
 GAGAAGCTCT TCCTGTCTCT TTAATCTAG AATGATGTAA AGTTTGAAT AAGTTGACTA 1620
 TCTTACTCA TGCAAGAGAG GGACACATAT GAGATTCATC ATCATAGAG ACAGCAATAA 1680
 CTAAGAGTGT AATTTGATTA TAAGAGTTTA GATAAATATA TGAATGCAA GAGCCACAGA 1740
 GGGATGTTT ATGGGGCAGC TTGTGAAGCC TGGGATGTGA AGCAAGGCA GGGAACTCA 1800
 50 TAGTATCTTA TATAATATAC TTCAITTTCT TATCTCTATC ACAATATCCA ACAAGCTTTT 1860
 CACAGAATTC ATGAGTGCA AATCCCCAAA GGTAACCTTT ATCCATTCCA TGGTGAGTGC 1920
 GCTTTAGAA TTTGGCAAT CATACTGGTC ACTTATCTCA ACTTTGAGAT GTGTTTGTC 1980
 TTGTAGTTAA TTGAAAGAAA TAGGGCACTC TTGTGAGCCA CTTTAGGGTT CACTCCTGGC 2040
 AATAAAGAAT TTACAAGAG CTACTCAGGA CCAAGTTGTA AGAGCTCTGT GTGTGTGTGT 2100
 55 GTGTGTGTGT GAGTGTACAT GCCAAAGTGT GCCTCTCTCT CTGACCCAT TATTCAGAC 2160
 TTAACAAGAG CATGTTTCA AATGGCACTA TGAGCTGCCA ATGATGTATC ACCACCATAT 2220
 CTCATTATTC TCCAGTAAAT GTGATAATAA TGTCATCTGT TAACATAAAA AAAGTTTGAC 2280
 TTCACAAAAG CAGCTGGAAG TGGACAACCA CAATATGCAT AAATCTAACT CCTACCATCA 2340
 GCTACACACT GCTTGACATA TATGTTAGA AGCACCTCGC ATTTGTGGGT TCTCTTAAAG 2400
 60 AAAATACTTG CATTAGTCTC CAGCTGGGGC TGTGCATCAG GCGGTTTGAG AAATATTTCA 2460
 TTCTCAGCAG AAGCCAGAAT TTGAATTCCC TCATCTTTTA GGAATCATTT ACCAGGTTTG 2520
 GAGAGGATTC AGACAGCTCA GGTGCTTTCA CTAATGTCTC TGAACCTCTG TCCTCTTTG 2580
 TGTTTATGGA TAGTCCAATA AATAATGTTA TCTTTGAACT GATGCTCATA GGAGAGAATA 2640
 TAAGAACTCT GAGTGATATC AACATTAGGG ATTCAAAGAA ATATTAGATT TAAGCTCACA 2700
 65 CTGGTCAAAA GGAACCAAGA TACAAAGAAC TCTGAGCTGT CATCGTCCCC ATCTCTGTGA 2760
 GCCACAACCA ACAGCAGGAC CCAACGCATG TCTGAGATCC TTAATCAAG GAAACCAAGT 2820
 TCATGAGTTG AATTCTCTTA TTATGGATGC TAGCTTCTGG CCATCTCTGG CTCTCTCTT 2880
 GACACATAIT AGCTTCTAGC CTTTGTCTCC ACGACTTTTA TCTTTTCTCC AACACATCGC 2940
 TTACCAATCC TCTCTGTCT CTGTTGCTTT GGACTTCCCC ACAAGAATT CAACGACTCT 3000
 70 CAAGTCTTTT CTCCATCCC CACCACTAAC CTGAATGCCT AGACCCTTAT TTTTATTAAT 3060
 TTCCAATAGA TGCTGCCTAT GGGCTATATT GCTTTAGATG AACATTAGAT ATTTAAAGCT 3120
 CAAGAGGTTT AAAATCCAAC TCATTATCTT CTCTTCTTT CACCTCCCTG CTCTCTCTCC 3180
 TATATTACTG ATTGCACTGA ACAGCATGGT CCCCATGTGA GCCATGCAAA TGAGAAACCC 3240
 AGTGGCTCCT TGTGGTACAT GCATGCAAGA CTGTGAAGC CAGAAGGATG ACTGATTACG 3300
 CCTCATGGGT GGAAGGGGACC ACTCTGGGC CTTCGTGATT GTCAGGAGCA AGACCTGAGA 3360
 75 TGCTCCCTGC CTCGATGCT CTCTGCATCT CCCCTTCTA ATGAAGATCC ATAGAATTG 3420
 CTACATTGGA GAATTCGAAT TAGGAACTCA CATGTTTTAT CTGCCCTATC AATTTTTTAA 3480
 ACTTGCTGAA AATTAAGTTT TTCAAAATC TGTCTTGTA AATTACTTTT TCTACAGTG 3540
 TCTTGGCATA CTATATCAAC TTGATTCTT TGTTACAACT TTCTTACTC TTTATCACC 3600

5 AAAGTGGCTT TTATCTCTT TATTATTATT ATTTCTTTT ACTACTATAT TACGTTGTTA 3660
 TTATTTTGGT CTCTATAGTA TCAATTTATT TGATTTAGTT TCAATTTATT TTTATTGCTG 3720
 ACTTTTAAAA TAAGTGATTG GGGGGGTGGG AGAACAGGGG AGGGAGAGCA TTAGGACAAA 3780
 TACCTAATGC ATGTGGGACT TAAACCTAG ATGATGGGTT GATAGGTGCA GCAAACCACT 3840
 ATGGCACACG TATACCTGTG TAACAAACCT ACACATCTCTG CACATGTATC CCAGAACGTA 3900
 AAGTAAAAAT TAAAAAAG TGA

10 PEZ6 Protein sequence:
 Protein Accession #: none

SEQ ID NO:164 PEZ6 DNA SEQUENCE

15 Nucleic Acid Accession #: AB028945
 Coding sequence: 1-3765 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 20 ATGATGATGA ACGTCCCGGG CGGAGGAGCG GCCGCGGTGA TGATGACGGG CTACAATAAT 60
 GGTGCGCTGTC CCCGGAATTC TCTCTACAGT GACTGCATTA TTGAGGAGAA GACGGTGGTC 120
 CTGCAGAAAA AAGACAATGA GGGCTTTGGA TTCTGTCTTC GAGGGGCCAA AGCTGACACA 180
 CCCATTGAAG AATTACACCC AACACCGGCT TTCCAGCCCT TACAGTACCT GGAGTCCGTG 240
 GATGAAGGTG GGGTGGCGTG GCAAGCCGGA CTAAGGACCG GGGACTTCTT GATTGAGGTT 300
 AACAATGAGA ATGTTGTCAA AGTCGGCCAC AGGCAGGTGG TGAACATGAT CCGGCAGGGA 360
 GGGAAATCACC TGGTCCCTAA GGTGGTCAAG GTGACCAGGA ATCTGGACCC CGACGACACC 420
 25 GCCAGGAAGA AAGTCCCGCC GCCTCCAAAG CGGGCACCAG CCACAGCCCT CACCCTGCGC 480
 TCCAAGTCCA TGACCTCGGA GCTGGAGGAG CTCGTGGATA AAGATAAACC CGAGGAGATA 540
 GTCCCGGCTC CCAAGGCCCT CCGCGCTGCT GAGAACATGG CTGTGGAAAC GAGGGTGGCG 600
 ACCATCAAGC AGCGGCCAG CAGCCGCTGC TTCCCGCGCG GCTCAGACAT GAATCTGTG 660
 TACGAACGCC AAGGAATCGC CGTATGACG CCCACTGTTT CTGGGAGGCC AAAAGCCCGC 720
 30 TTTCTGGGCA TCCCTCGAGG TACGATGCGA AGGCAGAAAT CAATAGACAG CAGAATCTTT 780
 CTATCAGGAA TAACAGAGGA AGAGCGGCAG TTCTGGCTC CTCCATGCT GAACTTCACC 840
 AGAAGCCTGT CCAATGCCGA CACTCTGAG GACATCCCCC CTCCACCGCA GTCTGTGCC 900
 CCGTCCCCAC CACCACCTTC CCAACCACT TACAACCTGCC CCAAGTCCCC AACTCCAAGA 960
 GTCTACGGGA CGATTAAGCC TGCCTCAAT CAGAATCTTG CCGCAAGGT GTCCCCCGCC 1020
 35 ACCAGGTCCG ACACCGTGGC CACCATGATG AGGGAGAAGG GGATGTACTT CAGGAGAGAG 1080
 CTGGACCGCT ACTCCTTGA CTTCTAAGAC CTCTACAGTC GGAATGCCGG CCCGCAAGCC 1140
 AACTTCCGCA ACAAGAGAGG CCAGATGCCA GAAAACCCAT ACTCAGAGGT GGGGAAGATC 1200
 GCCAGCAAAG CCGTCTACGT CCCGCCAAG CCCGCCAGGC GGAAGGGGAT GCTGGTGAAG 1260
 40 CAGTCCAAAG TGGAGGACAG CCCGAGAAAG ACCTGCTCCA TCCCTATCCC GACCATCATC 1320
 GTGAAGGAGC CGTCCACCAG CAGCAGCGGC AAGAGCAGCC AGGCAGCAG CATGGAGATC 1380
 GACCCCAAG CCCCGGAGCC ACCGAGCCAG CTGCGGCTG ACGAAAGCCT GACCGTCAGC 1440
 AGCCCTTTG CCGCCGCCAT CGCCGAGCC GTCCGCGACC GTGAGAAGCG GCTGGAAGCC 1500
 AGGAGGAACT CCGCGCTTCT CTTCTCCACA GACTTGGGGG ATGAGGATGT GGGCTTGGGG 1560
 45 CCACCCGCC CCAGGACCGG GCCTCTCATG TTCCCGGAGG AGGGGGATTI TGCTGACGAG 1620
 GACAGCGCTG AGCAGCTGT ATCCCCATG CCGAGTGCCA CGCCAGGGA GCCGAAAAAC 1680
 CATTTCTGG GTGGCGCCGA GGCACGTCT CCGGGTGAGG CTGGGAGGCC GCTGAATICC 1740
 ACGTCCAAAG CCCAGGGGCC CGAGAGCAGC CCAGCAGTGC CCTCCGCGAG CAGCGGCACA 1800
 GCGCGGCCCG GGAATTATGT CCACCACTC ACAGGGCGGC TGCTTGATCC CAGCTCCCCG 1860
 50 CTGGCCCTGG CACTCTCCG AAGGGACCGA GCCATGAAG AGTCTCAACA GGGACCCAAA 1920
 GGGGAGGCC CCAAGGCCGA CCTCAACAAA CCTCTTTACA TTGATACCAA AATGCGGCC 1980
 AGCCTGGATG CCGGCTTCCC TACGGTACC AGGCAGAAAC CCGGGGACC CTTGAGCGCG 2040
 CAGGAGACCG AGAACAAGTA CGAGACCGAC CTGGGCGGAG ACCGGAAGG CGATGACAAG 2100
 AAGAATGAC TGATCGACAT CATGGACAG TCCCAGCAGA AGTCGGCTGG CTTGCTGATG 2160
 55 GTGCACACCG TGGACGCCAC TAAGCTGGAC AACGCCCTGC AGGAAGAGGA CGAGAAGGCA 2220
 GAGGTGGAGA TGAAGCCAGA CAGCTCGCG TCCGAGGTGC CAGAAGGTGT TTCCGAAACC 2280
 GAAGGTGCTT TACAGATCTC CGTGCCCCC GAGCCACCA CCGTGCCCGG CAGAACCATC 2340
 GTCGCGGTGG GCTCCATGGA AGAGGCGGTG ATTTTGCCAT TCCGCATCCC TCCTCCCCCT 2400
 CTGGCATCCG TGGACTTGA TGAGGATTTT ATTTTACAG AGCCATTGCC TCCTCCCCCTG 2460
 60 GAATTGTCAA ATAGTTTTGA TATCCCGAT GACCGGGCAG CTTCTGTCCC GGCTCTCTCA 2520
 GACTTAGTGA AGCAGAAGAA AAGCGACACC CCTCAGTCCC CTTCTGTGAA CTCCAGCCAA 2580
 CCAACCAACT CTGCAGACAG CAAGAAGCCA GCCAGTCTTT CAAACTGTCT GCCTGCCTCA 2640
 TTCTGCCAC CCCCTGAAAG CTTTGACGCC GTCGCGACT CTGGATCGA GGAGGTGGAC 2700
 AGCCGGAGTA GCAGCGACCA CCACCTCGAG ACGACCAGCA CTATCTCCAC CGTGTCTAGC 2760
 65 ATCTCCACCC TGTCTTCCGA AGGTGGAGAG AATGTGGACA CTTGCACAGT CTATGCAGAT 2820
 GGGCAAGCAT TTATGGTTGA CAAACCCCA GTACCTCTTA AGCCAAAAAT GAAGCCCATC 2880
 ATTCACAAAA GCAATGCACT TTATCAAGAC GCGCTCGTGG AAGAAGATGT AGATAGCTTT 2940
 GTTATCCCCC CGCCCGCTCC CCGCCCGCG CCGGCGAGT CCCAGCTGG GATGGCCAA 3000
 GTTCTCCAGC CAAGGACCTC CAAGTTGTGG GCGCAGCTCA CAGAGATCAA AAGCCCGATT 3060
 CTCTCAGGCC CAAAGGCAA CGTTATTAGT GAATTGAACT CTATCTTACA GCAATGAAC 3120
 70 CGAGAGAAAT TGGCAAAGCC GGGGAAGGA CTGGATTAC CAATGGGAGC CAAGTCCGCC 3180
 AGCCTCGCTC CAAGAAGCCC GGAGATCATG AGCACCATCT CAGGTACAG GAGCAGCAG 3240
 GTCACCTTCA CTGTTCCGCC CGGCACCTCC CAGCCCATCA CCTGCAGAG CCGGCCCCCC 3300
 GACTATGAAA GCAGGACCTC AGGAACAAGA CGTGCCCAA GCCTGTGGT CTCGCCAACA 3360
 75 GAGATGAAA AAGAGACCTT GCCCGCCCC CTGCTGCTG CCACCGCTC TCCTTCTCCC 3420
 GCTCTCTCAG ATGTTCTTAG CCTTCAAAG CAGCCCTT CTGGGATCT ATTTGGCTTG 3480
 AACCAGCGG CAGCAGTAG GTCCCATCC CCTTCGATAC TGCAACAGCC AATCTCAAT 3540
 AAGCTTTTAA CAATCAACC TGTCCACCTG TGGACTAAAC CAGATGTGGC CGATTGGCTG 3600
 GAAAGTCTAA ACTTGGGTGA ACATAAAGAG GCCTTCATGG ACAATGAGAT CGATGGCAGT 3660
 CACTTACCAA ACCTGCAGAA GGAGGACCTC ATCGATCTTG GGGTAACTCG AGTCGGGCAC 3720

AGAATGAACA TAGAAAGGGC TTTGAAACAG CTGCTGGACA GATAAGGACG GCTGCTCTCC 3780
 ACCTCGCAGA CTGCTCTTGT TATAAGTAGA GATGGGCTCG TGCTGAAACA TCTGAATGCC 3840
 AAGCGAAGTC TGTGAGCATC AACCCCACTC CATGGGTTTG TCTCTGGTA CCCAAAGAAA 3900
 TACTGAGTTG TGTCCACAAC ATGGCTGGGT CTTCAGACCC CTGGCTCACC ATGTGGGTGT 3960
 5 CTGGGCAGT TCTATCACA CATGGGACAA GGGGAGGGAG TTTTCTAAC ATGGA AAAAG 4020
 ATTCCAGGCC TGCCGCCAG CATGCAGGTG GCCTCGCTT GCCGGGTCCG AGAGGCTCCC 4080
 CGTCAATTT GCACGGGATC CTAGCTCTTG TAGGCAGACA CCAGTGCCTC CTAGATACCT 4140
 10 CCTGAGACCT CCGTCTCTG CTTCGGGGC AGCTCTCACC ACCCCAGGCC CCGGCATGAG 4200
 GCCTTCTCTC AGTCTGTGG CCTCTCAGAG GACACCTGAT GCTCACCTGC CCCTCTTCT 4260
 CCTGCCTTG GCTTGCAGTG AGATGCTCCC AGATGCATTT GTCCAGTGCC CCATCATGGG 4320
 CCTGAAAGGC AGAGAAACTT TTCTCTACAC AGATTCTTTT CCCCATCTCC TCTGTGGTT 4380
 TGCATCCATG GCTCTTGGC CATGAGGTTT CTGGCAGTGC TGGGAGTTTG GATGGGATCG 4440
 TGCCAGCTT TGCTTAGCTT TCTTATTTC TGCAAATCTG TTAGCATAAT TCCAAGGTGG 4500
 15 CCAAGCAGAT GTCACATGGA GTTAGTCAAA GCACAAAGTC ACGATTCCAC AATGGAGGGG 4560
 AGACCTGGCC AAGGGAGCCA GCCAGCGTGC AACTGCCCAA GCTCCAGGTC TCCAGGACAA 4620
 GAGCAGTTGT CTGCCATGAG CACCCATCCA GGATGGAGAA TAAGGGCTTC TCTGCCTCTC 4680
 AGAATCTTT TTAATTGAAG ATGTCTTGG CTCTGCAAAG ATCAGAGCAG GTGAGCATCC 4740
 ACTTTGACAT GAAGGACAAAG AAGACGCATG GCTCATGGCG GGCACATGCG GCTGCCAGTG 4800
 20 AGACAGCGTC TCTCTGGGA GCTGGGCGGG CACAGCATCC TCAGTCTTGT GCCAGCCAA 4860
 GGGTGAGCAT CTCTGCTGAG ACAGTCTTTT TGCTCTCGGA GGCCAGGGAA GATGGTACTT 4920
 AGAGCTTTT CCCTTATCG CTCTGGGTGC TAGGAATCCC ACCAGCTTGT CTTAACAGTA 4980
 CAACAGCTTC TTTGAGGACC CAGTGGGTAT GGAGTATAGA CAGAAGCCAG GGTGAGAAC 5040
 AGAAGGTGGG CGGCAGGATC AGAGTGAAG CAGAGGCGTG AGGAGAGGAA AGCAGGGAGG 5100
 25 TCTCTGGGC TGCCAGGTCA GCCTCTCTGG CAAGGCTTTC TTGAGCCCG CCCCTTCTT 5160
 TCCCAGGAGT CCTCCACCC CATAACAATA CCTCGAATT CCAAAAGAGG TCACCAGATG 5220
 CACATGGGCC GAAAAACACA CAGTCAGGCT TCCAGCACAT TCTCCCCAT TTGGAGGATA 5280
 CTGGAATGTC AGCTTTTGG TTTTATTATT ATTTGAGAAC TAGCTCAGCC CATCTCTAAT 5340
 TATAAAACAT GGTTTTGTTT TTTTCTTCT CTCTTCTCT TGATTAGGTC TGGAACAGCT 5400
 30 CTAGAATGAA CACATAAAAT TTAGCAATT AAAATCTTTC TTTACTGCAA GTTAAATAG 5460
 TTGTACAGAT AGTTTATAAG CACAATATTT TAAGAAAAAA AAGTGGCTGG TCTACTAGGC 5520
 AGCCTTTGTG CCATCTCAGT GCTAGAAAAG TAAAGAAAAA AAAACTTTTG TGATTATAA 5580
 ATACTATTTC TGTGGAATAA TTATAAAAGT ATGACCTTTT TAAATCAACC TTATTGGAT 5640
 GCATCTGAAC CAGCAGAGCT GTGTATATT TCTATCTTT GCTAGAACTT CGTCATTGAA 5700
 35 GGACAATTC TTCAAAGTGG TTCAATTC TAATGCAGCA GTTCTCCAA AAAACAAAAA 5760
 AAAACACACA CCACACACAC GCGCTTTTC AGTCACACAC CCTGATGTT GGAACCAAGT 5820
 TTTTGGACCT TCTGTCCAA AACCTTTTC AGGTCAATCT TTGTATTGA AATGATCCAA 5880
 TCCAATCTGA AGTCAATTGA ATATTAAGGC GCTTACTTC CGTGTGCTT CAGTTTTTC 5940
 ATCATGAGAT GAATGAGCAT TACTCTAGAT AAATTTCAAG ACAGGATACT ACAGGTGGCC 6000
 40 TGCTGAGGCT GCCCATATT TTAGAAAATG TAAAAATGGT GGTTTGGCCA TTAATTTGTC 6060
 TTCCATTGA TGATACCGCA AAATTCGCTG AGTCCATTCC TTGGCATGG CACTTCCCT 6120
 GGGCTACAG TTGTATTAC CTCTGTGCTC AGTGCCAGGC AAAACACTAG CTCAAAGGAG 6180
 AGTCAAGGAA ACCGCTGGCA GACGATAACC AGTGAAGTCT CGTGACTTCG GTTTGTTGAA 6240
 CTTTGGCAGC CAGTTGGTGA GGGCCAGATG TTATCCCTT TCTTAAAGAT ACTCCAAGCC 6300
 45 ACATGCCACT AACCACAAGC AAGCTGGCTG CAAGACTAAA GAGCTGATAA CATAGTTTAT 6360
 TTTTCACTG TCTTATTATA GAGAAGTAAT AGACCTATCA GAACCTGCAC TGACCAACAA 6420
 ATAAACACAT GTTGCCAAGA TGAATCGGTC TCTATCTCTA TCTGCTTATT TTGGTACTGA 6480
 AAGCAATAGT TCCTCATTTCA AATCACCACC CACTGTTCTC CCCCTTTGGG ACATGTTAGG 6540
 ACGAGGCCCT ATTCATGCC CCTCTTTAAT GGTGGAACAA ATGTTAACT GCTCATCTAA 6600
 50 AGATCATGTT GATATTATTC CAGGTTTAA GATCAACTTT GTTACATAC TGAATTTAA 6660
 ATAACTGCA TTTACATGCC TAGTTCTGT AATATTGTGT ATACAAAACC CAAATCTCTC 6720
 AAAATGTAAA TTATGTATAC CTGCCAAGAT ACCTTTTCCA GGGTGTCTGC GCACATTTTA 6780
 AGTTAATTC CATAATATAA AAATTACTCA ATGTGACTGT TGATTGCTG AACTTTACAT 6840
 ATCACAAGT GAATTATTG TGATACITTA GTTAATAAAA TGGTAAATTT TTTTCTCAGT 6900
 55 TATTGAACAA GCAAGCATT TCCAGTTGAT CTGGCAATGA CTTTGTGTGT GTGGGCCACA 6960
 ATATTGATT TCCCATTAAC AATTTTTTTT TGTTTTTTAA ATACTAATAT GTTTCACACT 7020
 ATAGTTGTG TAACAACACG TGTTCGATT ATCTATGTTG CTGTTACTTT TGTGCTTTTA 7080
 TTCTTTTAG ACTTTATAA AAAAAAAGC AGCTCTCTGA ATTTGCATT TCTCCCAATC 7140
 CTTAAATCTC TTGTATGGCA ACCAAAATTA CTGTAAAAA ATAAATATAC TATTGCACTA 7200
 60 AGGTGTGGT TCTGATTGCA AACAAACAGT GAACACTGTC TGAATTAAC AAAAAGCTGC 7260
 CCGACTGCA ATCTAATGTA GATTATCTCA GGCATTGTGG CCAGCTCTGC CTCTCTAAAA 7320
 CTGACAGAA AAATCTCTCT CATCGAGTAA ACAGGCTCCT GTCAGTGC TAATCTGCCT 7380
 TGGTTCATT TCTTATTCT CAATTTATCA ATGGATACGT GCATGTTATT TCAGAATTAT 7440
 GCAAAACGTC AAAATCTGCT TCTGTGACCG CTGCTATAGG CGTGGAGCTG AGGCTCGGCT 7500
 65 TTTCTTTTG TTTGGGTGG AAGCAGCGGT GCCGCGGAGG GCCAGCCAGA TCCGAGCCCT 7560
 TCCCTTAGGG TCCAGTCTCC CCACACCCA GCAGGGTGT TCTAGCCAT AAGGCCAAGG 7620
 GAGTGGCAGA ACTGGGCCG CTCTCTGTT GACAAGCAAA CCACATGCTA AGGCTTGGAG 7680
 CAAGAGAGAA TTGTGTCTA TTGGCAAAGA ACTAAGCCAG GAAGACATGG GCCATCCCTC 7740
 CGCTTAGGG AAGCATATT TAAACCTAAA CGTTGAACCT CTCTTTGGC CTCACCATG 7800
 70 AAAACTTGT TCTTTAGTT CCTAAAGTT CTCTACTTT GGCACATTCC CCAGTTGAGC 7860
 AGCAGCCTCT ATGCTCCAC GTTCAGGAAA AATTCAGTC CTCATATCTT TTGTAGTTCA 7920
 CCCTCAAGCT CTCCCGCTTC ACCATCCAAT AGTTTCTCCC AAACCTTGGC ACCCCCTAG 7980
 ACTTTGTC CAATGGTTTC TTCCAGACCA CTTTCTAG ATGAATATAT TCGTTTACCT 8040
 TACTAGGAAA ATTATTGGA GATTTTTCT TTTACTTGA ATTGGAGGCA TTTAATAAC 8100
 75 TGGCGAAGCT GAATGTGTTT CTGTATTGT AGACAACCAT GTACCATGC AAGTAGGTGA 8160
 ACATTCCACA GTGGCTGGT GACCACAGCA GCTGCATGCA GACAGGAGT CCCGTGCTT 8220
 GTGGGGAATC AGAGAAATTC CAACTTGT TCTCAGACT CCGCAGATCT CATCACTTTG 8280
 ATTCTAAT CATGTGAT TGGTATTTT GTTATCGTT CCGTGAACCT GTTCTACAT 8340
 CCACAGTCT TACCGTTT TGTTCAAAAT TACAACAATC CTGTCCATT GATTCCACTC 8400
 TGGAACTCT TGTTCATGCC AATTTTGAAA TTTAATACG AGCCTTCAA TAAACACAGA 8460

AAAGAAAAAA AAAAAAAAAA AAAAAAAAAA

5 **SEQ ID NO:165 PEZ6 Protein sequence:**
Protein Accession #: BAA82974.1

```

1      11      21      31      41      51
|      |      |      |      |      |
10 MMNMNVPGGGA AAVMMTGYNN GRCPRNSLYS DCIEEKTVV LQKKDNEGFG FVLRGAKADT 60
   PIEEFTPTPA FPALQYLESV DEGGVAWQAG LRTGDFLIEV NNENVVKVGH RQVVNMIRQG 120
   GNHLVLKVVV VTRNLDPDDT ARKKAPPPPK RAPTTALTLR SKSMTSELEE LVDKDKPEEI 180
   VPASKPSRAA ENMAVEPRVA TIKQRPSSRC FPAGSDMNSV YERQGIAMVT PTVPGSPKAP 240
15 FLGIPRGTMF RQKSIDSRIF LSGITEEERQ FLAPPMLKFT RSLMPDTSE DIPPPQSV 300
   PSPPPSPPTT YNCPKSFTPR VYGTIKPAFN QNSAAKVSPA TRSDTVATMM REKGMFYFRE 360
   LDRYSLDSED LYSRNAGPOA NFRNKRQOMP ENFYSEVGKI ASKAVYVPK PARRKGMLVK 420
   QSNVEDSPEK TCSIFIPTII VKEPSTSSSG KSSQSSSMEI DPQAPPPSQ LRPDES LTVS 480
   SPFAAAIAGA VRDREKRLEA RRNSPAFLST DLGDEDVGLG PPAPRTRPSM FPEGDFADE 540
20 DSAEQLSSPM PSATPREPEN HFVGGAEASA PGEAGRPLNS TSKAQGPSS PAVPSASSGT 600
   AGPGNVVHPL TGRLLDPSSP LALALSARDR AMKESQQGPK GEAPKADLNK PLYDTKMMP 660
   SLDAGFTVT RQNTGRPLRR QETENKYETD LGRDRKGGDK KNMLDIDMT SQQKSAGLLM 720
   VHTVDATKLD NALQDEDEKA EVEMKPDSSP SEVPEGVSET EGALQISAAP EPTTVPGRTI 780
   VAVGMEEAV ILPFRIPPPP LASVDLDEDF IFTEPLPPPL EFANSFDIPD DRAASVPALS 840
25 DLVKQKKSDDT PQSFSLSNSQ PTNSADSKKP ASLNLCLPAS FLPPESFDA VADSGIEVD 900
   SRSSSDHILE TTSTISTVSS ISTLSSEGG NVDCTCTVYAD GQAFMVDKPP VPPKPKMKPI 960
   IHKSNALYQD ALVEEDVDSF VIPPPAPPPP PGSAQPGMAK VLQPRTSKLW GDTVTEIKSPI 1020
   LSGPKANVIS ELNSILQQMN REKLAKPGEG LDSPMGAKSA SLAPRSPEIM STISGTRSTT 1080
   VTFTVRPGTS QPITLQSRPP DYESRTSGTR RAPSPVVSFT EMNKETLPAP LSAATASPS 1140
30 ALSDVFLSPS QPPSGDLFGL NPAGRSRSPS PSILQQPISN KPFTTKPVHL WTKPDVADWL 1200
   ESLNLGEHKE AFMDNEIDGS HLPNLQKEDL IDLGVTRVGH RMNIERALKQ LLDR

```

SEQ ID NO:166 PEZ4 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_000024
Coding sequence: 220-1461 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40 ACTCGGAAGC GGCTTCTTCA GAGCACGGGC TGGAACTGGC AGGCACCGCG AGCCCTAGC 60
   ACCCGACAAG CTGAGTGTGC AGGACGAGTC CCCACCACAC CCACACCACA GCGCTGAAT 120
   GAGGCTTCCA GCGCTCCGCT CGCGGCCCGC AGAGCCCGCG CGTGGGTCCG CCCGCTGAGG 180
   CGCCCCCAGC CAGTGCCTT ACCTGCCAGA CTGCGCGCCA TGGGGCAACC CGGGAACGGC 240
   AGCGCCTTCT TGTGGGCACC CAATAGAAGC CATGCGCCGG ACCACGACGT CACGCAGCAA 300
   AGGGACGAGG TGTGGGTGGT GGGCATGGGC ATCGTCATGT CTCTCATCGT CCTGGCCATC 360
45 GTGTTTGGA ATGTGCTGGT CATCACAGCC ATTGCCAAGT TCGAGCGTCT GCAGACGGTC 420
   ACCAACTACT TCATCACTTC ACTGGCCTGT GCTGATCTGG TCATGGGCTT GGCAGTGGTG 480
   CCCITTGGGG CCGCCCATAT TCTTATGAAA ATGTGGGACTT TTGGCAACTT CTGGTGGCAG 540
   TTTTGGACTT CCATTGATGT GCTGTGCGTC ACGGCCAGCA TTGAGACCTT GTGCGTGATC 600
   GCAGTGGATC GCTACTTTGC CATTACTTCA CCTTTCAAGT ACCAGAGCCT GCTGACCAAG 660
50 AATAAGGCCG GGGTGATCAT TCTGATGGTG TGGATTGTGT CAGGCCTTAC CTCCTTCTTG 720
   CCCATTGAGA TGCACTGGTA CCGGGCCACC CACCAGGAAG CCATCAACTG CTATGCCAAT 780
   GAGACCTGCT GTGACTTCTT CACGAACCAA GCCTATGCCA TTGCCTCTTC CATCGTGTCC 840
   TTCTACGTTT CCTGGTGAT CATGGTCTTC GTCTACTCCA GGGTCTTTCA GGAGGCCAAA 900
55 AGGCAGCTCC AGAAGATTGA CAAATCTGAG GGCCGCTTCC ATGTCCAGAA CCTTAGCCAG 960
   GTGGAGCAGG ATGGGCGGAC GGGGCATGGA CTCGCAGAT CTTCGAAGTT CTGCTTGAAG 1020
   GAGCACAAGC CCTCAAGAC GTTAGGCATC ATCATGGGCA CTTTACCCTT CTGCTGGCTG 1080
   CCCTTCTTCA TCGTTAACAT TGTGCATGTG ATCCAGGATA ACCTCATCCG TAAGGAAGTT 1140
   TACATCTCTT TAAATTGGAT AGGCTATGTC AATTCTGGTT TCAATCCCCT TATCTACTGC 1200
60 CGGAGCCAGG ATTTCAGGAT TGCCTTCCAG GAGCTTCTGT GCCTGCGCAG GTCTTCTTTG 1260
   AAGGCCTATG GGAATGGCTA CTCCAGCAAC GGCAACACAG GGGAGCAGAG TGGATATCAC 1320
   GTGGAACAGG AGAAAGAAAA TAAACTGCTG TGTGAAGACC TCCCAGGCAC GGAAGACTTT 1380
   GTGGGCCATC AAGGTACTGT GCCTAGCGAT AACATTGATT CACAAGGGAG GAATGTAGT 1440
   ACAAATGACT CACTGCTGTA AAGCAGTTTT TCTACTTTTA AAGACCCCCC CCCCCCAAC 1500
65 AGAACACTAA ACAGACTATT TAACTTGAGG GTAATAAACT TAGAATAAAA TTGTAATAAT 1560
   TGTATAGAGA TATGCAGAAG GAAGGGCATC CTCTGCCCTT TTTTATTTT TTAAGCTGTA 1620
   AAAAGAGAGA AACTTATTT GAGTGATTAT TTGTTATTTG TACAGTTCAG TTCCTCTTGT 1680
   CATGGAATTT GTAAGTTTAT GTCTAAAGAG CTTTAGTCCT AGAGGACCTG AGTCTGCTAT 1740
   ATTTTCATGA CTTTCCATG TATCTACCTC ACTATTCAAG TATTAGGGGT AATATATTGC 1800
70 TGCTGGTAAT TTGATCTGA AGGAGATTTT CCTTCTTACA CCCTTGGACT TGAGGATTTT 1860
   GAGTATCTCG GACTTTTCAG CTGTGAACAT GGACTCTTCC CCCACTCTC TTATTTGCTC 1920
   ACACGGGGTA TTTTAGGCAG GGATTTGAGG AGCAGCTTCA GTTGTTTTCC CGAGCAAAGG 1980
   TCTAAAGTTT ACAGTAAATA AAATGTTTGA CCATG

```

75 **SEQ ID NO:167 PEZ4 Protein sequence:**
Protein Accession #: NP_000015.1

1 11 21 31 41 51

5 MGQPGNGSAF LLAPNRSHAP DHDVTQQRDE VVVVGMGIVM SLIVLAIVFG NVLVITAIAK 60
 FERLQTVTNY FITSLACADL VMGLAVVPFG AAHILMKMWT FGNFWCEFWT SIDVLCVTAS 120
 IETLCVIAVD RYFAITSPFK YQSLLTKNKA RVILMVWIV SGLTSFLPIQ MHWYRATHQE 180
 AINCYANETC CDFFITNQAYA IASSIVSFYV PLVIMVFVYS RVFQEAQRQL QKIDKSEGRF 240
 HVQNLSQVEQ DGRGTGHGLRR SSKFCLKEHK ALKTLGIIMG TPTLCWLPFF IVNIVHVIQD 300
 NLRKEVYIL LNWIGYVNSG FNPLYCRSP DFRIAFQELL CLRRSSLKAY GNGYSSNGNT 360
 GEQSGYHVEQ EKENKLLCED LPTGTEDFVGH QGTVPFSDNID SQGRNCSTND SLL

10
 15 Nucleic Acid Accession #: NM_004457
 Coding sequence: 143-2305 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 GAATTCGTTG TTGGGAAGGA CTGGGGAAC AGCTGTAACA TTTGCCACCC TCAGAAGCTG 60
 CTGGTCCTGT GTCACACCAC CTAGCCTCT TGATCGAGGA AGATTCTCGC TGAAGTCTGT 120
 TAATCTACT TTTGAGTAC TTAGAATAA CCACGTGTCT TCAAAACCAT CTACCATGAA 180
 GCTAAACAT ACCATCAACC CTATCTTTT ATATTTTATA CATTITCTAA TATCACTTA 240
 TACTATTTA ACATACATTC CGTTTTATT TTTCTCCGAG TCAAGACAAG AAAAATCAA 300
 25 CCGAATTAAG GCAAAGCCTG TAAATTCAA ACCTGATTCT GCATACAGAT CTGTTAATAG 360
 TTTGGATGGT TTGGCTTCAG TATTATACCC TGGATGTGAT ACTTTAGATA AAGTTTTTAC 420
 ATATGCAAAA AACAAATTTA AGAACAAAAG ACTCTTGGGA ACACGTGAAG TTTTAAATGA 480
 GGAAGATGAA GTACAACCAA ATGGAAAAAT TTTTAAAAAG GTTATTCTTG GACAGTATAA 540
 TTGGCTTCC TATGAAGATG TCTTTGTTC AGCCTTTAAT TTTGAAATG GATTACAGAT 600
 30 GTTGGGTGAG AAACCAAAAG CCAACATCGC CATCTCTGT GAGACCAGGG CCGAGTGGAT 660
 GATAGCTGCA CAGGCGTGT TTAGTATAA TTTTCAGCT GTTACATTAT ATGCCACTCT 720
 AGGAGGTCCA GCCATTGTT ATGCATTAA TGAACACAGAG GTGACCAACA TCATTACTAG 780
 TAAAGAACTC TTACAACAA AGTTGAAGGA TATAGTTTCT TTGGTCCAC GCCTGCGGCA 840
 CATCATCACT GTTGATGGAA AGCCACCGAC CTGGTCCGAC TTCCCAAGG GCATCATTTG 900
 35 GCATACCATG GCTGCAGTGG AGGCCCTGGG AGCCAAGGCC AGCATGGAAA ACCAACCTCA 960
 TAGCAAAACA TTGCCCTCAG ATATTGCAGT AATCATGTAC ACAAGTGGAT CCACAGGACT 1020
 TCCAAAGGGA GTCATGATCT CACATAGTAA CATTATGTCT GGTATACTG GATGGCAGA 1080
 AAGGATCCCA GAATAGGAG AGGAAGATGT CTACATTGGA TATTTGCCCT TGGCCATGT 1140
 TCTAGAATTA AGTGCTGAGC TTGTCTGTCT TTCTACCGGA TGCCGCAATT GTTACTCTTC 1200
 40 ACCACAGACT TTACGAGATC AGCTTTCAA AATTAAAAAA GGAAGCAAAG GGGATACATC 1260
 CATGTTGAAA CCAACACTGA TGGCAGCAGT TCCGGAATC ATGGATCGGA TCTACAAAAA 1320
 TGTCATGAAT AAAGTCAGTG AAATGAGTAG TTTTCAACGT AATCTGTTTA TTCTGGCCTA 1380
 TAATTACAAA ATGGAACAGA TTTCAAAAGG ACGTAATACT CCACTGTGCG ACAGCTTTGT 1440
 TTTCCGGAAG GTTCGAAGCT TGCTAGGGGG AAATATTCGT CTCTGTTGT GTGGTGGCGC 1500
 45 TCCACTTTCT GCAACCACGC AGCGATTAT GAACATCTGT TCTGCTGTC CTGTTGGTCA 1560
 GGGATACGGG CTACTGTAAT CTGCTGGGC TGGAAACAAT TCCGAAGTGT GGGACTACAA 1620
 TACTGGCAGA GTGGGAGCAC CATTAGTTTG CTGTGAAATC AAATAAAAAA ACTGGGAGGA 1680
 AGGTGGATAC TTTAATACTG ATAAGCCACA CCCCAGGGGT GAAATTCITA TTGGGGGCCA 1740
 AAGTGTGACA ATGGGGTACT ACAAATGA AGCAAAAACA AAAGCTGATT TCTCTGAAGA 1800
 50 TGAATATGGA CAAAGGTGGC TCTGACTGG GGATATTGGA GAGTTTGAAC CCGATGGATG 1860
 CTTAAAGATT ATTGATGTA AAAAGGACCT TGTAATACTA CAGGCAGGGG AATATGTTTC 1920
 TCTTGGGAAA GTAGAGGCAG CTTTGAAGAA TCTTCACTA GTAGATAACA TTTGTGCATA 1980
 TGCAACAGT TATCATCTT ATGTCATTG ATTGTTGTG CCAATCAA AGGAACATAAC 2040
 55 TGAAGTACT CGAAGAGAA GACTTAAAG GACTTGGGAG GAGCTGTGTA ACAGTTGTGA 2100
 AATGGAAAAT GAGGTACTTA AAGTGCCTTC CGAAGCTGCT ATTTACAGCA GTCTGGAATA 2160
 GTTTGAAATT CCAGTAAAAA TTCGTTTGG TCTGAAACCG TGGACCCCTG AAATGTTCT 2220
 GGTGACAGAT GCCTTCAAGC TGAACGCAA AGAGCTTAAA ACACATTACC AGGCGGACAT 2280
 TGAGCGAATG TATGGAAGAA AATAATTATT CTCTCTGGC ATCAGTTTGC TACAGTGAGC 2340
 60 TCACATCAAA TAGGAAAATA CTTGAAATGC ATGTCTCAAG CTGCAAGGCA AACTCCATTC 2400
 CTCATATTAA ACTATTACT CTCATGACGT CACCATTTT AACTGACAGG ATTAGTAAAA 2460
 CATTAAAGCA GCAAACTTGT GTCTGTCTCT TCTTTCATT TCCCGGCCAC CAACTTACTT 2520
 TACCACCTAT GACTGTACTT GTCAGTATGA GAATTTTCT GAATCATATT GGGGAAGCAG 2580
 TGATTTTAAA ACCTCAAGTT TTTAAACATG ATTTATATGT TCTGTATAAT GTTCAGTTTG 2640
 65 TAACTTTTTA AAAGTTTGG TGTATAGAG GATAAATAGG AAATATAAGA ATTGTTATT 2700
 TGGGGGCTTT TTTACTTACT GTATTTAAA ATACAAGGT ATTGATATGA AATTATGTAA 2760
 ATTTCAAATG CTTATGAATC AAATCATTTG TGAACAAAAG ATTGTGTCT GTGTAAATTAT 2820
 TGTCTTTGAT GCATTTGAGA GAAATAAATA TACCATACT TATGTTTTAA GAAGTTGAGA 2880
 TCTTGTGAAT ATATGCTGT CAGTGTCTT TTTATATATT TATTTTTAT TAGAAAAAAT 2940
 70 GAAGTTTGGT TGTGTATGA TGAACAAA TAGCAAGAGA GGGTTATAGT TTAATAGTAA 3000
 GGGAGATAAC ACAGCATGTG TAGCACCAGT TGATAATTGG TCTCTAGTAG CTACTGTCA 3060
 AAATGTTCAA TGAAGTCTTC GTTTCATCTG TTGAAACTAG GAAATATACC AAACCTTAAAT 3120
 GGAAGAATTC TGAAGAGAG GATAGAATTT AAAGAACAAG AGTATATAA GTTATCTTT 3180
 GAATATTTCT TTAGTATAT GTACATTGAG TATCTATAT TTGTAACAA ATTAGTCATG 3240
 75 GAAAATTATT CTATTTCAA GCTCTTTT AGTCTAGATA ATCATTAATT CATTTTAAAA 3300
 TTAGTGTTTT TACTAGTTTG CACTGATGCG TGTATGGATG TGTGTGAGTC AGTGGTAGCT 3360
 TATTTAAAAA GCACCTTATC CTTTCTCCA TAACCTTTGT AACTAAAAA ATGAAAGAAT 3420
 TTAGAATGTA TTGATGATA GCATCTCAC TAAGACACAT GAGAATTATA CTTTATAACC 3480
 GCGTGAGTTA AGATTTAATT CATAGTTTT GATGTCATTG TTGAAGTTAT TGTAAATCA 3540
 GAAACCTTGC TTGTGTGATA CATAGTAAGT CTCTTCATT ATTACTGCTT GCCTGTTGTT 3600

ATATCTGGAT TATCAAAAGC AATAGTGCAC CAATTAAGAT GTGCTCAAAT CAGGACTTAA 3660
ATCATAGGCA CCACATTTTT CATGTCAGAC TAGTTACTTT GTTGATTCTC AGTTACTGTA 3720
GGCATCAAAA GGCAAAAATC A

5

SEQ ID NO:169 PEZ1 Protein sequence:
Protein Accession #: NP_004448.1

10

15

20

25

1 11 21 31 41 51
MNNHVSSKPS TMKLKHTINP ILLYFIHFLI SLYTILTYIP FYFFESRQE KSNRIKAKPV 60
NSKPDAYSRS VNSLDGLASV LYPGCDTLDK VFTYAKNFKF NKRLLTREV LNEEDEVQPN 120
GKIFKKVILG QYNWLSYEDV FVRAFNFONG LQMLGQKPKT NIAIFCETRA EWMIAAQACF 180
MYNQLVLTLY ATLLGGPAIVH ALNETEVTNI ITSKEILLQTK LKDIVSLVPR LRHIITVDGK 240
PPTWSDFPKG IIVHTMAAAVE ALGAKASMEN QPHSKPLPSD IAVIMYTSQS TGLPKGVMS 300
HSNIIAGITG MAERIPELGE EDVYIGYLP L AHVLELSAEL VCLSHGCRIG YSSPQTLDQ 360
SSKIKKSGSK DTSMLKPTLM AAVPEIMDRI YKNVMNKVSE MSSFQRNLFI LAYNYKMEQI 420
SKGRNTPICD SFVFRKVRSL LGGNIRLLLC GGAPLSATTQ RFMNICFCCP VGQGYGLTES 480
AGAGTISEVW DYNTGRVGP LVCCEIKLN WEEGGYFNTD KPHPRGEILI GGQSVTMGY 540
KNEAKTKADF SEDENGQRWL CTGDIGEFEP DGCLKIIRK KDLVKLQAGE YVSLGKVEAA 600
LKNLPLVDNI CAYANSYHSY VIGFVVPNQK ELTELARKKG LKGTWEEELN SCEMENEVLK 660
VLSEAAISAS LEKFEIPVKI RLSPEPWTP E TGLVTDAPKL KRKELKTHYQ ADIERMYGRK

SEQ ID NO:170 PCQ7 DNA SEQUENCE

Nucleic Acid Accession #: none found
Coding sequence: 38-1075(underlined sequence corresponds to start and stop codon)

30

35

40

45

50

55

60

65

70

75

1 11 21 31 41 51
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCTGCTGG 60
CCTGCTGCTG AGCAGCGCCG CCGAGAGCCA GCTGCTCCCG GGAACAACT TCACCAATGA 120
GTGCAACATA CCAGCAACT TCATGTGCAG CAATGGACGG TGCATCCCG GCGCTGGCA 180
GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
GTGCAATGT GGCACCACT TCTTCCCTG TGCCAGCGGC ATCCATGCA TCATTTGCTG 300
CTTCCCGTGC AATGGGTTC AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AAACCCCTCG CTCTGCTCCA CCGCCCGCTA CCACTGCAAG AACGCCCTCT GTATTGACAA 420
GAGCTTCATC TGGGATGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
AAGTTCTCAA GAACCCGCGA GTGGGACGGT GTTTGTGACT TCAGAGAAC AACCTGTGTA 540
TTACCCGAGC ATCACTATG CCATCATCGG CAGTCCGCT ATTTTGTGTC TGGTGGTGGC 600
CCTGCTGGCA CTGGTCTTGC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
GCACCGGCTG CAGCACCTGT TGCTGCTGTC CCGCTGGTG GTCTGGGACC ACCCCACCA 720
CTGCAACGCT ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
GAATGCGTGC AAGTAGGCT CCCCACCTC CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840
TGCGTGTGAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
CGACCTGCCC CCGTACCGCT CCGGTTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
CAGCAGGCTC CTGAGCGTGG AAGACACGAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
AGTTATTTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTGT 1140
TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
AACTATCTCT GCATTCCTCT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
TGACATGATC TGTGTGCGT CTTTCTGTCT AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320
CACCTCATTT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
CGCTGGACCC AATCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTGGGTTAG 1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTTGAGC 1560
ATCAAAACCT CTCTTGCACA ATCCTATTGG ATGCCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
AAGAAACCTT TGGACGTGAG TAACACCCCT CAGCAGTCCG AACGTTATTT TGGTTTGTG 1680
AAGGACTCTG AAACCATCTA CCCTGTATAA ATCTGGCTT TAGAAATTTG CCCAAGAATG 1740
CTCATTTCTG GAGCTTTCTT CAGCAGCATA TATCATCAGC CTCATCTAA AATAGGCAGG 1800
GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCCAGCTG 1920
ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
GTATGTCCCT GTGGCCACA CCGAGCCTGT CTGCTCATTT CATGCAGCCT CAACACTGGC 2040
CTCCAAAGTT CCGTTAACAC TTGCAAGTTC CTTTCTTACCT GTGCATTTGG ACTTGAGGAC 2100
ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
CTGCACTGTG CACGCTCTCT TTCCCAAGGT CCAATACCA GCACCTCTAG TTAGAGTTAG 2220
GGTCAGGGTC AGGCCCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
AGACAATTG GAGTCAAGAT TTTCATTTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
TGAAACAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATG 2460
ACACCCCTTG CCGCTGAGC CCGTGATATA CAGTCACTC CAGACTAACC TGTGTGCCAG 2520
ACATTTGTGC ATTGTGTCAC TTGAGGTTA TTATTTATCA AGTCTTTGAA GGAAGCAGAA 2580
AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
TTCTCTGTGT CAGTCAAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGA CCAGGTAGAG 2760
CCACTCCGGC CAGCTGTCAC CCATTCAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGCTAAAG TGGCATTCAG 2880
TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940

5	AAGCTAGCCA	CTGGTATTTT	GTTTGTGTTA	AAAAAAAAAA	GAAAGAAAGA	AAGAAAGAAA	3000
	AACGGAAAGG	AACCTAGCTG	CCTGTATCTT	TCATTTTAA	AATAGCACCT	GAGTTATTTT	3060
	CTGAGTAATC	CAATAAAGAA	CYTTTGATGA	CAGCCAGAA	TGTTTAGAAC	TCTGGCTGAA	3120
	CATTTCACT	CCTGTGAGTC	AGAAGGGCTT	TATTTCTCCC	TTTGATGGGG	CCCCCTCTTC	3180
	TTTCTGGTGC	TCTGGAAGTT	GTTTAGAGGA	AAGAATCTTA	ATTTTAATTA	ATTGCGCAGT	3240
	GAGTTAATCT	CACCTCGCTT	TCTGCTTCCA	GGCATCTTAG	GAAAAACAAA	TGGTTTGTAGT	3300
	AGATAAGGGA	TCCCTACTAA	TGCTTTTATA	AAACAACACG	GGACATTTT	ATTATAGATT	3360
	TGATTTTATT	AATGAATGTT	TTTAAAAATA	TATAAATAGG	ACACCAAAGC	GGCAGGGTTT	3420
10	TTTGTGGGGG	GAGGGGGT	GTTTTCACAC	TCAAGATGGC	ACATTAAGTG	CCAGCAATAT	3480
	TTTTTAACTC	ATTTCAACCA	GGAAGCTTTT	TTATACATMG	CCTAAATCTA	CGCCAACACG	3540
	AAAATAGTCT	CATCTCTTTT	TTTCTCAAA	GAGATCCGTG	TTTATTTTAA	GCATTAATTT	3600
	AGTTACACTG	TGATGACTGG	CCTATTACCT	GACTCAGCTC	CCTCTACCTT	GAAATTGACA	3660
	TTTTTAAAAA	ATGCAACTAA	GTGGTTAATA	GTGTGTGACG	CTCAAAGTTA	ATGTAAACTG	3720
	GAAAGGTTGT	GTGTCGTGTC	TTTTTGTGTT	TTGGTTAGCG	TTGGTTTGT	TTTTTAATTT	3780
15	TTATACTTTC	TAATAAATTT	GCAGTTTCAT	TCTTCTGTTT	TGTGCAAAWG	GWMCTAMARM	3840
	AAMMAAAAC	AWYWTGGGG	GGGCTTGGGC	CTCGGAAAAA	GTTTTTAACA	CCACTTCGGG	3900
	TGGGGCGGGG	GGGCCCCAGT	AGGTACGGCG	ACCACGCGGG	CCCAACCGGG	ACCCAGAGAG	3960
	GAAACCTCGG	CCAAGAAAAA	GGTGGCGAGA	ATTCTCCACA	CCAGAAAAAA	ACGCGCCGGG	4020
20	GGAAACCGCA	GAGTGTGCG	TAAACACAC	CCGAAGAGAG	AACCTAGAAG	CACACAACCG	4080
	GGACTCAACC	AGGAGGACCC	AAGGGAACCC	GATAGAGTAC	G		

25 SEQ ID NO:171 PCQ7 Protein sequence:
Protein Accession #: none found

30	1	11	21	31	41	51	
	MWLLGFLCLL	LSSAAESQLL	PGNNFTNECN	IPGNFMCNSG	RCIPGAWQCD	GLPDCFDKSD	60
	EKECPKAKSK	CGPTFFPCAS	GIHCLIGRFR	CNGFEDCDPDG	SDEENCTANP	LLCSTARYHC	120
	KNGLCIDKSF	ICDQGNQCQD	NSDEBSCSSS	QEPGSGQVVF	TSENQLVYYP	SITYAIIIGSS	180
	VIFVLVAVLL	ALVLHHQRKR	NNMLTLPVHR	LQHPVLLSRL	VLDHPHHCN	VTYNVNNGIQ	240
35	YVASQAEQNA	SEVGSPPSYS	EALLDQRPAW	YDLPPFPYSS	DTESLNQADL	PPYRSRSGSA	300
	NSASSQAASS	LLSVEDTSHS	PGQPGPQEGT	AEPRDSEPSQ	GTEEV		

40 SEQ ID NO:172 PEL3 DNA SEQUENCE
Nucleic Acid Accession #: NM_005856.1
Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

45	1	11	21	31	41	51	
	GTCATATTGA	ACATTCAGAA	TACCTATCAT	TACTCGATGC	TGTTGATAAC	AGCAAGATGG	60
	CTTTGAACCT	AGGGTCACCA	CCAGCTATTG	GACCTTACTA	TGAAAACCAT	GGATACCAAC	120
	CGGAAAACCC	CTATCCCGCA	CAGCCCACTG	TGGTCCCCAC	TGTCTACGAG	GTGCNTCCGG	180
	CTCAGTACTA	CCCCTCCCCC	GTGCCCCAGT	ACGCCCCGAG	GGTCTTGACG	CAGGCTTCCA	240
	ACCCCTCCGT	CTGCACGACG	CCCAAAATCCC	CATCCGGGAC	AGTGTGCACC	TCAAAGACTA	300
50	AGAAAGCACT	GTGCATCAAC	TTGACCCCTG	GGACCTTCCT	CGTGGGAGCT	CGCGTGGCCG	360
	CTGGCCCTACT	CTGGAAGTTC	ATGGGCAGCA	AGTGCTCCAA	CTCTGGGATA	GAGTGGGACT	420
	CCTCAGGTAC	CTGCATCAAC	CCCTCTAACT	GGTGTGATGG	CGTGTACAC	TGCCCCGGCG	480
	GGGAGGACGA	GAATCGGTGT	GTTCGCCCTC	ACGGACCAAA	CTTCATCCCT	CAGATGTACT	540
	CATCTCAGCA	GAACTCTCTG	CACCCCTGTG	GCCAAGACGA	CTGGAACGAG	AACCTACGGC	600
55	GGGCGGCCCT	CAGGACCATG	GGCTATAAGA	ATAATTTTAA	CTCTAGCCAA	GGAATAGTGG	660
	ATGACAGCGG	ATCCACCAGC	TTTATGAAC	TGAACACAAG	TGCCGGCAAT	GTGATATCT	720
	ATAAAAAACT	GTACCACAGT	GATGCCCTGT	CTTCAAAAGC	AGTGGTTTCT	TTACGCTGTT	780
	TAGCCCTGCG	GGTCAACTTG	AACTCAAGCC	GCCAGAGCAG	GATCGTGGGC	GGTGAGAGCG	840
60	CGCTCCCGGG	GGCCTGGCCC	TGGCAGGTCA	GCCTGCACGT	CCAGAACGTC	CACGTGTGCG	900
	GAGGCTCCAT	CATCACCCCC	GAGTGGATCG	TGACAGCCCG	CCACTGCGTG	GAAAAACCTC	960
	TTAACAATCC	ATGGCATTTG	ACGGCATTTG	CGGGGATTTT	GAGACAATCT	TTTATGTTCT	1020
	ATGGAGCCGG	ATACCAAGTA	CAAAAAGTGA	TTTCTCATCC	AAATTATGAC	TCCAAGACCA	1080
	AGAACAATGA	CATTGCGCTG	ATGAAGCTGC	AGAAGCCTCT	GACTTTCAAC	GACCTAGTGA	1140
	AACCAAGTGT	TCTGCCCAAC	CCAGGCATGA	TGCTGCAGCC	AGAACAGCTC	TGCTGGATTT	1200
65	CCGGGTGGGG	GGCCACCGAG	GAGAAAGGGA	AGACCTCAGA	AGTGTCTGAAC	GCTGCCAAGG	1260
	TGCTTCTCAT	TGAGACACAG	AGATGCAACA	GCAGATATGT	CTATGACAAC	CTGATCACAC	1320
	CAGCCATGAT	CTGTGCCCGG	TTCTTGCAAG	GGAACGTCGA	TTCTTGCCAG	GGTGACAGTG	1380
	GAGGGCTCT	GGTCACTTCG	AACACRATA	TCTGGTGGCT	GATAGGGGAT	ACAAGCTGGG	1440
	GTCTGTGGCT	TGCCAAAGCT	TACAGACCAG	GAGTGTACGG	GAATGTGATG	GTATTCACGG	1500
70	ACTGGATTAA	TCTGACAAAT	AAGGCAACCG	GCTAATCCAC	ATGGTCTTCG	TCCTTGACCT	1560
	CGTTTTCACAA	GAAACCAATG	GGGCTGGTTT	TGCTTCCCGG	TGCATGATTT	ACTCTTAGAG	1620
	ATGATTCAGA	GGTCACTTCA	TTTTTATTA	ACAGTGAAC	TGTCTGGCTT	TGGCACTCTC	1680
	TGCCATFACTG	TGCAGGCTGC	AGTGGCTCCC	CTGCCACGCC	TGCTTCCCTT	AACCCCTTGT	1740
	CCGCAAGGGG	TGATGGCCGG	CTGGTTGTGG	GCACCTGGCG	TCAATTGTGG	AAGGAAGAGG	1800
	GTGGAGGCT	CGCCCAATGG	AGATCTTCCT	GCTGAGTCTT	TTCCAGGGGC	CAATTTTGA	1860
75	TGAGCATGGA	GCTGTCACTT	CTCAGCTGCT	GGATGACTTG	AGATGAAAAA	GGAGAGACAT	1920
	GGAAAGGGAG	ACAGCCAGGT	GGCACTTGCA	CGCGCTGCC	TCTGGGGCCA	CTTGGTAGTG	1980
	TCCCCAGCCT	ACTTCAACAAG	GGGATTTTGC	TGATGGGTTT	TTAGAGCCCT	AGCAGCCCTG	2040
	GATGGTGGCG	AGAAATAAAG	GGACCAAGCC	TTTATGGGTG	GTGACGTGGT	AGTCACTTGT	2100
	AAGGGGAACA	GAAACATTTT	TGTTCTTATG	GGGTGAGAAT	ATAGACAGTG	CCCTTGGTGC	2160

5 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
 CATTGGGTGG GGCCTCTGGG AGGGAGACTC AGCCTTCCTC CTACATCCTCC CTGACCTCTG 2280
 TCCTAGCACC CTGGAGAGTG AATGCCCTTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
 ATGCTCGGCT CTTGAGGCTT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGGTACAC TGTATCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
 CTGAGTTCAA AGCCATCTTT

10 SEQ ID NO:173 PEL3 Protein sequence:

Protein Accession #: NP_005647.1

15 1 11 21 31 41 51 60
 MALNSGSPPA IGFYYENHGY QPENFYPAQP TVVPTVYEVH PAQYYPSEVP QYAPRVLTA 60
 SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCINPS NWCADVSHCP GGEDENRCVR LYGNFILQM YSSQRKSWHP VCQDDWNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSLRVGGE SALFGAWPWQ VSLHVQNVHV CGSSIITPEW IVTAHCVCK 300
 PLNNFWHTA FAGILRQSFY FYGAGYQVQK VISHENYDSK TKNNDIALMK LQKPLTFNDL 360
 VKPVCLNPNP MMLQBEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRYVVDNLI 420
 TPAMICAGFL QGNVDSQCGD SGGPLVTSNN NIWWLIGDTS WSGSCAKAYR PGVYGNVMVF 480
 TDWIYRQMK NG

25 SEQ ID NO:174 PBJ4 DNA SEQUENCE

Nucleic Acid Accession #:

Al694767

Coding sequence:

130-1086 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51 60
 CAGAGAGGCT GTATTTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
 GGGGTCACAC ATTCCTTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTACACAGTTC 120
 AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCTCA 180
 35 ATAGGCTTCC CTGGTTTAGA AGAGGCTCAG TTCCTGGTTGG CCTTCCCATTT GTGCTCCCTC 240
 TACCTTATTT CTGTGCTAGG TAACCTTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC 300
 CTGCATGAGC CCATGTATAT ATTTCCTTGC ATGCTTTCAG GCATGTACAT CCTCATCTCC 360
 ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
 GATGCTTGTC TGCTACAGAT GTTTGCCATC CACTCCCTAT CTGGCATGGA ATCCACAGTG 480
 40 CTGCTGGCCA TGGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGCG CCATGCCACA 540
 GTACTTACGT TGCCCTCGTG CACCAAAATT GGTGTGGCTG CTGTGGTGGC GGGGGCTGCA 600
 CTGATGGCAG CCTTCTCTGT CTTCAATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660
 TCCCATTCCT ACTGCCTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
 AATGTCGTCT ATGGCCTTAT CGTCATCATC TCCGCCATTG GCCTGGAGTC ACTTCTCATC 780
 45 TCTTCTCAT ATCTCTTAT TCTTAAGACT GTGTGGGCT TGACACGTGA AGCCAGGCC 840
 AAGGCATTG GCATCTCGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900
 ATTGGATGT CATAGGTGCA TCGCTTAGC AAGCGGCGTG ACTCTCCACT GCCGCTCATC 960
 TGGCCAAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
 50 ACAAGAGAGA TTGACACGGC CATCCTTCGA CTMTTCCATG TGGCCACACA CGCTTCAGAG 1080
 CCTTAGGTGT CAGTGATCAA ACTTCTTTTC CATTCAGAGT CCTCTGATTC AGATTTTAAT 1140
 GTTAACATTT TGAAGACAG TATTCAGAAA AAAAAATTC TTAATAAAAA TACAACTCAG 1200
 ATCCCTTCAA TATGAACCTG GTTGGGGAAT CTCATTTTTC TCAATATTAT TTTCTTCTTT 1260
 GTTTCTTTCG TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATATC 1320
 55 TTTTCATTTT ACCATGCAGT CCAAACTCAA ACTGCTTCTA CTGATGGTTT ACAGCATTTCT 1380
 GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440
 TAAACACAGA ATATAATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500
 ACTCCCAACC ACATTTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560
 60 AAATAAATTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
 AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
 ATGGACCTCT TTTTCTCTAT TTAATTTTCT TATCAACCTT TTAATTAGGC AAAGATATTA 1740
 TTAGTACCCT CATTGTAGCC ATGGGAAAAA TGATGTTTCA TGGGGATCAG TGAATTAAT -1800
 GGGGTCATAC AAGTATAAAA ATTAAAAAAA AAGACTTCA TGCCCAATCT CATATGATGT 1860
 65 GGAAGAACTG TTAAAGAGAC CAACAGGGTA GTGGGTTAGA GATTTCAGAG GTCTTACATT 1920
 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGATTTTAG GAATTTCTCT 1980
 GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGCTCTGG TCCAAATTGCC 2040
 AATTACCTGT GTCITGGGAG AAGTGATTTT TAGGTTTACC ATTATGGAAG ATTCTTATTC 2100
 AGAAAGTCTG CATAGGGCTT ATAGCAAGTT ATTATTTTTT AAAAGTTCCA TAGGTGTTTC 2160
 70 TGATAGCAGC TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
 TGAAGATAAC ATTGGCTTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTTCAGG 2280
 ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGAACAGGG ACTTTGAGAC CGGGAAGCA 2340
 ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTCACATA 2460
 75 TACTAAAAA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTCATAT CCTCAGGTTT 2520
 CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCTTTTTC TAATGGATAT CATATTGGA 2580
 AATGCCATT TAATACCTGT ATTTGCTGCT GGAAGTAAAG CCCATGAGGG CACTGTTTAT 2640
 TATTGAATGT CATCTCTGTT CATCATTTGAC TGCTCTTTGC TCATCATTTA ATCCCCAGC 2700
 AAAGTGCTTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTC TCAAACTTGA 2760
 80 TTCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTCTTTTTCG TTGGGTATTA 2820
 TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAAGTGC ATGTGCAATT TTATACCTG 2880
 GCTCATAAAA CCTTCCCATG TGACGCTTTT CATGTTGACA TTAATATGTA CTTGGGAAGC 2940

TATGTGTAC ACAGAGTTAA TTAACCGAA AGGCCTGGNA ATTTTGTGNN AANNAACTG 3000
 TGGCCNNGAG GCCCNCAACC CTTTINNA ATTTGGCAAN NTCCCACTTT GTANTTTGGT 3050
 AAGGAGGCCA GTTGATAAG TGAAAAATAA AGTACTATTG TGTC

5

Protein Accession #: SEQ ID NO:175 PBJ4 PROTEIN SEQUENCE
 not available, cloned at Eos

10

15

20

1	11	21	31	41	51	
MVDPNGNESS	ATYFILIGLP	GLEEAQFWLA	FPLCSLYLIA	VLGNLTIYI	VRTEHSLHEP	60
MYIFLCMLSG	IDILISTSSM	PKMLAIFWFN	STTIQFDACL	LQMFIAHSL	GMESTVLLAM	120
AFDRYVAICH	PLRHATVLT	PRVTKIGVAA	VVRGAALMAP	LPVFIKQLPF	CRSNILSHSY	180
CLHQDVVKLA	CDDIRVNVVY	GLIVIIISAIG	LDLLISFSY	LLILKTVLGL	TREAQAKAFG	240
TCVSHVCAVF	IFYVFFIGLS	MVHRFSKRDR	SPLFVILANI	YLLVPPVLNP	IVYGVKTKEI	300
RQRILRLFHV	ATHASEP					

25

30

35

40

45

50

55

60

65

70

SEQ ID NO:176 PM72 DNA SEQUENCE
 NM_004624.1
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

TCGGAGCCTG	CGGAGGGTGG	TGGTGGTGGT	GGTGGTGGCC	CTCGCCCGCC	CTACTCATGC	60
CTCCTCCTCC	TCTGCTCTCG	CTCAGGCGCC	TCGGTGGCGG	TGGTGGCGCG	GTACGCGCGC	120
TGGTGGTCCG	GGCGGGCGGG	GCTCGCTCTC	GGGAGGCGCG	GGCGGATCTC	CGCGGCGCAG	180
CGCGGGCGGG	CCGAGGTGGG	GTCGCGCGGC	GGAGGCGGCT	CGAGCTTCGT	GCTGCGCGCT	240
CGCTCTTGGG	CTCTCGCTCG	CAGGAGGAGT	GTGACTATGT	GCAGATGATC	GAGGTGCAGC	300
ACAAGCAGTG	CCTGAGGAGG	GCCAGCTGGG	AGAATGAGAC	AATAGGCTCG	AGCAAGATGT	360
GGGACAACCT	CACCTGCTGG	CCAGCCACCC	CTCGGGGCCA	GGTAGTTGTC	TGGCCTGTCT	420
CCCTCATCTT	CAAGCTCTTC	TCTCCATTC	AAGGCCGCAA	TGTAAGCCGC	AGTGCACCG	480
ACGAAGGCTG	GACGACCTTG	GAGCCTGGCC	CGTACCCCAT	TGCTGTGGT	TGGATGACA	540
AGGCAGCGAG	TTTGGATGAG	CAGCAGACCA	TGTTCTACGG	TTCTGTGAAG	ACCGCTACA	600
CCATTGGCTA	CGGCTGTGCC	CTCGCCACCC	TCTGGTCTGC	CACAGCTATC	CTGAGCCTGT	660
TCAGGAAGCT	CCACTGCACG	CGGAACCTACA	TCCACATGCA	CCTCTTCATA	TCCTTCATCC	720
TGAGGCTCTG	CGCTGTCTTC	ATCAAAGACT	TGGCCCTCTT	CGACAGCGGG	GAGTCGGACC	780
AGTGTCTCCA	GGGCTCGGTG	GGCTGTAAAG	CAGCCATGGT	CTTTTCCCAA	TATGTGTCTA	840
TGGCTAACTT	CTTCTGGCTG	CTGGTGGAGG	GCCTCTACCT	GTACACCTCT	CTTGCCTCTT	900
CCCTCTCTCT	TGAGCGGAAG	TACTTCTGGG	GGTACATACT	CATCGGCTGG	GGGGTACCCA	960
GCACATTCAC	CATGGTGTGG	ACCATCGCCA	GGATCCATTT	TGAGGATTAT	GGTCTGTCTA	1020
GGTGTCTGGA	CACCATCAAC	TCTTCACTGT	GGTGGATCAT	AAAGGGCCCC	ATCCTCACCT	1080
CCATCTTGGT	AAACTTCATC	CTGTATTATT	GCATCATCCG	AATCTGCTTT	CAGAACTGCT	1140
GGCCCCCAGA	TATCAGGAAG	AGTGACAGCA	GTCCATACTC	AAGGCTAGCC	AGGTCCACAC	1200
TCCTGTCTGAT	CCCCCTGTTT	GGAGTACACT	ACATCATGTT	CGCCTTCTTT	CCGGACAATT	1260
TTAAGCCTCA	AGTGAAGATG	GTCTTTGAGC	TCGTCTGGGG	GTCTTTCCAG	GGTTTTGTGG	1320
TGGCTATCTT	CTACTGCTTC	CTCAATGGTG	AGGTGCAGGC	GGAGCTGAGG	CGGAAGTTGG	1380
GGGCTGTGCA	CCTGCAGGGC	GTCTGTGGCT	GGAAACCCAA	ATACCGGCAC	CCGTGGGGAG	1440
GCAGCAACGG	CGCCACGTGC	AGCACGCGAG	TTTCCATGCT	GACCCGCGTC	AGCCCAGGTG	1500
CCCGCCGCTC	CTCCAGCTTC	CAAGCCGAAG	TCTCCCTGGT	CTGACCACCA	GGATCCACAG	1560
CCAAGCGGGC	CCTCCCGCCC	CTTCCCACTC	GCAGCAGACG	CCGGGGACAG	AGGCCTGCCC	1620
GGGGCGGCCA	GCCCCCGCCC	TGGGCTCGGA	GGCTGCCCCC	GGCCCCCTGG	TCTCTGGTCC	1680
GGACACTCCT	AGAGAACGCA	GCCCTAGAGC	CTGCCCTGGG	CGTTCTTAGC	AAGTGAGAGA	1740
GATGGGAGCT	CCTCTCTCTG	AGGATGCAGG	TGGAACCTAG	TCATTAGACT	CCTCCTCCAA	1800
AGGCCCCCTA	GCCTCAATCA	GGGCAAAAAG	TCTACATACT	TTTATCTCTA	CTCTGCCCCC	1860
TGCTGTGCTT	TCTGCTCAAT	TGGAGGAAAG	CAACCGGTGG	ATCCTCAAAC	AACACTGGTG	1920
TGACCTGAGG	GCAGAAAGGT	TCTGCCCGGG	AAGGTCACCA	GCACCAACAC	CACGCTAGTG	1980
CCTGAAATTT	CACCATGTCT	GTCAAGTTCC	TTTGGGTAA	GCATTACCAC	TCAGGCATTT	2040
GACTGAAGAT	GCAGCTCACT	ACCCATTTCT	CTCTTTTACG	TTAGTTATCA	GCTTTTATAA	2100
GTGGGTATT	CTGGAGTTT	TGTTTGGAGA	GCACACCTAT	CTTAGTGGTT	CCCCACCGAA	2160
GTGGACTGGC	CCCTGGGTCA	GTCTGGTGGG	AGGACGGTGC	AACCAAGGA	CTGAGGGACT	2220
CTGAAGCCTC	TGGGAAATGA	GAAGGCAGCC	ACCACGGAAT	GCTAGGTCTC	GGACTAAGCC	2280
TACCTGCTCT	CCAAGTCTCA	GTGGCTTCAT	CTGTCAAGTG	GGACTCTGTC	ACACGAGCCA	2340
TTCTTATCTC	TCTGTGCTGT	GGAAAGCAACA	GGAAATCAAGA	GACTGCCCCC	CTTGTCCACC	2400
CACCTATGTG	CCACTGTGTT	TAACTAGGCT	CAGAGATGTG	CACCCATGGG	CTCTGACAGA	2460
AAGCAGATCC	TCACCTTGCT	ACACATACAG	GATTTGAAC	CAGATCTGTC	TGATAGGAAT	2520
GTGAAAGCAC	GGACTCTTAC	TGCTAACTTT	TGTGTATCGT	AACACGCCAG	ATCCTCTTGG	2580
TTATTTGTTT	ACCACTTTGA	TTATTAATGC	CAATATCCCT	GAATTTCCCT	TGCCACCCCA	2640
CCCTCCCTGG	AGTGTGGCTG	AGGAGGCCTC	CACTCTATGT	ATCATCTGGA	TAGGAGCCTG	2700
CTGGTCACAG	CCTCCTCTGT	CTGCCCTTCA	CCCCAGTGGC	CACCTAGCTT	CCTACCCACA	2760
CTCTGCCAG	AAGATCCCTT	CAGGACTGCA	ACAGGCTTGT	GCAACAATAA	ATGTGGCTTT	2820
GGAAAAAAA	AAAA					

75

80

SEQ ID NO:177 PM72 Protein sequence:
 Protein Accession #: JC2195

1	11	21	31	41	51	
MPPPPLLSLR	RLGGGWSAVT	RLVVAAAGAR	SRGGRRGSRG	AGGGRRGGVA	RRRRLRLRAA	60
RLLLGSSLQE	ECDEVQMEV	QHKQCLEEAQ	LENETIGCSK	MWDNLTCWPA	TFRGQVVVLA	120

5	CPLIFKLFSS	IQGRNVSRSC	TDEGWHLEP	GPYPIACGLD	DKAASLDEQQ	TMFYGSVKTG	180
	YTIYGYLSLA	TLIVATAILS	LFRKLHCTR	YIHMHLFISF	ILRAAAVFIK	DLALFDSGES	240
	DQCSEGSVGC	KAAVFFQYC	VMAFFWLLV	EGLYLYTLA	VSFFSERKYF	WGYILIGWGV	300
	PSTFTMVWTI	ARIHFEDYGL	LRCWDTINSS	LWVIKGPIL	TSILVNFILF	ICIIRILLQK	360
	LRPPDIRKSD	SSPYSLRLRS	TLLLIPLFGV	HYIMFAFFPD	NFKPEVKMVF	ELVVGSEFGF	420
	VVAILYCFIN	GEVQAELEPK	WRRWHLQGV	GNPKYRHP	GGSNATCST	QVSMLETRVSP	480
	GARRSSSFQA	EVSLV					

10 Nucleic Acid Accession #: AL133619
 SEQ ID NO:178 BFF8 DNA SEQUENCE
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

15	1	11	21	31	41	51	
20	ATGAGCGGTG	CGGGGGTGGC	GGCTGGGACG	CGGCCCCCA	GCTCGCCGAC	CCCGGGCTCT	60
	CGGCGCCGGC	GCCAGCGCCC	CTCTGTGGGC	GTCAGTCCT	TGAGGCCGCA	GAGCCCGCAG	120
25	CTCAGGCAGA	GCGACCCGCA	GAAACGGAAC	CTGGACCTGG	AGAAAAGCCT	GCAGTTCCTG	180
	CAGCAGCAGC	ACTCGGAGAT	GCTGGCCAA	CTCCATGAGG	AGATCGAGCA	TCTGAAGCGG	240
30	GAAAACAAGG	GTGAGCCGGC	GCGGGGCCCT	AGGCCGGCCC	TGCTTCCCA	GGCACACTCA	300
	ACACTGCCGC	TCCCGCAGCA	CAGAAACACA	GCCATCAACT	CCAGCACACG	CCTGGGCTCA	360
35	GGGGGAACAC	AGGACGGGGA	GCCCCCTCAG	ACTGTCCCTG	CCCACCTGGC	TGCAGTGGCC	420
	CCTGTATGCC	AACCCAGTGG	GTACAGGTTC	TGGGGGACCT	GGACAGATGC	CGCTACCTCT	480
40	AGCCGTGGCT	GGACGATGTT	ATGCAGCCAA	GCACAGCAGC	TGCTGTCTCT	GGGAAGCCCA	540
	GGGCTTGGG	TCAITGACAG	GCGGCAGGTG	GCCACAGGGT	GCTCCCCAGA	CCTCCCTCCT	600
45	CCAAGTAGAG	CTGAAATGGG	AAGGAACCCC	TGGGACAGCC	CCTGCCCTGC	TAGATCTTTG	660
	CCTCAGATTG	CTGCTGTGGC	CAGGCCCAGG	ATTTCACGCC	CTATGGCTCT	GAGTCTCTAC	720
50	ATGCTGGGGG	CCCAGGGGAT	ATGGACACAC	TCCATCCAGG	GATCCCTTCC	TGCCATCTGG	780
	GCAGCAACCA	TGGGGACAAA	GGGAGGAAGC	AGAGTCTTGT	TTCTTGGCCA	CTTCTCCAAG	840
55	GCACCTTCCC	ATCTGTACAG	CGGCCCCAC	CCAGCCCAGG	ATCCTGGGCT	GTGGTCTCAA	900
	GCTCACTTCC	CATTATCTTT	GGGGCTGGGG	CTGACATCAG	GAGGACATCT	GACTGTGTGA	960
60	TGGAGCCAGC	CTGGGAACAT	CGCAGCTGGG	GCAGTGCCTA	GGGCTCTCCC	TTCCAGGGA	1020
	GACATGGAGA	AGGGGGTTGA	GGGAGGGCCC	TTCCCTAGCC	GCTGTGGCAA	CTCCAGTGAG	1080
65	CTGTCTTGGG	CAAAGTGTGG	CCCAAGTCGG	CAGCCCCAGC	CCTGCAGTGC	TGGGGACGCT	1140
	GACAGGACAC	GGGAAGAGGC	CATGCTTTCC	CTCGGGACCT	GCTGTCCCAT	GTGTCCCAAG	1200
70	CCCTCTGTCT	TCCAGATGGG	CCCTCTAGGA	AACCACTTTT	CCAGGGCCCT	TGCTCCCTTG	1260
	GGCGCTCGCT	GGGTCTGCAT	CAACGGAGTG	TGGGTAGAGC	CGGGAGGACC	CAGCCCTGCC	1320
75	AGGCTGAAGG	AGGGCTCCTC	ACGGACACAC	AGGCCAGGAG	GCAAGCGTGG	GCGTCTTGGC	1380
	GGCGGTAGCG	CGGACACTGT	GCGCTCTCCT	GCAGACAGCC	TCTCCATGTC	AAGCTTCCAG	1440
80	TCTGTCAAGT	CCATCTCTAA	TTCAAGCAAC	TCTCAAGGCA	AGGCCAGGCC	CCAGCCCGGC	1500
	TCCTTCAACA	AGCAAGATTG	AAAAGCTGAC	GTCTCCCAAG	AGGCGGACCT	GGAAGAGGAG	1560
85	CCCTACTTTC	ACAACAGCAA	GCTGGACAAA	GTCTCTGGGG	TACAAGGGCA	GGCCAGAAAG	1620
	GAGAAAGCAG	AGGCCTCTAA	TGCAGGAGCT	GCCTGTATGG	GGAACAGCCA	GCACCAGGGC	1680
90	AGGAGATAGG	GGGCGGGGGC	ACACCCCCCA	ATGATCCTGC	CCCTTCCCTT	GCGAAAGCCC	1740
	ACCACACTTA	GGCAGTCCGA	AGTGTCTATC	CGCAGCTGTG	GGAATACCAA	CCTCTGTCAG	1800
95	ACCCAAGAGC	TGCGGCACCT	CAAGTCCCTC	CTGGAAGGGA	GCCAGAGGCC	CCAGGCAGCC	1860
	CCGGAGGAAG	CTAGCTTTCC	CAGGGACCAA	GAAGCCACGC	ATTTCGCCAA	GCTCTCCACC	1920
100	AAGAGCCTCT	CCAAGAAATG	CCTGAGCCCA	CCTGTGGCGG	AGCGTGCCAT	CCTGCCCGCA	1980
	CTGAAGCAGA	CCCCGAAGAA	CAACTTTGCC	GAGAGGCAGA	AGAGGCTGCA	GGCAATGCAG	2040
	AAACGGCGCC	TGCATCGCTC	AGTGCTTTGA				

SEQ ID NO:179 BFF8 Protein sequence:

Protein Accession #: T43457

55	1	11	21	31	41	51	
60	MSGAGVAAAT	RPPSSPTPGS	RRRRQRPSVG	VQSLRPQSPQ	LRQSDPQKRN	LDLEKSLQFL	60
	QQQHSEMLAK	LHEIEHLKR	ENKGEFARGP	RPALPPQAH	TLPLPQHRNT	AINSSSTRLGS	120
65	GGTQDGEPLQ	TVLAHLAALA	PVCQPSGYRF	WGTWDAATS	SRGWTMLCSQ	AQHVLLSGSP	180
	GPEVIAGRQV	ATGCSPLDLP	PSRAEMGRNP	WDSPCPARSL	PQIAAVARPR	ISSPMALSPH	240
70	MLGAQGIWTH	SIQGSPLPAIW	AATMGTKGGS	RVLFPCHLSK	ALPHPDGSGFH	PAQDPGLWSQ	300
	AHFPLSLGLG	LTSGGHITGG	WSQPGNIAAG	AVPRALPSQG	DMEKGVGGFP	FPSRCGNSSE	360
75	LFWAKCGPSR	QPQPCSGADA	DRTREEAMLS	LGTCCSMCPK	PSCFPDGPSP	NHLSRASAPL	420
	GARWVCINGV	WVEPGGSPSA	RLKEGSSRTH	RPGGKRGLA	GGADTVRSP	ADSLSMSSFP	480
80	SVKSISSNSAN	SQKARPQPG	SFNKQDSKAD	VSQKADLEEE	PLLHNSKLDK	VFGVQGGARK	540
	EKAESASNAGA	ACMGNSQHQG	RQMGAGRPP	MILPLPLRKP	TTLRQCEVLI	RELWNTNLLQ	600
85	TQELRHLKSL	LEGSQRQAAA	PBEASFPRDQ	EATHFPKVST	KSLSKKCLSP	PVAERAILPA	660
	LKQTFNNFA	ERQKRLQAMQ	KRLRLRSVL				

SEQ ID NO:180 BCR4 DNA SEQUENCE

Nucleic Acid Accession #: NM_012319.2

Coding sequence:

138-2405 (underlined sequences correspond to start and stop codons)

75	1	11	21	31	41	51	
80	CTCGTGGCCG	ATTTCGGCACG	AGACCGCGTG	TTCGCGCCTG	GTAGAGATT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACTTGGC	CGCGTGGCCG	GGCCGTGGGA	CAACGAGGCC	120

60 Protein Accession #: NP_036451 SEQ ID NO:181 BCR4 PROTEIN SEQUENCE

1	11	21	31	41	51	
MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QTTEKISEPNW	ESGINVDLAI	STRQYHLQQL	60
FYRYGENNSL	SVEGFRKLLQ	NIGIDKIKRI	HIHHDHDHHS	DHEHSDHDER	HSDHEHHSDH	120
EHHSDDHDHS	HHNHAASGKN	KRKALCTPRD	SDSSGKDPRN	SQGGKAHRPE	HASGRNVKD	180
SVASSEVST	VYNTVSEGTH	FLETIETFP	GKLFPEKDVSS	STPPSVTFSK	RVSLRAGRKT	240
NESSVEPRKG	KFYSRTNEN	PQECFNASKL	LTHSGMGIQV	PLNATSEFNYL	CPAINIQIDA	300
RSCLIHTSEK	EMAPIPKTYS	LQIAVNSAGL	AISSISFLSL	LGVLIVLPMN	RVFVFFLLFS	360
LVALAVGTLS	GDYFLLHLP	SHASHHHSK	HEEPAMEMKR	GPLFSLHSSQ	NTEESAIFYDS	420
TKWGLTALGK	LDFMFLVEHV	DLTIKQFKDK	KKKNQKKPEN	DDIVEIKKLN	SKYESQLSTN	480
EEKVDTDDRT	EGYLRRDSQE	PSFEDSQPPA	LEEESEVMIA	HAHPQEVNE	YVPRGCKNKC	540
HSHFHDTLGQ	SDDLIHHHHD	YHHTLIHHHH	QNHHPHSHS	RYRSLEEKDA	GVATLAVMVI	600
MGDGLHNFSK	LGAIGAAPTE	GLSSGLSTV	AVFCHELPE	LGDFAVLLKA	GMTVYQAVLY	660
NALSAMLAYL	GMLTGFIFIG	YAENVSMWIF	ALTALGFMVY	ALVDMVPEML	HNDASDHGCS	720
RNGYFFLONA	GMAITGFGIML	LISIFEHKIV	PRINF			

SEQ ID NO:182 BCY2 DNA sequence

Nucleic Acid Accession #:

NM_001203

Coding sequence:

274-1782 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
 | | | | |
 CGCGGGGCGG GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGGGAGA CCGCGGCGCT 60
 GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
 10 GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
 CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGAGCACA 420
 15 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
 GGTTCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACTCCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA 600
 CTGCCTCCAT TGA AAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
 20 ATATCTGTGA CTGCTCTGTG TTGCTCTGTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720
 TATAAAGAGC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGA AACTTAC 780
 ATTCTCTCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGG 840
 TCAGGCCCTC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG 900
 ATTGGAAGG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCCTGGCGA AAAGGTAGCT 960
 GTGAAAGTGT TCTTCACAC AGAGGAAAGC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
 25 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
 GGGTCTCTGA CCCAGTTGTA CTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAAT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
 AGTGGCTTAT GTCAATTACA CACAGAAATC TTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 CATCGAGATC TGA AAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
 GACCTGGGCG TGGCTGTGTA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 30 ACTCGAGTTG GCACCAACCG CTATATGCCT CCAGAAAGTG TGGACGAGAG CTTGAACAGA 1440
 AACTCACTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTGGGAG 1500
 GTTGTAGGA GATGTGTATC AGGAGGTATA GTGAAGAAAT ACCAGCTTCC TTATCATGAC 1560
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGAT CAAGAAGTTA 1620
 35 CGCCCTCAT TCCCAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACCT 1680
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740
 ACACCTGCCA AAATGTCAGA GTCCCAGGAC ATAAACTCT GATAGGAGAG GAAAAGTAA 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTGTGG GCAGAGCAAA AGACATCAAA 1860
 TAAGCATCCA CAGTACAGC CTGAACATC GTCCCTGCTC CCAAGTGGGT CAGACCTCAC 1920
 40 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTA GCGGAGAAAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

SEQ ID NO:183 BCY2 Protein sequence

Protein Accession #:

NP_001194

45 1 11 21 31 41 51
 | | | | |
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHOPE DSVNNICSTD GYCFIMIED 60
 DSGLPVVTSG CLGLEGSDQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
 50 GPIHHRALLI SVTVCSLLLV LILFCYFRY KRQETRPYRS IGLEQDETYI PPGESLRDLI 180
 EQSQSSSGS GLPLLVRQTI AKIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFITEAS 240
 WFRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSSIF STQGKPAIAH RDLKSKNIV KKNGTCCIAH LGLAVKFISD 360
 55 TNEVDIPNT RVGTFKRYMP EVLDESILNRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
 EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPRNWSSD ECLRQMGKLM TECWAHPAS 480
 RLTAIRVKKL LAKMSESQDI KL

60 SEQ ID NO:184 CBF9 DNA sequence

Nucleic Acid Accession #:

AC005383

Coding Sequence:

328-2751 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 | | | | |
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
 TTTTATTTGC AGACCTGGGC CGATCGCGCT TTA AAAAACG CGAGGGGCTC TATGCACCTC 120
 70 CCTGGCGGTA GTTCTCCGA CCTCAGCCGG GTCGGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAAAACAGT GTCCACCGTG GCAGCCGCGC CCGGGGCGCC CCTCTGTGA TCCCGTAGCG 240
 CCCCCTGGCC CGAGCCGCGC CCGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
 TCGCCGCTCT CCTTCGGTTA TATCAACATG CCCCCTTCC TGTGTCTGGA GGCCGTCTGT 360
 GTTTCTCTGT TTTCCAGAGT GCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420
 75 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCAAG 540
 CACTTGCACA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTCCAC TCCTCATCTG GAATCCCTT TGGATTCAAT TTC AACCACA 660

CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGGCGCAC GGAGACGGAA 720
 CTGTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCC 780
 CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGGTGGGAG 900
 5 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTGGC TGAGCAGGTG 960
 GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCACAGGCC 1020
 ACGCCAGACT GCAGGGTCTGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080
 GAGTTGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCCCTGC GGTGCTGGCT 1140
 0 GCACACTGTG CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTTGC CACCTGCTAC 1200
 AGGACCACCT GCCCAGGGCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
 CCAGAAGGAC TGGACGGCTA CCAGTGCCTC TGCCCGCTGG CCTTGGAGG GGAGGCTAAC 1320
 TGTGCTCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGCT GGACAGCTCT 1380
 GCGGGCACC ACTCTGACGG CTTCCTGCGG GCCAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
 5 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
 CTGGTGGCGG TGCCGTGTGG GAGGTACAGG GATGTGCTG ACCTGGTCTG GAGCCTCGAT 1560
 GGCAATCCCT TCCGTGGTGG CCCCACCTG ACGGGCAGTG CCTTGGCGCA GCGGCGAGAG 1620
 CGTGGCTTCG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTGTG 1680
 CTCACTGAGT CACACTCCGA GGATGAGGTT GCGGGCCAG CGCGTCACGC AAGGGCCGGA 1740
 10 GAGCTGCTCC TGCTGGTGTG AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATGCTCAGG ATCTGTTCAA CCAATCCCT 1860
 GAGCTGCGAG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920
 CTCGTCTTCA TGTGAGCAC CTCTGCCCTA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGGCG 2040
 15 CTGGTGGTGT ATGGCAGCCA GGTGCAAGT GCCTTCGGGC TGGACACCAA ACCCAGCCGG 2100
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
 ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
 GTCCCAAGAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280
 GCGCAGAGGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGCGGTGGG GCTGTGCTTA 2340
 30 AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CCGGATTTCC TGATCCACGT GGCAGCTTAC 2400
 GCGGACTGCG GGTACCCACA GGCAGGTGCT ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG 2460
 CCGATCAACC TCTGCAAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520
 GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGATATC TTGAGACGCC CCTGAGGCAC 2640
 35 ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCTCCCA GCAACTACAG AGAAGGCGCT 2700
 GGCACAGAAA TGGTGCCTAC CTCTTGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760
 TTCCCGCCGT GGCCAGGACC ACTATCTCTA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT 2880
 TTGATGTGTA AGTAATATCC CACTTCTGT ACCTGTGTGT CCTTGTGAG GCTATGTCTAT 2940
 40 CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTCTAAG ACTTAATTT AGCGGCGTGA 3000
 CGTTCCTTTG CACACAATCA ATGCTGCCCA GAATGTGTGT GACACAGTAA TGCCAGCAG 3060
 AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAGACA 3120
 GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAGGGGG 3180
 CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGGAAA 3240
 45 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GCGGCTGAGT 3300
 TGTGATGGG CCCAGGTCTG GAGGGCCACG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360
 ACCTTGAAGG TCTTC

SEQ ID NO:185 CBF9 Protein sequence
 Protein Accession #: none found

1 11 21 31 41 51
 | | | | |
 55 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGNS 60
 SVKGSGFERS KHFATVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
 MVFKGGRTEB ELALKYLLHR GLPGGRNASV PQLLIIVTDG KSQGDVALPS KQLKRGVTV 180
 FAVGVFRPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
 50 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL 360
 RAKVVFVKRFV RAVLSDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPIFRGGPT 420
 LTGSALRQAA ERGFGSATRT GQDRFRRVVV LLTESHSEDE VAGPARHARA RELLLLVGVS 480
 EAVRAELEEI TGSPKHVMVY SDFQDLFNQI PELQGLKCSR QRPGRCTQAL DLVFMLD TSA 540
 SVGPENFAQM QSFVRSALQ FEVNPVTVQ GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 65 APYLGGVGS A GTALLHIYDK VMTVQRGARF GVPKAVVVL T GGRGAEDAAV PAQKLRNNGI 660
 SVLVVGVGVP LSEGLRRLAG PRDSLHVA A YADLVYHQDV LIEWLCEBAK QPVNLCRPS 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPENYREG LGTEMVPTFW NVCAPEP

SEQ ID NO:186 PAV1 DNA sequence

Nucleic Acid Accession #:

Coding Sequence:

AF272890

87-1520 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 75 TGCTACCCGC GCCCGGGCTT CTGGGGTGT CCCCACCCAG GCGCCAGCCC TGCCACCCC 60
 CCGCCCCCG GCCTCCGAG CTGGGATGG GCGGGGGGT GCTCGTCTG GCGGCTCCG 120
 AGCCCGGTAA CCGTCTGCTG GCGGCACCG TCCCGGACG GCGGCGCAC GCGGCGCGG 180

5 TGCTGGTGCC CGCGTCGCGG CCCGCCCTCGT TGCTGGCTCC CGCCAGCGAA AGCCCCGAGC 240
 CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGCTCA 300
 TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC 360
 TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCCGACCT GGTTCATGGG CTGCTGGTGG 420
 TGCCGPTCCG GGGCCACATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
 TTGCCCTGGA CGGCTACCTC GCCATCACCT CGCCCTTCGG CTACCAAGAG CTGCTGACGC 600
 GCGCGCGGGC GCGGGGCTTC GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGTCTCTCC 660
 10 TGCCCATCCT CATGCACTGG TGGCGGGCGG AGAGCGACGA GCGCGCGCCG TGCTACAACG 720
 ACCCCAAGTG CTGCGACTTC GTCAACCAAC GGGCTTACGC CATCGCCTCG TCCGTAGTCT 780
 CCTTCTACGT GCCCTGTGTC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCC 840
 AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGCGCGC CCAGCGCGGC 900
 CGCCCTCGCC CTCGCCCTCG CCCGTCCCGG CGCCCGCGCC GCGCGCCGGA CCGCGCGGCC 960
 15 CGCGCGCGCC CGCCGCCACC GCGCCGCTGG CCAACGGGCG TGCGGGTAAG CGCGGGCCCT 1020
 CGCGCCCTCGT GCGCCTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
 TCTTCAAGCT CTGCTGGGCTG CCCTTCTTCC TGGCCAACGT GGTGAAGGCC TTCCACCGCG 1140
 AGCTGGTGCC CGACCGCTTC TTCTGTCTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT 1200
 TCAACCCCAT CATCTACTGC CGCAGCCCGC ACTTCCGCAA GGCTTCCAG GACTGTCTCT 1260
 20 GCTGCGCGCG CAGGGCTGCC CGCCGCGGCC ACGCGACCCA CGGAGACCGG CCAGCGCCCT 1320
 CGGGCTGTCT GCGCCGCGCC GAGCCCGGCC CATCGCCCGG GCGCGCCTCG GACGACGACG 1380
 ACGACGATGT CTGCGGGGCC ACGCCGCGCG CGCGCCTGCT GGAGCCCTGG GCGGCTGCA 1440
 ACGCGCGGGC GCGCGCGGAC AGCGACTCGA GCCTGGACGA GCGGTGCCCG CCGCGCTTCG 1500
 25 CCTCGGATC CAAGGTGTAG GCGCCGCGCG GGGCGCGGGA CTCGGGCGAC GGCTTCCAG 1560
 GGGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACCTCA AGCCCACAAT 1620
 CCTCGTCTGA ATCATCCGAG GCAAGAGAGA AAGCCACGGA CCGTTCACAA AAAAGGAAAG 1680
 TTTGGGAAGG GATGGGAGAG TGGCTTGCTG ATGTCTCTTG TTG

30

SEQ ID NO:187 PAV1 Protein sequence

Protein Accession #:

AA011176

35 1 11 21 31 41 51
 | | | | |
 MGAGVLVLGA SEPNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG 60
 MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMLL VVFGATIVV 120
 WGRWEYGSFF CELWTSVDVL CVTASLETLC VIALDRYLAI TSPFRYQSL TRARARGLVC 180
 TVWAIASLV FLPILMHWR AESDEARRY NDPKCCDFVT NRAYAIASSV VSFVPLCIM 240
 40 AFVYLRVFRE AQKQVKIDS CERRFLGGPA RPPSPSPSEV PAPAPPPGPP RPAATAATAP 300
 LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVPDRLFV 360
 FFWNLGYANS AFNPIIYCRS PDKRAFGQL LCCARRAARR RHATHGDRPR ASGCLARPGP 420
 PPSGAASDD DDDVVGATP PARLLEPWAG CNGGAADSD SSLDEPCRFG FASESKV

45

SEQ ID NO:188 BC02 DNA sequence

Nucleic Acid Accession #: AJ400877

Coding sequence:

81-3080 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 GCGCTCCGCG CACACCTCCC CGCGCCGCGG CGGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CGCAACCCGC TGAGCCATCC ATGGGGTTCG CGGGCCGCAA CCGTCCCGGG GCGGCTGGG 120
 CCGTGTCTGT GCTGTCTGCT GTGCTGCCGC CACTGTCTGT GCTGGCGGGG GCGTCCCGC 180
 55 CCGGTCCGGG CCGTCCCGCG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
 TCAATGGAGG CTGTGTCCAT GACTGTITTA ATATTCCAGG CAATTATCGT TGCACTTGTT 420
 TTGATGGCTT CATGTGGCT CATGACGGTC ATAATGTCT TGATGTGGAC GAGTGCCTGG 480
 60 AGAACATGG CGGCTGCCAG CATACTGTG TCAACGTCAT GGGGAGCTAT GAGTGTCTGT 540
 GCAAGGAGGG GTTTTCTCTG AGTGACAATC AGCACACCTG CATTACCCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCGCCAAGGG 660
 GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 65 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCGCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGAGAGGA CACTGTCTCT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTAACAAT GGAGGCTGTG 960
 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCTGT GTGATCACTC 1020
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
 70 GTGATCATTT TCGCAAAAAA ATCGTGGGCA GTTTGACTG CGGCTGCAAG AAAGGATTTA 1140
 AATTATTAA AGATGAGAAAG TCTTGCCAAG ATGTGGAATG GTGCTTTTG GATAGGACCT 1200
 GTGACCAAG CTGCAATCAAC CACCCTGGCA CATTGTCTTG TGCTTGCAAC CGAGGGTACA 1260
 CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CTTGGGTACA 1380
 75 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GTCTCTGCC ACAAAGTGTG 1440
 CACCCCGTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500
 GTCACTCTGG CATTACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560
 AGCTAAATGA AGGCAAGTGT AGTTTAAAAA ATGCTGAGCT GTTCCCAG AGGCTGCGAC 1620
 CAGCACTACC AGAGAAGCAG AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680
 80 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740
 TTATCACTGT TGAGTTTGA CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTGTGAC 1800

5 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860
 AGGCCCGTCCA CAGGGAGCAG TTTCACCTCC AGCTCTCAGG CATGAACCTC GACGTGGGTA 1920
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCATG 1980
 CAGAAAACCA ATGTGTCAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100
 GCCCAAGACC AGGAAATCTT GGGGCCCTGA AGACCCCAAG AGCTTGAAT ATGTCTGAAT 2160
 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGACCTT TGCCAGCTCT 2220
 GTGCCCTGGG CACGTTCCAG CCTGAAGCTG GTCGAACCTC CTGCTTCCCC TGTGGAGGAG 2280
 GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340
 10 GTTCACCTGG ACATTCTAC AACACCACCA CTCACCGATG TATTGTTGC CCAGTGGGAA 2400
 CATACCAGCC TGAATTTGGA AAAAAATAAT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460
 ACTTTGATGG CTCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520
 GAGATTTTAC TGGGTACATT GAATCCCAA ACTACCCAGG CAATTACCA GCCAACACCG 2580
 AGTGTACGTG GACCATCAAC CCACCCCAAG AGCGCCGAT CCTGATCGTG GTCCTGAGA 2640
 15 TCTTCTGCCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTTCTCAT 2700
 CCAATTTCTGT GACAAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACTT 2760
 CCAGGTCAAA GAAGCTGTGG ATTCAATGA AGGGAACAGC GCTAGAGGGT 2820
 TCCAGTCCC ATACGTGCA TATGATGAG ACTACAGGA ACTCATGAA GACATAGTTC 2880
 GAGATGGCAG GCTCTATGCA TCTGAGAAC ATCAGGAAAT ACTTAAGGAT AAGAAACCTA 2940
 TCAAGGCTCT GTTGTAGTTC CTGGCCCATC CCCAGAACTA TTCAAGTAC ACAGCCCAAG 3000
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
 GGTGGTGGG ACAGAGCTGT CTTCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC 3180
 CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGTAATAAT 3240
 25 GAACTTGGTT TTCTTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
 CAGCTTCTCA CTCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT 3360
 TTGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCC TCAAGGAGTC 3420
 TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540
 CAAGAGGGGA GGAAGGAGA CCCCTGCAGG CTCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTATCC CAGGAACCTG 3660
 AGTTCTAAGC AGTCTCTGTG AAAAAAAAAA GCAGAAAGAA TTAGAAATAA ATAAAAACTA 3720
 AGCACTTCTG GAGACAT

35 SEQ ID NO:189 BCO2 Protein sequence
 Protein Accession #: CAB92285

40 1 11 21 31 41 51
 | | | | |
 MGAVAGNRNP AAWAVLLLLL LLPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTSYK CSCKPGYQGE GRQCEIDDEC GNELNGGCVH DCLNIPGNRY CTFDFGFLA 120
 HDGHNCLDVG ECLENNNGCQ HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSCMNK 180
 45 DHGCSHICKE APRGSVACBP RPFELAKNQ RDCILTCNHG NGGCOHSCDD TADGPECSCH 240
 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300
 STGVHCSPV GFILQLDGT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
 SCQDVDECSL DRICDHSCIN HPGTAFACAN RGYTLYGFTH CGDINECSIN NGGCOQVCVN 420
 TVGSYECQCH PGYKLHWK KDCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 50 SSDVTITRS VTFKLNKGK SLKNALFPE GLRPALEKH SSVKESFRYV NLTCSSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPRTS ERQAESCQVG QGHAENQCVS CRAQTYDGA RERCILCPNG 660
 TFQNEEGQMT CEPCPRPNS GALKTPAWN MSECGLCQF GEYSADGFAP CQLCALGTFQ 720
 PEAGRTSCFP CGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYPQEPF 780
 55 KNNVCSPGN TITDFDGSIN ITQCKNRRCG GELGDFTYGIESPNYPGNYP ANTECTWTIN 840
 PPPKRLIV VPEIFLPIED DCGDYLVMRK TSSNSVTY ETCQTYERPI AFTSRSKLW 900
 IQFKSNEGNS ARGFPQVYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFKY TAQESREMPF RSFRLRLSK VSRFLRPYK

60 SEQ ID NO:190 BFG1 DNA sequence
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

65 1 11 21 31 41 51
 | | | | |
 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
 CTGGACCACT GCATGACCGC CTTGGACCTC TTCTCACCA ACCAGTTCTC AGAAGCACTC 120
 AGTACCTCA AGCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
 CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
 ATGAAGGAGG CACAGATGCT GTGTCAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
 70 TTCAGCAGCC TGGTGAACCG CCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360
 GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCTC GCAGGACGAG 420
 AACATGTGGA GCTTCTCAA AGGCGGCATC AAAGTTCTGA ACAGCTACCA GACCTACAAG 480
 GAGCTGGACA GCCTTGTTC GTCTCACA TACTGCAAGG GTGAGAACCA CCCGCACTTT 540
 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600
 75 AGGATCCTGA GCTTGTGGA GTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
 CAGCTGGAGG AGGGAGCGTC AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720
 CTGTGCTACC ACACCTTCTT CACCTTCTGT CTCGGTACTG GGAACGTCAA CATCGAGGAG 780
 GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCCTA AGGGTGCCAT CTTCTCTGTC 840
 TTTGACGGGA GGATTGAAGT CATTAAAGGC AACATTGATG CAGCCATCCG CGGTTTCGAG 900

5 GAGTGTGTG AGGCCAGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
 ATGTGGTGTCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTACGC CGACCTGCTC 1020
 AGCAAGGAGA ACTGTCTGGT CAAGGCCACC TACATTACAA TGAAGGCCGC CTACCTCAGC 1080
 ATGTTTGGGA AGGAGGACCA CAAGCCGTTT GGGGACGACG AAGTGGAAAT ATTTCGAGCT 1140
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTCGCATC 1200
 CGGAAGTCCC GGCCTACTT CTCTCCAAC CCTATCTCGC TGCCAGTGCC TGCTCTGGAA 1260
 ATGATGTACA TCTGGAACGG CTACGCCGTG ATTGGGAAGC AGCCGAAACT CACGGATGGG 1320
 ATACTTGAGA TTACTACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCCAGA GAACGAGTAC 1380
 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440
 10 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCTGCTGCT TATGGAGCAA 1560
 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC 1620
 TCCATGGAGT CAAGGACACA CTTCGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
 CTAGAGAACA GCAGGACATA CTGGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740
 15 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCTT 1800
 CCCCTGCCC TGCCCTGCCT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
 TGTATCCGTG CAGAAGCCGA GCTGGCATT TCCACAGTGT AGCCAAGGGC CTTTGCCAAG 1920
 GGCAGAGCAG GTGGAGCCCT CTGCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980
 GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCTT TAGAAATACA TTGATGGGAT 2040
 20 CACAGTTGGC TTTAAAAACC AACAACAATC AACCACCTGT AAGTCTTTGT CTTCACCTAT 2100
 TATCATCTGG AGTTAAATCT CTTTATATGA TGATGCCAAA GGGCAAATTG CTTTCAAAAT 2160
 TCAGCAAGTT CTCAGCTGTG GTGACGGAAG GTCTTCAGA GGACCTGAGG AATGCCTGGG 2220
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTGGGG ATGAGGATGT ACACAGACAC 2280
 CCCTACCTT ACTACTACA CTTCATTTC CTTCTTTTGT AAATTTCCAA TTTAAAAATC 2340
 25 AAGCACGTCT TTTTAGTGAG ATAAAACTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
 AGTAGAAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
 AAATTTGGGG GGCAGGAGGA GGTTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
 CTGAAACCAC TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA 2580
 30 CATTGCTTA CTGACAGCAT TTTTGTTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAAAA 2640
 AA

SEQ ID NO:191 BFG1 Protein sequence

Protein Accession #: AAC39582

35 1 11 21 31 41 51
 | | | | |
 MTALDLFLTN QSEALSULK PRKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA 60
 40 QMLCQRHRRK SSVTDSFSL VNRPTLGQFT EEEHAEVCY AECLLQRAAL TFLQDENMVS 120
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSMLPTRILR 180
 LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGTG NVNIEEAELK 240
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEBCEC AQHWHKQFHH MCYWELMWCF 300
 TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAYLSMFGK EDHKPFGDDE VELFRAVPGI 360
 45 KLKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420
 ITKABEMLEK GFENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
 LIPNALLELA LLLMEQDRNE EAIKLLESAK QNYKNYSMES RTHFRIQAAT LQAKSLENS 540
 SRSMVSSVSL

SEQ ID NO:192 BFO8 DNA sequence

Nucleic Acid Accession #:

NM_032583

Coding sequence:

1-4044 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 ATGACTAGGA AGAGGACATA CTGGGTGCCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC 60
 ATCGACATAG GCGATGACAT GGTTCAGGA CTTATTATA AAACCTATAC TCTCCAAGAT 120
 GGGCCCTGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGGAGGCAGC TGTCACCCG 180
 60 TGGGGGAAGT ATGATGCTGC CTGAGAACC ATGATTCCTT TCCGTCCCAA GCCGAGGTTT 240
 CTTGCCCTCC AGCCCTGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300
 ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTTCCACTG 360
 TCAGTCCATG ATGCCCTAGA CAAAAATGTC CAAAGGCTTC ACCGCCTTTG GGAAGAAGAA 420
 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480
 65 ACAAGGTGTA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540
 CCAATATTGA TTATACCAAA GATCCTGGAA TATTAGAAG AGCAGTTGGG GAATGTTGTC 600
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660
 TCCTCCAGTT GATCATATCA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTTCTCTC 720
 TTTGCCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780
 ATCAGCTTCT TCACCGGTGA GTAAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
 70 GTACTGATCA CTTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCTACTT CATTATTGGA 900
 TACTGTCAT TTATTGCCAT CTTATGCTAT CTCCTGGTTT TCCCACTGGC GGTATTCTAT 960
 ACAAGAAATG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT 1020
 GTGACCAGTG AAGTCTCTAC TTGCATTAAG CTGATTAATA TGTACACATG GGAGAAACCA 1080
 75 TTGCAAAAAA TCATTGAAGG TATGGAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC 1140
 ATGGCCTTCA GCATGCTGGC CTCCTTGAAT CTCCTTCGGC TGTCAGTGTT CTTTGTGCTT 1200
 ATTGCAGTCA AAGGTCTCAC GAATTCGAAG TCTGCAATGA TGAGGTTCAG GAAGTTTTC 1260
 CTCAGGAGA GCCCTGTTT CTATGTCCAG ACATTACAAG ACCCCAGCAA AGCTCTGGTC 1320
 TTTGAGGAGG CCACCTTGTG ATGGCAACAG ACCTGTCCCG GGATCTGCTA TGGGGCACTG 1380
 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCCTAGAGA TGCCCTCGGG 1440

CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500
 AAGGGGATGA TGTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTTGTCA 1560
 GCCATCTGG AGGAGATGCA CTTGCTCGAG GGCTCGGTGG GGGTGCAGGG AAGCCTGGCC 1620
 TATGTCCCCC AGCAGGCTG GATCGTCAGC GGAACATCA GGAAGAATCA CCTCATGGGA 1680
 5 GGGCATATG ACAAGGCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740
 CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCCT CAACCTCTCT 1800
 GGGGGGCGA AACAGAGGAT CAGCCTGGCC CGCGCCGCTCT ATCCGACCG TCAGATCTAC 1860
 CTGCTGGACG ACCCCTGTC TGCTGTGGAC GCCACGTGG GGAAGCACAT TTTTGAGGAG 1920
 10 TGCATTAAGA AGACACTCAG GGGGAAGACG GTCGTCCTGG TGACCCACCA GCTGCAGTAC 1980
 TTAGAATTTT GTGGCCAGAT CATTITGTGG GAAAATGGGA AAATCTGTGA AAATGGAACT 2040
 CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCAAC TTATCCAGAA GATGCACAAG 2100
 GAAGCCACTT CGGACATGTT GCAGGACACA GCAAAGATAG CAGAGAAGCC AAAGGTAGAA 2160
 AGTCAGGCTC TGGCCACCTC CCTGGAAGAG TCTCTCAACG GAAATGCTGT GCCGGAGCAT 2220
 15 CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCACCAC 2280
 TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGATAAA TTTTCTTCTT CGTGGTGTCT 2340
 ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGGTGGGA GCAGGGCTCG 2400
 GGGACCAATA GCAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAC 2460
 AATCTCTAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CCTCATCTGT 2520
 20 GTGGGGGTCT GCTCCTCAGG GATTTTCACC AAAGTCACGA GGAAGGCATC CACGGCCCTG 2580
 CACAACAAGC TCTTCAACAA GGTITTCGCG TGCCCCATGA GTTCTTTTGA CACCATCCCA 2640
 ATAGGCCGCG TTTTGAAGCT CTTCGACGGG GACTTGAAC AGCTGGACCA GCTCTTGCCC 2700
 ATCTTTTTCAG AGCAGTCTCT GGTCTGTGTC TTAATGGTGA TCGCCCTCTCT GTTGATTGTC 2760
 AGTGTGCTGT CTCATATAT CCGTGTAAAT GGAGGCATAA TCATGGTAT TTGCTTCATT 2820
 25 TATTATATGA TGTTCAGAA GGCCATCGGT GTGTCAAGA GACTGGAGAA CTATAGCCGG 2880
 TCTCTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940
 GGAAAACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000
 CTGCTGTGT TCTATCTTC CACACGATGG ATGGCATTGA GGTGGAGAT CATGACCAAC 3060
 CTGTGACCT TGCTGTGTC CCGTGTCTGG GCTTTTGCCA TTCTCTCCAC CCCTACTCC 3120
 30 TTTAAAGTCA TGGCTGTCAA CATCGTGTG CAGCTGGCGT CCAGTTCCA GGCCTGTC 3180
 CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG 3240
 AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAGTGTCC CCAGGGGTGG 3300
 CCACAGCATG GGAATAATCAT ATTCAGGAT TATCAGATGA AATACAGAGA CAACACACCC 3360
 ACCGTGCTTC ACGGCATCAA CCGTACCATC CGCGGCCACG AAGTGTGGG CATCGTGGGA 3420
 35 AGGACGGGCT CTGGGAAGTC CTCCTGGGC ATGGCTCTCT TCCGCTGCTT GGAGCCCATG 3480
 GCAGGCCGGA TTCTCATTGA CGCGGTGGAC ATTTGCAGCA TCGGCTGGA GGAAGTGGG 3540
 TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600
 CTAGATCCCT TTAGCCGTC CACTGACCAG CAGATCTGGG ATGCCTTGA GAGGACATTC 3660
 CTGACCAAGG CCATCTCAAA GTTCCCAAAA AAGCTGCATA CAGATGTGGT GGAACACGGT 3720
 40 GGAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780
 TCCAAGATCA TCCTATTCGA TGAAGCCACA GCTCCATTG ACATGGAGAC AGACACCTCG 3840
 ATCCAGCGCA CAATCCGTGA AGCCTCCAG GGCTGCACCG TGCTCGTAT TGCCACCGT 3900
 GTCACCACTG TGCTGAAGT TGACCACATC CTGGTATGG GCAATGGGAA GGTGGTAGAA 3960
 TTTGATCGG CGAGGTACT GCGGAAGAAG CTTGGGTCAT TGTTCGAGC CCTCATGGCC 4020
 45 ACAGCCACTT CTCACGTAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG 4080
 CTCAGAGGTT CACACAGTGT CAGCTTCGAG GCCACAGTC TGCACCTTC TTGTTTGGAG 4140
 ATGAGAAGCT TCCTGGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA 4200
 ACCCTGGAAT AGGCTACTTG ATGGCTCTCA AGACCTTGA ACCCCAGAAC CATCTAAGAC 4260
 50 ATGGGATCA GTGATCATGT GGTCTCTCT TTAACCTACA TGCTGAATAA TTTTATAATA 4320
 AGGTAAGAGC TTATAGTTTT CTGATCTGTG TTAGAAGTGY TGCAATGCT GTACTGACTT 4380
 TGTAAATAT AAAACTAAGG AAAACTCAAA AAAAAAAAAA AAAAAA

SEQ ID NO:193 BFO6 Protein sequence

Protein Accession #: NP_115972.1

55 1 11 21 31 41 51
 | | | | |
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQRNP EAPGRAAVFP 60
 WGKYDAALRT MIFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL 120
 60 SVHDASDKNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180
 PILIPIKILE YSEELGNV HGVGLCFALF LSECVKLSLF SSSWIINQRT AIRFRAAVSS 240
 FAFELKIQKF SVIHITSGEA ISFTGDVNY LFEGVICYGL VLITCASLVI CSISSYFIIG 300
 YTAFIALCY LMVFLAVFM TRMAVKAQHH TSEVSDQRI VTSEVLTCTIK LIKMYTWEKP 360
 FAKIEGMES LTFCKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF 420
 65 LQESPVFYVQ TLQDPSKALV FEEATLSWQQ TCPGIVNGAL ELERNHASE GMTRPRDALG 480
 PEEEGNSLGP ELHKINLVVS KGMMLGVCN TGSGKSSLLS AILEEMHLLS GSVGVQGSLS 540
 YVPQQAIVS GNIRENLMG GAYDKARYLQ VLHCCSLNRD LELPFQDMT EIGERGLNLS 600
 GGQKQKRLA RAVYSDRQY LDDPLSAVD AHVGKHIFEE CIKTLRGT VVLVTHQLQY 660
 LEFCGQILL ENGKICENG HSELMQKKGK YALQIKMHK EATSDMLQDT AKIAEKPKVE 720
 70 SQALATSLEE SLNGNAVPEH QLTQEEEMEE GSWRVVYHH YIQAAGGYMV SCIFFFVVL 780
 IVFLTIFSW WLSYWLQGS GTNSSRESNG TMADLGNAD NPQLSFYQLV YGLNALLIC 840
 VGVCSGIFT KVTRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLP 900
 IFSEQLVLS LMVIAVLLV SVLSPYILL GAIMVICH YNMMFKKAIG VFKRLNYSR 960
 SPLFSHILNS LQGLSIHVY GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALREIMTN 1020
 75 LVTLAVALFV AFGISSPYPS FKVMANVNL QCLASSFQATA RIGLETEAQF TAVERILQYM 1080
 KMCVSEAPLH MEGTSCPGW PQHGEHFQD YHMKYRDNT TVLHGINLTI RGHEVVGIVG 1140
 RTGSGKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDF VLLSGTIRFN 1200
 LDPFDRHLDQ QIWDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIAVAVLRN 1260
 SKIILDEAT ASIDMETDTL IQRITREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNKGKVE 1320
 FDRPEVLRKK PGSFLAALMA TATSSLR

SEQ ID NO:194 BHB8 DNA sequence

Nucleic Acid Accession #:

AA983251

Coding sequence:

1-1749 (underlined sequences correspond to start and stop codons)

5
10
15
20
25
30
35
40
45
50
55
60
65
70

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCTGTCGTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCAGG 60
GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCAGAG GCGAGGCAGC 120
GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
CCGCCGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300
CGCCTGCGTC CTGAGACGTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCCA GATTTCATC AGCGAGTGCA 420
ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
GCTCCTGGAC CTAGGGCCCG GCCTCGTCCG CTCTGGGCGT TCGCGGCAGA GGGGAGTGGC 540
CCGCCGCGGA AGCGCCGCGG GACAGTCAGT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600
CTTCTCGGAG ACCGTCCGTC GCTCTCTGGA GACGCGCTGT CCGCGCCACG GGTGGTGCCA 660
TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCTCGGAA CGCCGCTTCG CTCTGCAGC 720
TGTGCTGGCG TCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGTCTCCAGT GTCCCGAGCG CTTGACGGC 840
GGCGACGCCA CCATCTGCTG CGCAGCTGCG GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
GCGCGCTGCG ACCAGGGCGG CTGCACAAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGCTCTAG GGTACCCAA 1020
GGAGACGGCG AGGGTGCGCC CCCACCGGTG AGGGCTGGC AGCGGTGCTC CCTGGAAGGC 1080
TCCCCGAAAG GAAGCGAGCT CCTCAGGGCT TCCCCGGGCG TGTGTCGCCG TGCCAGACGC 1140
CGCGGATTCC CATCTCTCC ACGCCGCGGC CCTCTCCCTC TGCAGCGGCC CGCCTTGCCC 1200
ATCTACGTGC GGTTCCTCAT TGTGGCTTCC GTGTTGTCG CCTTATCAT CTTGGGGTCC 1260
CTGCTGGCAG CCTGTGCTG CAGATGTCTC CGGCTTAAGC AGGATCCCCA GCAGAGCCGA 1320
GCCCGAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380
CGGGGCTCGT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAATCC 1440
GGGGCCCGGG CGCCCCAAC AAGGTACAGC ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500
AACACAGTGT ATGTCAACAT GCCACGAAT TTCTCTGTGC TGAACGTGCA GCAGGCCACC 1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG 1620
CAGGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
AGGCAGATTC AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTTA TGGCAGGATT CTTTGGATG 1860
GCTTCAATTTG CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCCT AGCTGGAGAT GACTGTGATG 1980
TTGCTGATGG GTGTATACCA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTTAT TTGTTATTAT TATTCTTTT 2100
TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
TTTMTTTTTT TTTTMTTAA TCAGACAGGG TCTTGTCTCG TTGCCCAGGC TGGAGTGCAG 2220
TGGTGGCAGT TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCTGCCTC 2280
AGCCTCCACG GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT 2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
TCTGCCGTGC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
TGAGCCTTTT TTTTCTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
ATTCTAAAG GAAACCTGTT TGAACCTGTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
GGGCTTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
TTAAAAGAG ACTGAAATAA ATGTATAGT TACTTAACATA ATGAAGACAT TTCAGAACTC 2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAACCAAT CATCCCCTTC 2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATCTTTTTT 2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
TGGTTATGGT TTGGCGTTTC CTCTGTGTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTT 3000
GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
AAAAATTTT TGTCTCTAGT TATAAAATTT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180
GCAGATCATA AGGCTTTTAA TACTCTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
GATTGTAAAG AGAAAAAGCT TTCAACGAAG GATTGCCCTT CTCTCCAC ACTGTTCTTG 3300
ATTTCCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATCCA TTGCCAATGT TCCAAATTAT 3360
CAAATTCAGT TGAATTTAT TGTGTGTTCT TTAATTATAT AAAAAAGAT AACTTTAAGG 3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480
GTATGTGATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540
TGTTTTATGA CTGAATAATG TAAAACCAAG GTTGGCAATT GGTATCATCA ATGATACTCA 3600
TTTTTTAATA ACCAAAGGCA GGGGAAAAAT ATTTTACTMA TTAATAAATA TTTTATGATG 3660
TGAAAAAAA AAAAAAAA AAAAAAAA

```

SEQ ID NO:195 BHB8 Protein sequence

Protein Accession #: none found

5	1	11	21	31	41	51	
	MLSGFLMSFS	TOHRAQYTPG	GKKLPWEAST	GAHSTRGRGS	DRBRERSRPEA	AGLLWDRAAA	60
10	GEAEKGNRGE	FPANWRAQQQ	PRPPPAGQAP	GTAAGGAQDP	RLRPGRSRGR	VRLEPVKPPEA	120
	SGRQPRGSPD	CIPRFPSSASA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
	PRGKRRGTVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAARPSF	HPGTPLRSCS	240
	CCWLRCWRRG	RGPSGEYCHG	WLDAQGVWRI	GFQCPERFDG	GDATICCGSC	ALRYCCSSAE	300
	ARLDQGGCDM	DRQQAGGEPG	RADKDGPRRL	GRASCLRGTQ	GDGEGAPPPV	RAWQRCSPG	360
15	SPKGRQLLRA	FPGLLPRARR	RGFFSSPRGG	PSPLQRPALP	IYVPFLIVGS	VFVAFILGS	420
	LVAACCCRCL	RPKQDPQQR	APGGNRLMET	IPMIPASASTS	RGSSSRQSSST	AASSSSSANS	480
	GARAPPTRSQ	TNCCLEPGTM	NNVYVNMPTN	FVVLNCQQAT	QIVPHQGGYL	HPPYVGYTVQ	540
	HDSVPMPTAV	PFMDGLQPGY	RQIQSPFFHT	NSEQKMYPAV	TV		

SEQ ID NO:196 CQA5 DNA SEQUENCE

Nucleic Acid Accession #:

AA088453

Coding sequence:

862-1995 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GCCCTTGGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAAG	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
	GCGCCGGGCG	CCGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCCGC	180
30	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAGGTGACA	AGAGGTGGCC	CGGTGCCCTG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCCGTCTCTC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
	ACCTACCCCC	CGGCTCGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
	CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAGTCG	480
35	GGGCTCATTA	AGCAGCTGTT	TGAGGCCCGC	GGCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
	GATTCCACCT	TCTATGATC	CTTGTGGGCC	CGGTGGGGCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCGA	GGGTGCGGCG	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCCCGGCAG	660
	GCCACGGCAC	AGTCCCGGAG	TGGGCGCCTT	CCTGCCGCCC	TTGCCAGATG	GGCTCCCCAG	720
	GCCCTGCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTTTGGGCTC	CTGGTTGYTG	780
40	ACATGGGGCT	GGGGCTCTCT	TGAGTCCGCA	TAGTCCCGCA	CTACTACTGC	CCGCTGTCTG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCGG	TTTCCAGCGG	TGCCCGCCCTG	900
	GGTCCCATCT	TCAGGGAAAG	GCAGTGCCCA	CGCCAGGCTG	CAGTTCCAAC	AACGGGCAGC	960
	AGAGGCGCGG	GGCGCGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TGGGACGGAC	GGAAAGTAGT	GGAGGGGGTG	GGGACGGCCT	1080
45	GTAAGCGGGG	GGTGCCTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTGCG	ACTTCAGGTT	1140
	CTGGCCAAAG	CTGAGGAGCC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GCGAGAGCTT	1200
	GGCCTGCATG	TGCTCTCCAC	AGACCTTGGG	GTGATGGCCT	TCCCTCTCTT	GGCCGGGACG	1260
	TTGCCCCACG	TTGAGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACGTGA	TAGGCAAAAG	CTGTTCCTCC	CGACTCAGGA	TTTCCAAGGC	1380
50	CTGGGGTCCCT	GCTCACCCCC	CTTTGCTCTC	ACGCCACGCC	TGTCCCCAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCCTGCCCA	GGCCCACTCC	CGCTGGTGCT	1560
	GGAGTAGCGA	CTGGTGGGGG	GGCCCTGTCT	AGCCCAACCT	GGAGGGTCCC	AGTGTCAACA	1620
	GAACCAAGGG	CAGCGCAACA	GCATCGATGG	GTTCCTGCAG	CCAGGGCCCC	CGATGCGGGG	1680
55	TCAGTGTGTG	TGGGGCGCAG	GGCCTCCGAT	GCGGGGTCAG	TGCGTGGGGG	GCGCAGGGCC	1740
	CCCGATGCGG	GGTCACTGCG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCACTTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGGGCCT	GGCAGGCAGC	GTGGCAACTC	1860
	CCTTCCGGAG	CCCAGCTCCA	TGCTAACCTG	CCCACAGCAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCCTG	GACAGGCCCA	AGTCAGCCCA	GCATGCAGCT	1980
60	GCCTCTCTAC	CCTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCCTGG	2040
	ACCTCTCTGG	CAGGAAAGGG	TGCAGGTCTT	GAGGGCCTGT	GCCCCACAGC	CCCAGCACCC	2100
	AGGTGGACTG	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCGTCAGCA	2160
	GGCTGGGGTC	TGCCCAACAG	GGCCTCCCCA	CGTCTGCCCT	TGAGGGTGCC	TGCCATGCCC	2220
	TGGGGGATCC	TGGCACTTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
65	GGTGACTTCA	TCAGGAGACC	GCCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCTCCG	GAAAAAAGTGC	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCCT	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
70	GAGCAGCGTC	CCTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACGT	2640
	GCCTGCACAC	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCTTGGGGGG	TCCCTGGGGG	2700
	CAGAAGTGTC	CCCAAGTTAG	AATCTGCCCC	AGAGGAACAC	ATCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTG	ATCAAGTTCC	AAGGAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCACTG	2820
	CTGGAATCCC	AGCATPTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
75	CCCCATCTCT	ACAAAAAAAA	AAAAAGAAAG	AAAGAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAAGCAAC	AGATTGACTC	3000
	TAGACCCAGA	TACTAGAAAT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTTCTG	GAAACATGAA	AAAAAA			

SEQ ID NO:197 LBG2 DNA SEQUENCE

Nucleic Acid Accession #: X83629
Coding sequence: 54-2543 (start and stop codons are underlined)

5 1 11 21 31 41 51
 | | | | |
 GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATG GGGC 60
 TCCTCTCGTG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCGG 120
 CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 10 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTAT GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCAGTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAT GGCAAGGGTC 420
 15 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTGAC AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660
 TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 20 GTGCTTTAGA GGGAGTCCCT CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 25 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCTGAG AATGCAAGTG 1080
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140
 GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTITGAG GCCAAAAACC 1260
 AGCACACCCT GTACGTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
 30 CCACAGCCAC CATAGTGGT CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTIGAGGTC CAGGAGGGCA TCCCACITGG GGAGCCTGTG TGTGCTACA 1440
 CTGCAGAGA CCTGACAAG GAGAATCAAA AGATCAGCTA CCGATCCTG AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTCGACC 1560
 35 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCCACCAT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAAAG 1680
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCGTGGCGCC 1740
 ACGTGCTGAA CATCAGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCACGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGCTG 1920
 40 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGGAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCTTGGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTGTTT GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAAGACT ATGACATCAC CCAGCTCCAC CGAGGCTTGG 2220
 45 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCAGATG AATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CACTACGACAC CCTCTTGGTG TTCGACTATG 2400
 AGGCGAGCGG CTCGAGCGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 50 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580
 CACAGAGCAT CTTCAAGGGG TCTCAGTTC CCCTTCAGCT GAGGACTTCG GAGCTTGICA 2640
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 55 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGTCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTCTTAG GCCTCCTGGT GCAACTTAAT TTTTITTTT AATGTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCA GA GCTGTGGGC CCACTGGCCG 3000
 TCTGCAATTT CTGTTTCCA GACCCCAATG CCTCCATTG GGATGGATCT CTGCGTTTTT 3060
 60 ATACTGAGTG TGCCTAGGTT GCCCTTATT TTTATTTTC CCGTTGGCT TGTATAGAT 3120
 GAAGGGTGAG GCAATCTGT TATATGTACT AGAAGCTTTT TATTAAAGAA A

SEQ ID NO:198 LBG2 Protein sequence:

Protein Accession #: CAA45177

65 1 11 21 31 41 51
 | | | | |
 MGLPRGPLAS LLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVMGCPG 60
 QEPALSTDN DDFVNRNGT VQERRSLKER NPLKIFSKR ILRRHKRDVW VAPISVPENG 120
 70 KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREEIAK 180
 YELFGHAVSE NGASVEDPMN IISIVTDQND HKPKFTQDIF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTS VISSGLDREK VPEYTLTQA 300
 TMDMDGSGST TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360
 75 AWRATYILMG GDDGDHFTIT THESNQGL TTRKGLDFEA KNQHTLYVEV TNEAFFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPKE NQKISYRILR 480
 DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIEYVMVLA MDNNGSPPTG TGTLLLTLD 540
 VNDHGFVPEP IQITICNIQSP VRHVLNITDK DLSPIHSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLVLLVRKK RKIKEPLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720

GLEARPEVVL RNDVAPTIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

SEQ ID NO:199 OB15 DNA SEQUENCE

5 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

```

10 1      11      21      31      41      51
    |      |      |      |      |      |
    CTTCCTTAAA TTTCCTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
    GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTCTGA TGACTGGACA 120
    GGAACAAAGC TTGTGATTGT TTGTGTGTGT GGGACGTTT TCTGCTGTGT TATTTTCTTT 180
    TCTAATTCTC TGGTCATGCG GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240
    TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTCGCTA TGTATTCCTG 300
    ATGTTTAAAC CAGGCCAGT TTCAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG 360
    GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGTTTAT CGCCGTGGAG 420
    AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAA GAGGGTGACA 480
    CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATATG GGGCGGTCCC CACACTGGGC 540
    TGGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCTCTG CCCCATTCTA CAGCAGGAGT 600
    TACCTTGTGT TCTGGACAGT GTCCAACTC ATGGCCTTCC TCATCATGGT TGTGGTGATC 660
    CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG 720
    TCATCATGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
    GCGTTTGTGG TATGTTGGAC CCGGGGCTTG GTGGTTCTGC TCCTCGACGG CCTGAAGTGC 840
    25 AGGCAGTGTG GGTGTCAGCA TGTGAAAGG TGGTTCTGTC TGCTGGCGCT GCTCAACTCC 900
    GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
    ATGATCTGCT GTTCTCTCTA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
    GTCTCAGACA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
    30 GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140
    GTCTTAGG
  
```

SEQ ID NO:200 OB15 Protein sequence:

Protein Accession #: NP_036284

```

35 1      11      21      31      41      51
    |      |      |      |      |      |
    MNECHYDKHM DFFYNRSNFD TVDDWTGTKL VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60
    FHFPFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
    40 LVIAVERHMS IMRMVRHNSL TKKRVTLLIL LWALALFMG AVPTLGWNCL CNISACSSLA 180
    PIYSRSLYVF WTVSNLMAPL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT 240
    VMTVLGAFFV CWTPLGLVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVP IYYSYKDEDM 300
    YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS
  
```

SEQ ID NO:201 PAA6 DNA SEQUENCE

Nucleic Acid Accession #: AA569531
 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

```

50 1      11      21      31      41      51
    |      |      |      |      |      |
    ATGACCTTACA GTTACTCATT TTTCAGGCCT GAGTTGATCG TTAATCATCT TAATTATGTT 60
    CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGTCTCTGCT TTCATTTCTT 120
    GATGAAACCT CTGGACTAAG CACACATCTT CCTTGTTTAT CTCTCTCAAA GGAGTGTTGA 180
    GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240
    55 CAGCTATACC TGTGGGACAT GGGTGGTTT ACAATATTTA AGAACCTGTG GATGAGCCTC 300
    ATACCCAGAG GGAACAAACG CTCCCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360
    AAGCAGAAGC AAAGTTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420
    CTCTCTTCAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTGGGCA 480
    60 GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTTCTTCA 540
    GCTACGTTGT CCCAGCATT CTCTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600
    AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTTAT TACTGAGCTG CTACCATATG 660
    CCAGCTACTC CTTCGATGTT GTTCATTTAT TTCTCAACAC TCAGCATATT TGCAATATGT 720
    TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTCTCT GCCAAACATC 780
    65 ACATGAGGAT GAACAATGAA ACCGATTGTA AACCAGGATT GTCTGATTCC AACATCTCTG 840
    GGTCTTTTTT CACTCTGATA TGCTGCAATT AAAAAGCCAT TTCTAAGACT GT
  
```

SEQ ID NO:202 PAA6 Protein sequence:

Protein Accession #: none found

```

70 1      11      21      31      41      51
    |      |      |      |      |      |
    MTYSYSFFRP ELIVNHLNV HSEANRRRTK KTLSSLSSFL DETSGLSSTHL PCLSLSKECG 60
    75 VLHLDIHKKK EDMRTQQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120
    KQKQSSKIQE ERRRESAGPN LSSFVFWGNA GRGDRPQIWA GSKQFSG
  
```

SEQ ID NO:203 PAB2 DNA SEQUENCE

Nucleic Acid Accession #: XM_050197
Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
| | | | | |
TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC 60
AGCCGCGCGC CTCGCCCAGG ATCTGAGTGA TGAGACGTGT CCCACTGAG GTGCCCCACA 120
GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAGGGGCT GGCAGAAATG 180
GGCGCCTGGC TGATTCTCTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCCG CAGCTTCTGG 240
AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCTGAGC CCTACCCGCC 300
TGGCCCACTA TGSTCCAGAG GCTGTGGGTG AGCCGCTGTC TCGGCACCG GAAAGCCACG 360
CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCGC AGGCATCACC 420
TATGTCCGCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTCATGAC CATGGTGTCTG 480
GGCAATTGGT CAGTGTCTGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540
TGGCGTGGAC GCTATGGCCG CCGCCGGCCC TTCTCTCTGG CACTGTCTTT GGCATCTCTG 600
CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCGGGATCCC 660
AGGCCCTGAG AGCTGGCACT GCTCATCTGT GGCGTGGGCG TGCTGGACTT CTGTGGCCAG 720
GTGTGCTTCA CTCCACTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
CGCCAGGCCT ACTCTGTCTA TGCCCTTCATG ATCAGTCTTG GGGGCTGCCT GGGCTACCTC 840
CTGCCCTGCC TTGACTGGGA CACCAGTCCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900
TGCCCTTTTG GCCTGCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGGTG 960
GCTGAGGAGG CAGCGCTGGG CCCACCGGAG CCAGCAGAAG GGCTGTGCGC CCCCTCTCTG 1020
TCGCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080
25 CCGCCGCTGC ACCAGCTGTG CTGCCGCACT GCCCGCACCC TGCGCCGCT CTTCGTGGCT 1140
GAGCTGTGCA GCTGGATGGC ACTCATGACC TTACAGCTGT TTACACGGA TTTCGTGGGC 1200
GAGGGGCTGT ACCAGGGCCT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT 1260
GATGAAGGCG TTCCGATGGG CAGCCTGGGG CTGTTCTTGC AGTGCGCCAT CTCCCTGGTC 1320
TTCTCTCTGG TCATGACCGG GCTGGTGCAG CGATTCCGCA CTGAGCAGT CTATTTTGGCC 1380
30 AGTGTGGCAG CTTCCTCTGT GGCTGCCGGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440
GTGACAGCTT CAGCCGCCCT CACCGGGTTC ACCTTCTCAG CCTGCAGAT CCTGCCCTAC 1500
ACACTGGCCT CCTCTTACCA CCGGGAGAAG CAGGTGTTCG TGCCCAAATA CCGAGGGGAC 1560
ACTGGAGGTG CTAGCAGTGA GGACAGCCTG ATGACCAGCT TCCTGCCAGG CCTAAGCCT 1620
35 GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCTGCT CCCACCTCCA 1680
CCCGCGCTCT GCGGGGCTTC TGCCCTGTGAT GTCTCCGTAC GTGTGGTGGT GGTGAGCCCC 1740
ACCGAGGCCA GGTGGGTTCG GGGCCGGGGC ATCTGCCTGG ACCTCGCCAT CCTGGATAGT 1800
GCCTTCTCTG TGTCACAGGT GGCCCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC 1860
CAGTCTGTCA CTGCCATATG GGTGCTTGCC GCAGGCTTGG GTCTGGTCCG CATTTACTTT 1920
40 GCTACACAGG TAGTATTGTA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAAACTTCC 1980
AGCACATTGG GGTGGAGGGC CTGCCTCACT GGGTCCCAGC TCCCCTGCC TGTAGCCCC 2040
ATGGGCTGCG CGGGCTGGCC GCCAGTTTCT GTTGCTGCCA AAGTAATGTG GCTCTCTGTG 2100
GCCACCTCTG GCTGCTGAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCCT 2160
CTCTCCCCAG TCTCTAGGGC TGCCCTGACTG GAGGCCTTCC AAGGGGGTTT CAGTCTGGAC 2220
45 TTATACAGG AGGCCAGAAG GGCTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280
ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT 2340
GGGAGCTGAA TAAACTCAGT CACCTGGTTT CCCATCTCTA AGCCCTTAA CCTGCAGCTT 2400
CGTTTAATGT AGCTCTTGCA TGGGAGTTTC TAGGATGAAA CACTCCTCCA TGGGATTTGA 2460
ACATATGAAA GTTATTGTGA GGGGAAGAGT CCTGAGGGGC AACACACAAG AACAGGTCC 2520
50 CCTCAGCCCC ACAGGCACTG GTCTTTTGTG CTNGANTCCA CCCCCCCCT CTTTACCCCT 2580
TT

SEQ ID NO:204 PAB2 Protein sequence:

Protein Accession #: XP_050197

55 1 11 21 31 41 51
| | | | | |
MVQLWVSR LRRKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVVE KFMTMVLGIG 60
60 PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120
ELALLILGVG LLDPCGQVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCLGYLLPA 180
IDWDTALAP YLGTQEELCF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240
CCPCRARLAF RNLGALLPRL HQLCCRMPT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300
65 YQGVPRAEFG TEARRHYDEG VRMGSLLGLFL QCAISLVFSL VMDRLVQRFG TRAVILASVA 360
AFPVAAGATC LSHSAVVTA SAALTGFTFS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420
ASSEDSLMTS FLPGPKFGAP FPNGHVAGG SGLLPPPPAL CGASACDVSV RVVVGEPTEA 480
RVVPGRGICL DLAILDSAF L SQVAPSLFM GSIIVQLSQSV TAYMVSAGL GLVAIYFATQ 540
VVFDSDLAK YSA

SEQ ID NO:205 PAJ3 DNA SEQUENCE

Nucleic Acid Accession #: AK002126
Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
| | | | | |
ATGGTTCCGC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60
TGCTGTGCTA TCTCTGTCTT GTACATGPTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120
80 CTGGCACTGC CCAGGCCCAA CAGCCCCACG GGAAGGAGG GGTACCAGGC CGTCTTCAG 180
GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240

5	AAGGAGGAGC	TGCAGGAGAG	GAGTGAGCAG	CTCAGGAATG	GGCAGTACCA	AGCCAGCGAT	300
	GCTGCTGGCC	TGGGTCTGGA	CAGGAGCCCC	CCAGAGAAAA	CCCAGGCCGA	CCTCCTGGCC	360
	TTCTTGCACT	CGCAGGTGGA	CAAGGCAGAG	GTGAATGCTG	GCGTCAAGCT	GGCCACAGAG	420
	TATGCAGCAG	TGCCCTTTCGA	TAGCTTTACT	CTACAGAAGG	TGTACCAGCT	GGAGACTGGC	480
	CTTACCCGCC	ACCCCGAGGA	GAAGCCTGTG	AGGAAGGACA	AGCGGGATGA	GTGGTGGAA	540
	GCCATTGAAT	CAGCCTTGGA	GACCCTGAAC	AATCCTGCAG	AGAACAGCCC	CAATCACCST	600
	CCTTACACGG	CCTCTGATTT	CATAGAAGGG	ATCTACCGAA	CAGAAAGGGA	CAAAGGGACA	660
	TTGTATGAGC	TCACCTTCAA	AGGGGACCAC	AAACACGAAT	TCAAACGGCT	CATCTTATTT	720
10	CGACCATTCG	GCCCATCAT	GAAAGTAAA	AATGAAAGC	TCAACATGGC	CAACACGCTT	780
	ATCAATGTTA	TCGTGCCTCT	AGCAAAAAGG	GTGGACAAGT	TCCGGCAGTT	CATGCAGAAT	840
	TTCAGGGAGA	TGTGCATTGA	GCAGGATGGG	AGAGTCCATC	TCACTGTTGT	TTACTTTGGG	900
	AAAGAAGAAA	TAAATGAAGT	CAAAGGAATA	CTTGAAACCA	CTTCCAAGC	TGCCAACTTC	960
	AGGAACCTTA	CCTTCATCCA	GCTGAATGGA	GAATTTTCTC	GGGGAAAGGG	ACTTGATGTT	1020
15	GGAGCCCGCT	TCTGGAAGGG	AAGCAACGTC	CTTCTCTTTT	TCTGTGATGT	GGACATCTAC	1080
	TTCACATCTG	AATTCCTCAA	TACGTGTAGG	CTGAATACAC	AGCCAGGGAA	GAAGGTATTT	1140
	TATCCAGTTC	TTTTCAGTCA	GTACAATCCT	GGCATAATAT	ACGGCCACCA	TGATGCAGTC	1200
	CCTCCCTTGG	AACAGCAGCT	GGTCATAAAG	AAGGAAACTG	GATTTTGGAG	AGACTTTGGA	1260
	TTTGGGATGA	CGTGTAGTGA	TCGGTCAGAC	TTTATCAATA	TAGGTGGGTT	TGATCTGGAC	1320
20	ATCAAAGGCT	GGGCGCGAGA	GGATGTGCAC	CTTTATCGCA	AGTATCTCCA	CAGCAACCTC	1380
	ATAGTGGTAC	GGAGCCCTGT	GCGAGGACTC	TTCCACCTCT	GGCATGAGAA	GCGCTGCATG	1440
	GACGAGCTGA	CCCCCGAGCA	GTACAAGATG	TGCATGCAGT	CCAAGGCCAT	GAACGAGGCA	1500
	TCCCACGGCC	AGCTGGGCTT	GCTGGTGTTC	AGGCACGAGA	TAGAGGCTCA	CCTTCGCAAA	1560
	CAGAAACAGA	AGACAAGTAG	CAAAAAACA	<u>TGA</u>			

SEQ ID NO:206 PAJ3 Protein sequence:
Protein Accession #: NP_060841

30	1	11	21	31	41	51	
	MVRRGLLAWI	SRVVLLVLL	CCAISVLYML	ACTPKGDEEQ	LALPRANSPT	GKEGVQAVLQ	60
	EWEEQHRNYV	SSLKRQIAQL	KEELQERSEQ	LRNGQYQASD	AAGLGLDRSP	PEKTQADLLA	120
	FLHSQVDAE	VNAGVKLATE	YAAVPFDSFT	LQKVYQLETS	LTRHPEEKPV	RKDKRDELVE	180
35	ALSALEFLN	NPAENSPNHR	PYTASDFIEG	IYRTERDKGT	LYELTFKGDH	KHEFKRLILF	240
	RPFGBIMKVK	NEKLNMANTL	INVIVPLAKR	VDKFRQFMQN	FREMCIEQDG	RVHLIVVVFG	300
	KEEINEVKGI	LENTSKAANF	RNFTFIQLNG	EFNRGKGLDV	GARFWKGSNV	LLFFCDVDIY	360
	FTSEFLNTR	LNTQPGKKVF	YPLVFSQYNP	GLIYGHDAV	PFLEQQLVIK	KETGFWRDFG	420
	FGMTQCYRSD	FINIGGFDDL	IKGWGGEDVH	LYRKYLHNSL	IVVRTPVRLG	FHLWHEKRCM	480
40	DELTPQYKYM	CMQSKAMNEA	SHGQLGMLVF	RHEIEAHLRK	QKQKTSKKKT		

SEQ ID NO:207 PAJ5 DNA SEQUENCE

Nucleic Acid Accession #: AF189723
Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

45	1	11	21	31	41	51	
	<u>ATGATTCCTG</u>	<u>TATTGACATC</u>	AAAAAAAGCA	AGTGAATTAC	CAGTCAGTGA	AGTTGCAAGC	60
50	ATTCCTCCAAG	CTGATCTPTCA	GAATGGTCTA	AAACAAATGTG	AAGTTAGTCA	TAGGCGAGCC	120
	TTTCATGGCT	GGAATGAGTT	TGATATTAGT	GAAGATGAGC	CACCTGTGAA	GAAGTATATT	180
	TCTCAGTTTA	AAAATCCCTT	TATTATGCTG	CTTCTGGCTT	CTGCAGTCAT	CAGTGTTTTA	240
	ATGCATCAGT	TTGATGATGC	CGTCAGTATC	ACTGTGGCAA	TACTTATCGT	TGTTACAGTT	300
	GCCTTTGTTC	AGGAATATCG	TTCAGAAAAA	TCTCTTGAAG	AATTGAGTAA	ACTTGTGCCA	360
55	CCAGAAATGCC	ATTGTGTGCG	TGAAGGAAAA	TTGGAGCATA	CACCTTGCCG	AGACTTGTTT	420
	CCAGGTGATA	CAGTTTGCTT	TTCTGTTGGG	GATAGAGTTC	CTGCTGACTT	ACGCTTGTTT	480
	GAGGCTGTGG	ATCTTTCCAT	TGATGAGTCC	AGCTTGACAG	GTGAGACAAC	GCCTTGTTCT	540
	AAGGTGACAG	CTCCTCAGCC	AGCTGCAACT	AATGGAGATC	TTGCATCGAG	AAGTAACATT	600
60	GCCTTTATGG	GAACACTGGT	CAGATGTGGC	AAAGCAAGGG	GTGTTGTGAT	TGGAACAGGA	660
	GAAAAATCTG	AATTITGGGA	GGTTTATAA	ATGATGCAAG	CAGAAGAGGC	ACCAAAAACC	720
	CCTCTGCAGA	AGAGCATGGA	CCTCTTAGGA	AAACAACCTT	CCTTTTACTC	CTTTGGTATA	780
	ATAGGAATCA	TCATGTTGGT	TGGCTGGTTA	CTGGGAAAAA	ATATCCTGGA	AATGTTTACT	840
	ATTAGTGTAA	GTTTGGCTGT	AGCAGCAATT	CCTGAAAGTC	TCCCCATTGT	GGTCACAGTG	900
65	ACGCTAGCTC	TTGGTGTAT	GAGAATGGTG	AAGAAAAGGG	CCATTGTGAA	AAAGCTGCCT	960
	ATTGTTGAAA	CTCTGGGCTG	CTGTAATGTG	ATTGTGTCAG	ATAAACTG	AACACTGACG	1020
	AAGAATGAAA	TGACTGTTAC	TCACATAATT	ACTTCAGATG	GTCTGCATGC	TGAGGTACT	1080
	GGAGTTGGCT	ATAATCAATT	TGGGGAAGTG	ATTGTTGATG	GTGATGTTGT	TCATGGATTC	1140
	TATAACCCAG	CTGTTAGCAG	AATTGTTGAG	GCGGGCTGTG	TGTGCAATGA	TGCTGTAAAT	1200
70	AGAACAATA	CTCTAATGGG	GAAGCCAACA	GAAGGGCCCT	TAATTGCTCT	TGCAATGAAG	1260
	ATGGGTCTTG	ATGGACTTCA	ACAAGACTAC	ATCAGAAAAA	CTGAATACCC	TTTTAGCTCT	1320
	GAGCAAAAGT	GGATGGCTGT	TAAGTGTGTA	CACCGAACAC	AGCAGGACAG	ACGAGGATT	1380
	TGTTTATGTA	AAGGTGCTTA	CGAACAAGTA	ATTAAGTACT	GTAATACATA	CCAGAGCAAA	1440
	GGGCAGACCT	TGACACTTAC	TCAGCAGCAG	AGAGATGTGT	ACCAACAAGA	GAAGGCACGC	1500
75	ATGGGCTCAG	CGGGACTCAG	AGTTCCTGCT	TTGGCTTCTG	GTCTGAACT	GGGACAGCTG	1560
	ACATTTCTTG	GCTTGGTGGG	AATCATTTGAT	CCACCTAGAA	CTGGTGTGAA	AGAAGCTGTT	1620
	ACAAACCTCA	TTGCTCAGG	AGTATCAATA	AAAATGATTA	CTGGAGATTC	ACAGGAGACT	1680
	GCAGTTGCBA	TCGGCAGTCG	TCTGGGATTT	TATTTCCAAA	CTTCCCAGTC	AGTCTCAGGA	1740
	GAAGAAATAG	ATGCAATGGA	TGTTTCAGCAG	CTTTTACAAA	TAGTACCAAA	GGTTCAGTA	1800
80	TTTTCACAGAG	CTAGCCCAAG	GCACAAGATG	AAAATATTATA	AGTCGCTACA	GAAGAACGGT	1860
	TCAGTTGTAG	CCATGACAGC	AGATGGAGTA	AATGATGCAG	TTGCTCTGAA	GGCTGCAGAC	1920

5 ATGGAGTTG CGATGGGCCA GACTGGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTTTCA AACCATATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT 2040
 AATAACATTA AAAATTTTCG TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACATTTA 2100
 ATCTCATGG CTACATTAAT GAACCTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
 ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
 GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
 CTTAAAATAC TTGTTTCATC AATAATCAT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
 TTTTGTGACA TGTTCATGCG ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
 10 GGACTCTGCA GTAATAGAAT GTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
 CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
 GATCTGTGTG TTTCTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
 15 CTGAAGTAT GA

SEQ ID NO:208 PAJ5 Protein sequence:

Protein Accession #: AAF27813

20 1 11 21 31 41 51
 MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHERRA FHGMNEFDIS EDEPLWKYVI 60
 SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP 120
 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSIDES SLTGTTTPCS 180
 25 KVTAPQPAAT NGBLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240
 PLQKSMDDLK KQLSFYSGFI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLEIVVTV 300
 TLALGVMRMV KKRAIVKKPL IVETLGCENV ICSDKTGTLT KNEMIVTHIF TSDGLHA EVT 360
 GVGYNQFGEV IVDGDIVHGF YNPVSRIVE AGVCNCDAVI RNNTLMGKPT EGALIALAMK 420
 MGLDGLQDDY IRKAIEYFSS BQKWMVAVCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 30 GQTLTLTQQQ RDVYQGEKAR MGSAGLRVLA LASGPGLQL TFLGLVGIID PPRTGVKEAV 540
 TLLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG BEIDAMDVQQ LSQIVPKVAV 600
 FYRSPRHKM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMGQGTGT DVCKEADMI 660
 LVDDDFQTIM SATIEGKGIY NNINKFVRFO LSTSLAALT LSLATLMNFP NPLNAMQILW 720
 INIMDGPFA QSLGVEPVKD DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
 35 ELRDNVITPR DTMTEITCFV FDFMFNALSS RSQTKSVFEI GLCSNRMEFY AVLGSIMGOL 840
 LVITYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIKI KVEREREKIQ KHVSTSSSF 900
 LEV

SEQ ID NO:209 PAV4 VARIANT 1 DNA SEQUENCE

40 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGA GAGGATTGCC TTATTCATATG 60
 AAGCAAGCTG GGTTTCCTTT GGAATATTT CTTTATTTCT GGGTTTCATA TGTTACAGAC 120
 TTTTCCCTTG TTTTATGTAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTCTG 240
 50 TATCTCTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAAGT 300
 TTTCAAAGAA TCCACGAGGT TGAATCTGAA AACGTGTTTA TTGGTCGCCA CTTCATTTAT 360
 GGACTTTCCA CAGTTACCTT TACTCTGCTT TATCTCTGTT ACCGAAATAT AGCAAGCTTT 420
 GGAAAGGCTC CCTCATCTC TACAGGTTTA ACAACTCTGA TTTCTGGAAT TGAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTCGAAAG 540
 CCAATGCGCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC 600
 55 TTTCTAGTTT ACAGTTCCTC AGAAGAACC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATCTTTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCCAAGG GGACTTATTT GAAATTTACT GCAGAAATGA TGACCTGGTA 780
 ACATTTGGAA GATTTTGTGA TGGTGTCACT GTCAATTTGA CATACCTCAT GGAATGCTTT 840
 60 GTGACAAGAG AGGTAATGCG CAATGTGTTT TTGGTGGGA ATCTTTCTATC GGTTTTCCAC 900
 ATTTGTTGTA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAAT CAATGGTGTG CTCTGTGCAA CTCCCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
 TCTTGTGTCA TGCTTCCCAT TGGTGTGTGT GTGATGGTTT TTGGATTCTG CATGGCTATT 1140
 65 ACAAACTACT AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTC 1200
 TCTCTCAAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

SEQ ID NO:210 PAV4 Variant 1 Protein sequence:

Protein Accession #: none found

70 1 11 21 31 41 51
 MGQRQEPVI PPQRGLPEYSM KQAGFPLGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60
 LVNKTFFGEG YLLLSVLQFL YPFIAMISYN ILAGDTLSKV FORIPGVDP NVEIGHRFII 120
 GLSTVTFPLP LSLYRNIAKL GKVSLLSTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK 180
 PNAIQAVGVM SFAFICHHSN FLVYSSLEEP TVAKWSRLIH MSIVISVPIC IFFATCGVLT 240
 75 FTGFTQGLDF ENYCRNDDLV TFRFCYGVV VILTYPMECF VTREVIANVF FGNLSSVFH 300
 IUVTVMTVIT ATLVSLLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
 80 SCVMLPIGAV VMVFGFVMAI TNTQDCETHGQ EMFYCFDNF SLTNTSESHV QQTQLSTLIN 420

ISIFQLE

5 Nucleic Acid Accession #: N62096
Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

SEQ ID NO:211 PAV4 VARIANT 2 DNA SEQUENCE

```

10 1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCCGC 120
TTTCCAGGAT ATCTGCTCCT CTCTGTTCTT CAGTTTITGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TCAAAGAAT CCCAGGAGTT 240
15 GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT 300
ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
ACAGGTTTAA CAACTCTGAT TCTTGGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTGCAAAAGC CCAATGCCAT TCAAGCGGTC 480
GGGTATATGT CTTTTCGATT TATTGCCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
20 GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCATCGT GATTTCGTGA 600
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660
GACTTATTTG AAAATTAAGT CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTATT 720
GGTGTCACTG TCATTTTGAC ATACCCATAT GAATGCTTTG TGACAAGAGA GGTAAATTGCC 780
25 AATGTGTTTT TTGTTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840
ATCACTGTAG CCACGCTTGT GTCAATGCTG ATTGATGGCC TCGGGATAGT TCTAGAACTC 900
AATGGTGTGC TCTGTGCAAC TCCCTTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC ACACCTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
30 GGTGCTGTGG TGGATTCGTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCAGAAA TACCTCAGAG 1140
TCTCATGTTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
TAA

```

SEQ ID NO:212 PAV4 Variant 2 Protein sequence:

35 Protein Accession #: none found

```

40 1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60
SYNIIAGDTL SKVFQRIQGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120
TGLTTLILGI VMARAILSLG HIPKTEDAW FAKPNAIQAV GVMSEAFICH HNSFLVYSSL 180
EEPFAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTGGRFCY 240
GVPVILTYPM ECFVTREVIA NVFFGNLSS VFHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
45 NGVLCATPLI PIIPSACYLK LSEERTHSD KIMSCVMLEI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLNTISE SHVQQTITQLS TLNISIFQLE

```

SEQ ID NO:213 PAV4 VARIANT 3 DNA SEQUENCE

50 Nucleic Acid Accession #: N62096
Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

```

55 1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATAC CTTTATAGC AATGATAAGT 120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTFC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTTCACACAG TACCTTTACT 240
CTGCCCTTAT CCTTGTACCG AAATATAGCA AAGCTTGGAA AGGTCCTCCCT CATCTCTACA 300
60 GGTTTAACAA CTCGTATCTT TGGAAATTGA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATCA AGCGGTCCGG 420
GTTATGTCCT TTGCATTAT TFGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTAC CCAAGGGGAC 600
65 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTATGGT 660
GTCACTGTCA TTTTGACATA CCTATGGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTT GTGGGAATCT TTCAATCGGT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAAGTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTTCCAT CAGCCTGTGA TCTGAAACTG 900
70 TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCCT GTGTCATGCT TCCCATTTGT 960
GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTCTTACTG CTTTCTCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTTCAGC AGACAACACA ACTTCTTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA

```

SEQ ID NO:214 PAV4 Variant 3 Protein sequence:

80 Protein Accession #: none found

```

80 1      11      21      31      41      51
|      |      |      |      |      |

```

MGVRQREFVI PPQVNTKFGF PGYLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIFGVD 60
 PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLGKVSLLST GLTTLILGIV MARAISLGPB 120
 IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
 ICIFPATCGY LTFITGFTQGD LFENYCRNDD LVTFRGRFCYG VTVILTYPME CFVIREVIAN 240
 VFFGNLSSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCAITPLIF IIPSAICYLKL 300
 SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360
 HVQQTQLST LNISIFQLE

10

SEQ ID NO:215 PAV4 VARIANT 4 DNA SEQUENCE:

Nucleic Acid Accession #: N62096
 Coding sequence: 1-1398 (underlined sequences correspond to start and stop codons)

15

1 11 21 31 41 51
 | | | | |
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGA GAGATTAGTA TGACAGAGAA 60
 ACCCTTGTTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAGCAAGCT 180
 GGGTTTCCTT TGGGAATATT GCPTTTATTC TGGGTTTCAT ATGTTACAGA CTTTTCCTT 240
 GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
 AAAACTPTCG GCTTTCAGG GTATCTGCTC CTCTCTGTC TFCAGTTTTC GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA 420
 ATCCCAGGAG TTGATCCTGA AAACGCTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTC 480
 ACAGTTACCT TPACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC 540
 TCCCTCATCT CPACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600
 TCACCTGGTC CACACATACC AAAACAGAA GACGCTTGGG TATTTCGAAA GCCCAATGCC 660
 ATTCAAGCGG TCGGGGTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTCTTAGTT 720
 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTCTG TATTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
 TTCACCCAAG GGGACTTATT TGAATAATTAC TGCAGAAATG ATGACCTGGT AACATTGGA 900
 AGATTTCGTT ATGGGTCTAC TGTCATTTTG ACATACCCTA TGGAAATGCTT TGTGACAAGA 960
 GAGGTAATG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCTA CATTGTTGTA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCATTGC TGATTGATTG CCTCGGGATA 1080
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTATCAT TCATCAGCC 1140
 TGTATCTGA ARCTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
 ATGCTTCCCA TTGGTGTGCT GGTGATGGTT TTTGGATTCT TCATGGCTAT TACAAATACT 1260
 CAAGACTGCA CCCATGGGCA GGAATGTTC TACTGCTTTC CTGACAATT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAA TATTAGTATC 1380
 TTTCAATGA

45

SEQ ID NO:216 PAV4 Variant 4 Protein sequence:

Protein Accession #: none found

50

1 11 21 31 41 51
 | | | | |
 MGVRQREFVI PPQRLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60
 GFPLGILLFF WVSIVTDFSL VLLIKGGALS GTDTYQSLVN KTFGFFGYLL LSVLQFLYFP 120
 IAMISYNIIA GDTLSKVFPQ IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIAKLGKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKENA IQAVGVMSFA FICHNSFLV 240
 YSSLLEPTVA KWSRLIHMSI VISVFICIFF ATCGYLITFG FTQGDLFENY CRNDDLVTFG 300
 RFCYGVTVIL TYPMCEVFTR EVIANVFFGG NLSSVFHIV TVMVITVATL VSLIDCLGI 360
 VLELNGVLCA TPLIFLIPSA CYLKLSEEP THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
 QDCTHGQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

60

SEQ ID NO:217 PAV9 DNA SEQUENCE

Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

65

1 11 21 31 41 51
 | | | | |
 ATGGAGGATG CTTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCAG 60
 GAGAAGCCCA CCGATGCCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120
 AATTTCCTCC GGCCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTACACAGC 180
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
 GTCTTCCAGA CTTGGCTGCA GGACCTGCTG CGTCTGTGGG TGGTGGGGGC TGCCACAGAGC 300
 ACAGGAGCCT GGATTGTCTAC TGGGGGTCTG CACACGGGCA TCGGCCGCGA TGTGTGTGTG 360
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACCA AGGTGGTGGC CATGGGTGTG 420
 GCGCCCTGGG GTGTGTCTCG GAATAGAGAC ACCCTCATCA ACCCAAGGG CTGTTCCCTT 480
 GCGAGGTACC GTTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAA 540
 TACTCGGCTT TCTTCTGTGT GGACGACGGC ACACACGGCT GCCTGGGGGG CGAGAACCCT 600
 TTCCGCTTGC CCCTGGAGTC CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGGACTGGA 660
 ATTGACATCC CTGTCTCTGT CCTCTGATT GATGGTGATG AGAAGATGTT GACGCGAATA 720
 GAGAAGCCCA CCCAGGCTCA GCTCCCATGT CTCTCTGTGG CTGGCTCAGG GGGAGCTGCG 780
 GACTGCCTGG CGGAGACCTT GGAAGACACT CTGGCCCCAG GGAGTGGGGG AGCCAGGCCA 840
 GCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCCAAAG GGGACCTTGA GGTCTGCAG 900
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTCTG CAGTCTATTC TTCTGAGGAT 960

80

5
10
15
20
25
30
35
40
45

GGGTCTGAGG AATTCGAGAC CATAGTTTTC AAGGCCCTTG TGAAGGCCTG TGGGAGCTCG 1020
GAGGCCCTCAG CTTACCTTGGG TGAGCTGCCG TTTGGCTGTGG CTTTGAACCG CGTGGACATT 1080
GCCCAGAGTG AACTCTTTTCG GGGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140
CTCATGGACG CCTTGTCTGAA TGACCGGCCCT GAGTTTGGTG GCTTGTCTCAT TTCCACGGGC 1200
CTCAGCCTGG GCCACTTCCCT GACCCCGATG CGCCTGGGCC AACTCTACAG CGCGGCGCC 1260
TCCAACTCCG TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAAGCC 1320
CCAGCCCTAA AAGGGGGAGC TCGCGAGCTC CGGCCCTCTG ACGTGGGGCA TGTGCTGAGG 1380
ATGCTGTGGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGGCGCCTG GGACCCCTAC 1440
CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCCCTC 1500
TCGCTGGATG CTGGCCCTCG GCAGGCCCTC TGGAGCGACC TGTCTCTTTG GGCAGCTGTT 1560
CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTCA 1620
GCTCTTGGGG CCTGTTTGCT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGCTGAGGAG 1680
GCAGCACGGA GGAAGACCT GGCCTTCAAG TTTGAGGGGA TGGGCGTTGA CCTCTTTGGC 1740
GAGTGTATC GCAGCAGTGA GGTGAGGGCT GCCCGCTTCC TCTTCCGTG CTGCCCGCTC 1800
TGGGGGGATG CCACCTTGCT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTCTTGCC 1860
CAGGATGGG GCTGCTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920
CCCATCTGGG CCTTGGTCTT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCCTCATC 1980
ACCTTCAGGA AATCAGAAGA GGAGCCACA CGGAGGAGC TAGAGTTTGA CATGGATAGT 2040
GTCATTAAAT GGAAGAGGCC TGTCCGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100
GTCCCGCGCC AGTGGGGCGG TCCGGGTTCG TCGGGGGGCC GCTCGGGGGG GCGCCGCTGC 2160
CTACGCCGCT GTTCTCACTT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGGTC 2220
AGCTACCTGC TGTTCCTGCT GCTTTCTCTG CGGGTGTCTG TCGTGGATTT CCAGCCGGCG 2280
CCGCCCGGCT CCTTGGAGCT GCTGCTCTAT TTTCTGGGCT TCACGCTGCT GTGCGAGGAA 2340
CTGCGCCAGG GCTCTGAGCG AGCGGGGGGC AGCCTCGCCA GCGGGGGGCC CGGCCCTGGC 2400
CATGCCCTAC TGAGCCAGCG CCTGCGCTC TACCTCGCGC ACAGCTGGAA CCAGTGGCAG 2460
CTAGTGGCTC TCACCTGCTT CCTCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTTGTAC 2520
CACCTGGGCC GCACGTCTCT CTGCATCGAC TTCATGGTTT TCACGGTGGC GCTGCTTAC 2580
ATCTTCACGG TCAACAACA GCTGGGGCCC AAGATCGTCA TCGTGGAGAA GATGATGAAG 2640
GACGTGTCTT TCTTCTCTCT CTTCCTCGGC GTGTGGCTGG TAGCCTATGG CGTGCCACG 2700
GAGGGGCTCC TGAGGCCAGG GACAGTGAC TTCCCAAGTA TCTTGGCCCG CGTCTCTAC 2760
CGTCCCTACC TGCAGATCTT CGGCGAGATT CCCAGGAGG ACATGGACGT GGCCTCATG 2820
GAGCACAGCA ACTGCTCGCT GGAGCCCGGC TTTCTGGCAC ACCCTCTGG GGGCCAGGCG 2880
GGCACCTGCG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTCT CATCTTCTG 2940
CTCGTGCCA ACATCTCTCT GGTCAACTTG CTCATTGCA TGTTCAGTTA CACATCTGGC 3000
AAGTACAGG GCAACAGCGA TCTTACTGG AAGCGCGAG GTTACCGCCT CATCCGGGAA 3060
TTCCACTCTC GGCCCGGCGT GGGCCCGCCC TTTATCGTCA TCTCCCACTT GCGCCTCTG 3120
CTCAGGCAAT TGTGACGGG ACCCGGAGC CCCCAAGCGT CCTCCCGGCG CCGGAGCAT 3180
TTCCGGGTTT ACCTTCTTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGATC 3240
AAGGAGAACT TCTTCTCTGG ACCTGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG 3300
AAGCGCACGT CCCAGAAGGT GGACTTGGCA CTGAAACAGC TGGGACACAT CCGCGAGTAC 3360
GAACAGCGCC TGAAGTGTCT GGAGCGGGAG GTCCAGCAGT GTAGCCGCGT CCGGGGTGG 3420
GTGGCGGAGG CCTTGAAGCG CTCTGCCCTTG CTGCCCCCAG GTGGGCGGCC ACCCCCTGAC 3480
CTGCTGGGT CCAAGACTG A

50
55
60
65
70

1 11 21 31 41 51
MEDAFGAADV TVWDSADHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAENLV VSVLGGSGGP VLQTLWQDLL RRLVRAAQS TGAWIVTGGL HTGIGRHVGV 120
AVRDHQMAST GGTQVVMGV APWGVVRNRD TLINPKGSFP ARYRWGDPE DGVQFPLDYN 180
YSAFFLVDDG THGCLGGENR FRLRLSEYIS QQTGTVGGTG IDIFVLLLI DGDEKMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLAELETDT LAPGSGGARQ GEARDRIIRF FPKGDLEVLQ 300
AQVERIMTRK ELLTVYSSSD GSEEFETIVL KALVKACGSS EASAYLDELRL LAVAWNVRDI 360
AQSEIFRQDI QWRSFHLEAS LMDALLNDRP EFVRLLSHSG LSLGHFLTPM RLAQLYSAAP 420
SNSLIRNLDD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQGFESMY LLSDKATSPL SLDAQLGQAP WSDLLWALL LNRAQMYAF WEMGSNAVSS 540
ALGACLLLRV MARLEPDAEE AARRKDLAFK FEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600
WGDATECLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASST PIWALVLAFF CPPLIYTRLI 660
TFRKSEEEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGGRR 720
LRRWFHFWGA PVTTFMGNNV SYLLFLLLS RVLLVDFQPA PPGSLELLLY FWAFTLLCEE 780
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRVLCID FMVFTVRLH IFTVKNQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT 900
EGLLRPRDS FFSILRRVFP RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPGGAQA 960
GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQNSDLWY KAQRYLIRE 1020
FHSRPLALPP FIVISHRLRL LRQLCRRPRS PQSSPALEH FRVYLSKEAE RKLLTWESVH 1080
KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLRE VQCSRVLGW 1140
VAEALSRSAL LPPGPPPPPD LPGSKD

75
80

SEQ ID NO:219 PBF1 DNA SEQUENCE
Nucleic Acid Accession #: AA054237
Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCTTGGGG 60
CTGCTCTGTA CGGCATCTTT CACCGACCAC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
GAGAGCTGCG AGCCAGACCG CGCGGCGGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG 180

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80

CCGCTGTGCG ACCTGCCTGCT GCGGGACTCG CCCCCGCTGG GCGGCCGGCT GCTCCCGGGC 240
GGCCCCGGGG GCGCCGACCC CGAGTCCCTGG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC 300
GCCGAGTGGC GCCGGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCATCG ACCGGGACAT CGACACCCCTC ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGTTTGCAGG ACATTCTTTT TAATTTAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTTATTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
TGACCATTTT CCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCTGTGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

SEQ ID NO:220 PBF1 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCBRSRAGA DPPDQKNRLM 60
PLSHLPLRDS PPLGRRLLPF GPGRADPESW RSLGLGLD AECGRPLFAT YSGLWRKCYF 120
LGIDRDIIDL ILKGIARQCT AIKYHFSQPI RLKNIPFNLT KTIQQDEWHL LHLRRITAGF 180
LGMMAVAVLLC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
KLITYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

SEQ ID NO:221 PCI4 DNA SEQUENCE

Nucleic Acid Accession #: NM_018570

Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCCCTTCCG 60
AAGGTTCCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTACAACTA TGGCTTTTATT AACCAATATG GAATCTCTAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
ACTGTTGCCA TGAAGTGTC AATATGTTGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420
CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
GATGATTCAT CACAGCTCTC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATATAA 540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCTAGAAAT AGATCATTTG 660
TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAAGTGA AAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCAATATTTT ATACAGTTG TGCCAACAAA ACTACATACA 780
TATAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAC 840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTCTCTCT 900
ATGGTGACAG TTAATGAGGA GCACATGCCA TTCTGGCAGT TTTTGTGAAG ACTCTGTGGT 960
ATTGTTGGAG GAATCTTTTC AACAAACAGGC ATGTTACATG GAATTGGAAG ATTTATAGTT 1020
GAATATATTT GCTCTCTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCTTTT 1080
GAGGATGGCC ACACAGACAA CCATTTACCT CTTTATAGAA ATAATACACA TGA

SEQ ID NO:222 PCI4 Protein sequence:

Protein Accession #: NP_057654

1 11 21 31 41 51
MRRLLNRKKTLL SVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
KYEYVDKDF SSKLRINIDI TVAMKCQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
KEWQRLQLI QSRLEEBHSL QDVIFKSAFK STSTALPPRE DDSSQSFNAC RIHGHLYVNK 180
VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGELVPAII NPLDGTEKIA 240
IDHNQMFQYF ITTVFTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRIG SYKPVNSVFP 360
EDGHTDNHLP LLENNTH

SEQ ID NO:223 PEZ3 DNA SEQUENCE

Nucleic Acid Accession #: NM_001935.1

Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGCGCGTCTC CGCCGCCCGC GTGACTTCTG CTTGCGCTCC TTCTCTGAAC GCTCACTTCC 60
GAGGAGACGC CGACGATGAA GACACCGTGG AAGATCTCTT TGGGACTGCT GGGTCTGCT 120
CGCTTGTCA CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180
ACAGCTGACA GTCCGCAAACT TACACTCTA ACTGATTACT TAAAAATATC TTATAGACTG 240
AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAT 300

5
10
15
20
25
30
35
40
45
50

ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360
GATGAGTTTG GACATCTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTTCTC 420
TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT 480
GATTTAAATA AARGGACGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540
ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAATGACAT TTAGTTTAAA 600
ATTGAACCAA ATTTACCAAG TTACAGAAATC ACATGGACGG GGAAGAAGA TATAATATAT 660
AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCTTACTC TGCTCTGTGG 720
TGGTCTCCAA ACGGCACTTT TTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780
ATTGAARTACT CCTTCTACTC TGATGAGTCA CTGCACTACC CAAAGACTGT ACGGGTCCA 840
TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAA TACAGACTCT 900
CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCCTGCTTC TATGTTGATA 960
GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAGAATTTTC TTTGCAGTGG 1020
CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGA 1080
AGATGGAACCT GCTTAGTTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140
AGATTTAGCG CTTCAGAAAC TCATTTTACC CTGTATGTTA ATAGCTTCTA CAAGATCATC 1200
AGCAATGAAG AAGGTTACAG ACACATTTGC TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACAG TGATTATCTA 1320
TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380
CTTATTGACT ATACAAAGT GACATGCCCTC AGTTGTGAGC TGAATCCGGA AAGGTGTGAG 1440
TACTATTCTG TGCTGATCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
GGTCTGCCCC TCTATACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCCCTGGA 1560
GACAATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAACTGGAC 1620
TTCAATTTAT TGAATGAAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCATTTTGAT 1680
AAATCCAAGA AATATCCTCT ACTATTAGAT GTGTATGTCAG GCCATGTAG TCAGAAAGCA 1740
GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAA CATTTATAGTA 1800
GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
AGAAGACTGG GAACATTTGA AGTTGAAGAT CAAATTTGAAG CAGCCAGACA ATTTTCAAAA 1920
ATGGGATTTG TGGACAACAA ACGAATTGCA ATTTGGGGCT GGTCTATAGG AGGGTACGTA 1980
ACCTCAATGG TCCTGGGATC GGGAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCCT 2040
GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCACT 2100
CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATTTT 2160
AAACAAGTTG AGTACCTTCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGAGATGG ATTTCCAGGC AATGTGGTAT 2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCACATG 2340
AGCCACTTCA TAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
AAGCTTTATTA AACTCATTTT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
TGATCTTTAA AATACACACT CAAATCAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCAACAAC GATTATTACC TTACAGAAAT 2580
TTGAATTATC CGGTCCGGTT TTATGTTTAA AATCATTTTC TGCATCAGCT GCTGAACAA 2640
CAAATAGGAA TTGTTTTCAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
TTTCTAATCG GACTGTTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCTCGG 2880
AGAAGAGCTG TTCACCACGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940
CAGGAAATCA AATATCGAAA GCACTGACTT CTAAGTAATC CACAGCAGTT GAAAGACTCC 3000
AAGAAATGT AAGGGAATCT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060
TGCTACAAA ACACAGCAAG GGTGATGGGA AAGCATTTGA AATGTGCTTT TAAAAA 3120
TACTGATGTT CCTAGTGAAA GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
CTGTAAAGAG ATGAAATAT TTGATATACA AATCTTAACT TGAAGGAGTC CTTGCATCAA 3240
TTTTTCTTAT TTCAATTTCT TGAGTGTCTT AATTAAGA ATATTTTAACT TTCTTGGAC 3300
TCATTTTAAA AATGGAACA TAAATACAA TGTATGTAT TATTATCCC ATTCTACATA 3360
CTATGGAAT TCTCCAGCTC ATTTAATAAA TGTGCTTCA TTTTTC

55
60
65
70

SEQ ID NO:224 PEZ3 Protein sequence:
Protein Accession #: NP_001926.1

1 11 21 31 41 51
MKTFWKILG LLGAAALVTI ITVFVVLNK GTDDATADSR KTYLLTDYLK NTYRLKLYSL 60
RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFGH SINDYSISPD GQPILLEYN 120
VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQVWTWSPV GHKLAYVWNN DIYVKIEPNL 180
PSYRIWTGK EDIYINGITD WYEEVFSY YSALWNSPNG TFLAYAQFND TEVELIEYSF 240
YSDESLOYPK TVRVVPYKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
CDVTWATQER ISLQWLRLRI NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360
EPHFTLDGNS FYKLIISNEB YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
EYKGMPPGGRN LYKLIQLIDYT KVTCLSCSELN PERCQYYSVS FSKEAKYYQL RCGPGLPLY 480
TLHSSVNDKG LRVLEDNSAL DKMLQNVOMP SKKLDIFILN BTKFWYQMLL PPHFDKSKKY 540
PLLLDVYAGP CSQKADTVFR LNWTYLAST ENLIVASFDG RSGVYQGDKI MHAINRRLGT 600
FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGYVTSMVL GSGGVFKCG IAVAPVSRWE 660
YDVSVTERY MGLTTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADBN VHFQQAQIS 720
KALVDVGVDV QAWYTTDEDH GIASSTAHQH IYTHMSHFIF QCFSLP

75
80

SEQ ID NO:225 PBJ2 DNA SEQUENCE

Nucleic Acid Accession #: none found
Coding sequence: 1-261 (undefined sequences correspond to start and stop codons)

1 11 21 31 41 51

5
10
15
20
25
30

ATGGCTCTGG	CGAAGGTGAG	GGAGCCAAAC	GCRAATGACA	ATGCCATCAG	AGTTGACAAC	60
AGAAGTGTGA	TTAAAGTGGG	TGCTAACCAG	TGTTCCCTGC	ATGAGGCAGA	AAGTGAATCC	120
AGAAACCCCTC	AGGAGCTCTG	GATGGGCGCTG	CTCCTCTTGA	TGGGGGTCTC	AGAAGCATGT	180
GTGGAAATGA	GGCCTCTGTC	AGTCTGGTCC	CTGAGAGATG	ACAAGGAGCA	GAGCCCCCAC	240
CAGCCACAC	TGGATGTCTA	A				

SEQ ID NO:226 PBJ2 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51

MALAKVREPN	ANDNAIRVDN	RSVIKVRANQ	CSLHEAESES	RNPQELWMGL	LLLMGVLEAC	60
VEMRPLSVWS	LRDDKEQSPH	QPTLDV				

SEQ ID NO:227 PBM2 DNA SEQUENCE

Nucleic Acid Accession #: none found

Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

<u>ATGCCAAATG</u>	CTGAGTTAGA	AGCAAGAGAGC	CTTGGGAAGCA	GTAATGTTTT	AAAACTGCT	60
CTCATACTTG	CTGTATGTTG	TGGATCAGCA	AATATAGTCA	GCCCTCTACT	TGAGCAAAAT	120
ATTGATGTAT	CTTCTCAAGA	TCTGGACAGA	CGGCCAGAGA	GTATGCTGTT	TCTAGTCATC	180
ATCATGTGGA	CCAGTTTGTG	GGAAGACAAAT	CTTTCCATGG	GCTGGGGGAA	GCTAGAAGAT	240
TTTATGGCTA	TTGAAGAAGA	AATGAAGAAG	CACGGAAGTA	CTCATGTGGG	ATTCCCAGAA	300
AACTGACTA	ATGGTGGCG	TGCTGGCAAT	GGTGTATGAT	GATTAATTC	TCCAAGGAAG	360
AGCAGAACAC	CTGAAAGCCA	GCAATTTCCT	GACACTGAGA	ATGAAGAGTA	TCACAGGTTT	420
GTCAAGATC	AGATAGTTGT	AGATATGCGG	CGTTATTTCT	<u>GA</u>		

SEQ ID NO:228 PBM2 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51

MPNAELEAKS	LGSSKCLKTA	LILAVCCGSA	NIVSFLLEQN	IDVSSQDLDR	RPESMLFLVI	60
IMWTSFVEDN	LSMGWGLKED	FMAIEEEMKK	HGSTHVGFPE	NLTNGAAGN	GDDGLIPFRK	120
SRIPESQQFP	DTENEYHRF	VKDQIVVDMR	RYF			

SEQ ID NO:229 PEZ2 DNA SEQUENCE

Nucleic Acid Accession #: NM_014253

Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

GACTGCTTGC	ATTAAAGGAC	TTCTCTCATCC	TTTTTTTCAT	GAAACTGAGC	TTGCTTAATC	60
AGAGATGGAG	CAAACTGACT	GCAAACCCCTA	CCAGCCCTCTA	CCAAAAGTCA	AGCATGAAAT	120
GGATCTAGCT	TACACCAGTT	CTTCTGATGA	GAGTGAAGAT	GGAAGAAAAC	CAAGACAGTC	180
ATACAACCTC	AGGGAGACCC	TGCACGAGTA	TAACCAAGGAG	CTGAGGATGA	ATTACAATAG	240
CCAGAGTAGT	AAGAGGAAG	AAGTAGAAAA	ATCTACTCAA	GAGATGGAAT	TCTGTGAAAC	300
CTCTCACACT	CTGTGCTCTG	GCTACCAAAC	AGACATGCAC	AGCGTTTCTC	GGCATGGCTA	360
CCAGCTAGAG	ATGGGATCTG	ATGTGGACAC	AGAGACAGAA	GGTGTGCTCT	CACCTGACCA	420
TGCACTAAGA	ATGTCGATAA	GGGGAATGAA	ATCAGAGCAT	AGTTCTCTGT	TGTCCAGCCG	480
GGCCAACTCT	GCATATCTCT	TGACTGACAC	TGACCATGAA	AGGAAGTCTG	ATGGGGAAAA	540
TGGTTTCAAA	TTCTCTCCTG	TTTGTGTGTA	CATGGAGGCT	CAAGCTGGGT	CTACTCAAGA	600
TGTGCAGAGC	AGCCCAACAC	ACCAGTTTAC	CTTCAGACCC	CTCCCACCGC	CACCTCCGCC	660
TCCTCATGCC	TGCACCTGTG	CCAGGAAGCC	ACCCCTTGCA	GCGGACTCTC	TTTCAAGGAG	720
ATCAATGACT	ACCCGACGCC	AGCCAGGCC	AGCTGCTCCA	GCTCCCCCAA	CCAGCACGCA	780
GGATTCAGTC	CATCTGCATA	ACAGCTGGGT	CCTGAACAGC	AACATACCAT	TGGAGACCAG	840
GCATTCCTTG	TTCAACATAG	GATCTGGTTC	CTCTGCGATC	TTCAGTGCAG	CCAGTCAGAA	900
CTACCTCTCT	ACATCCAATA	CCGTGTACTC	GCCCCCTCCC	AGGCCTCTTC	CTCGAAGCAC	960
CTTTTCCCGA	CCTGCCCTTA	CCTTTAACAA	ACCTTACAGG	TGCTGCAACT	GGAAGTGCAC	1020
AGCATTGAGC	GCCACTGCAA	TCACAGTGAC	TTTGGCCCTG	TTACTAGCCT	ATGTGATTGC	1080
AGTGCAATTG	TTCCGCCCTG	CTTGGCAGTT	GCAACCAAGT	GAAGGAGAGC	TGTATGCAAA	1140
TGGAGTTAGC	AAAGGGAACA	GGGGGACCGA	GTCCATGGAC	ACTACTTACT	CTCCAATTGG	1200
AGGAAAAGTT	TCTGATAAAT	CAGAGAAAAA	AGTGTTCAG	AAGGGACGGG	CGATAGACAC	1260
TGGAGAAGTT	GACATTTGGT	CACAGGTCAT	GCAGACCATT	CCACCTGGTT	TATTTCTGGCG	1320
TTTCCAGATT	ACTATCCACC	ATCCAATATA	TCTGAAGTTC	AATATTTCTT	TAGCCAAGGA	1380
CTCTCTGCTG	GGAAATTATG	GCAGAAGAAA	CATTCCACCT	ACACATACTC	AGTTTGTATTT	1440
TGTAAACTA	ATGGATGGCA	AACAGCTGGT	CAAGCAGGAC	TCCAAGGGCT	CTGATGATAC	1500
ACAGCACTCC	CCTCGGAACC	TGATCTTAAC	TTCCGCTTCAG	GAGACAGGTT	TCATAGAGTA	1560
TATGGATCAA	GGACCTTGGT	ATCTGGCGTT	TTACAATGAT	GGAAAAAAGA	TGGAGCAAGT	1620
ATTCGTGTTA	ATCAGACCAA	TTGAAATAAT	GGATGACTGT	TCAACCAATT	GCAATGGAAA	1680
TGGAGAGTGT	ATCTCTGGCC	ATTTGTCATTG	TTTCCCAGGA	TTCTCTGGAC	CTGACTGTGC	1740
TAGAGATTCC	TGCCCTGTGC	TGTGTGGTGG	GAATGGAGAA	TACGAGAAAG	GACACTGTGT	1800
CTGCCGCAT	GGCTGGGAAG	GGCCAGAGTG	TGACGTTCCG	GAAGAACAAAT	GCATTGATCC	1860
AACATGCTTT	GGCCACGGCA	CCTGCATCAT	GGGAGTCTGC	ATCTGTGTGC	CAGGATACAA	1920

	AGGAGAAATA	TGCGAGGAAG	AGGACTGCCT	AGACCCAAATG	TGTTCCAACC	ATGGCATCTG	1980
	TGTAATAAGGA	GAATGTCACT	GTTCCTACTGG	CTGGGGAGGA	GTTAACTGTG	AAACACCACT	2040
	TCCTGTATGT	CAAGAGCAGT	GCTCAGGACA	CGGAACCTTT	CTTCTGGAGC	CTGGAGTATG	2100
5	CAGCTGTGAT	CCCAAGTGGA	CAGGATCTGA	CTGCTCAACA	GAGCTGTGTA	CCATGGAGTG	2160
	TGGTAGCCAT	GGAGTCTGCT	CAAGAGGAAT	TTGCCAGTGT	GAAGAAGGCT	GGGTAGGACC	2220
	AACATGTGAG	GAACGCTCCT	GTCACTCTCA	TTGTACTGAG	CATGGCCAA	GCAAGATGG	2280
	AAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
10	AAATGGTTGG	CACGTGTGTT	GTCAAGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTCTAT	2460
	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GTTTAAACCG	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCTC	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTTCAG	AAAGCCRAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAAATTC	TCATTGGCAA	GGACAGTACT	CATGTCTATC	CTCCTGAGGT	2700
15	GTCAATTGAC	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
	TCCTCTGAGT	GGATGTGAAT	TCAGTTTCTT	GCACCACAGT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAAAGCTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCCTGC	CTGAGAAGAG	AACACTCTGG	TTGCCTTGGA	ATCAGTTTAT	2940
	TGTGGTAGAG	AAAGTCAACA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCCT	CGCATATCTC	3000
20	CAACTTTATC	AGCCCAAAAC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
	CTGTCCAGAG	AGGGGAACATA	TTGTTCTGTA	GCTGCAGGTT	GTACAGGAGG	AAATTCCCAT	3120
	TCCCTCCAGC	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAACCTT	3180
	GCTACGGATG	CTTCTGACAC	ATTCACAGAT	TCCCGTAGGC	ATGATAAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTGTCTTA	3300
25	CACATTGTCT	TGGAACAAGA	CGGATATCTA	TGGACAGAA	GTTTGGGGCC	TGGCAGAGGC	3360
	TTTGGTATCT	GTGGGATATG	AAATGAAAC	GTGCCCTGAC	TTTATCTCTT	GGGAGCAAG	3420
	GACAGTCGTT	TTACAAGGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACCATTAATG	GGTAATGGAC	ACCAAAGGAG	3600
30	TGTAGCCTGC	ACCAACTGCA	ATGGCCAGC	CCACAACAAC	AAACTCTTTG	CTCCTGTCCG	3660
	CTTAGCTTCT	GGCCCTGATG	GCAGTGTGTA	TGTTGGCGAC	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCCTCG	GGAAACTCCG	TTAGTATTTT	GGAATTAAGC	ACAAGTCCGT	CTCACAAATA	3780
	CTATCTGGCT	ATGGACCTGT	TGCTGTAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAAG	TTGAAATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAATGGT	3900
35	GGCAGGAAT	GGTGATCAGT	GCCTTCCCTT	TGACCAGAGT	CATTTGTGGAG	ATGGTGGGAG	3960
	AGCATCCGGA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTGTATAGGC	ATGGATTTAT	4020
	TTACTTTTGG	GAAAGGACTA	TGATTTCGAA	AATTGATGAG	AATGCTGTGA	TCACAACCTG	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCACCTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTCAGTG	CGATTAGAGT	GGCCAACAGA	CCTTGCAGTA	AATCCTATGG	ACAATTCATT	4200
40	GTATGCTTTG	GATAACAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTGGGATCAT	4260
	CGCAGGACGC	CCCATTCACT	GCCAGGTGCC	AGGCATCGAT	CATTTCCCTGG	TCAGCAAGGT	4320
	AGCAATTTAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTCCCAAC	CGGGCTGTCT	4380
	CTTCATAGCT	GAAACAGACG	AGAGGAAAGT	AAACCGCATT	CAGCAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATCGCTG	GTGCCCCCAC	TGACTGTGAC	TGCAAAATG	ATCCAAACTG	4500
45	TGACTGTTTT	TCAGGTGATG	GTGGCTATGC	CAAGATGCA	AAGATGAAAG	CCCTTCCCTC	4560
	CTTAGCAGTG	TCGCCTGATG	GAACCTCTTA	TGTGGCAGAC	CTCGGAAATG	TTGGAATTCG	4620
	TACCATCAGC	AGGAACCAAG	CCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACTGTACC	AGTTCACCTG	AAATGGAACC	CACCTACACA	CCCTGAACTT	4740
	GATTAACAAG	GACTATGTTT	ATAACTTCAC	CTACAATTTCT	GAAGGTGACT	TGGCGCGCAT	4800
50	TACCAGCAGC	AATGGCAATT	CAGTGCACAT	TCGCGGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
	GCTTGTGGTG	CCTGGCGGAC	AAGTATACCT	GCTGACTATA	AGCAGCAATG	GAGTCTTGAA	4920
	AAGAGTGTCA	GGCCAGGCTT	ATAATCCGCG	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCGTGCTACC	AAAAGTAACT	AAAATGGATG	GACAAACGTT	TATGAGTATG	ACCCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTCAGC	AGCTTCCACA	GTGACCTGGA	5100
55	GAAGCTGACA	AAAGTGTAGC	TAGATACTTC	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
	CTTGACGGCA	ACTAGTACCA	TATATATTTT	AAAACAAGAA	AATACTCAAA	GTACCTPATCG	5220
	GGTGAATCCA	GATGGTTCCC	TGCGTGTAC	TTTGGCCAGC	GGGATGGAGA	TCGGCCTCAG	5280
	CTCAGAGCCC	CACATCTCTG	CAGGGGCGAGT	CAACCTTACC	CTGGGCAAA	GCAACATCTC	5340
	ATTGCCCGGA	GAGCACAATG	CAACCTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
60	AGGCAATGTT	TCGGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
	AGATTTTGTAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCACCTT	5520
	TCGAATTTCT	TATGACCAGA	CTGGGCGACC	CATTCTGTGG	TCTCTGTAA	GCAGATATAA	5580
	TGAAGTGAAC	ATCACATATT	CACCTTCGGG	ATTGGTGACG	TTTATTCAAA	GAGGAACGTG	5640
	GAATGAAAAA	ATGGAATATG	ACCAGAGTGG	GAAATATATT	TCAAGAACTT	GGGCTGATGG	5700
65	GAAATTTTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTCTTAC	ACAGCCAGCG	5760
	GCGTTACATC	TTTGAGTATG	ACCAATCAGA	TTGCCCTGCTG	TCAGTTACCA	TGCCCTAGCAT	5820
	GGTGGCGCAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACCGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAGA	CTATAGTCGA	GATGGCCGAT	TGCTACAGAC	5940
	CCTGCACTCTG	GGGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAGCAAG	CAAGGCTTTC	6000
70	TGAGGTTCTC	TATGATACCA	CTCAGGTCAC	ATTAACATAT	GAAGAGTCTT	CTGGAGTGAT	6060
	TAAGACAATA	CACCTGATGC	ATGACGATT	CATCTGCACA	ATCAGATACA	GGCAACACAG	6120
	ACCTCTTATT	GGACGCGAGA	TTTTCAGATT	CAGTGAAGAA	GGCCTTGTGA	ATGCACGGTT	6180
	CGACTACAGC	TACACAATTT	TCCGAGTCAC	AAGCATGCAA	GCTGTAATCA	ATGAAACCCC	6240
	TTTGCCTATA	GATCTTTACC	GATATGTTGA	TGCTCTGGC	AGAACAGAGC	AGTTTGGAAA	6300
	ATTCAGTGTA	ATTAATTTACG	ATTTAAATCA	GGTCATAACT	ACTACAGTGA	TGAAACACAC	6360
75	CAAAATCTTC	AGTGGCAATG	GACAAGTCAT	TGAAGTCCAA	TATGAAATCC	TAAAGGCAAT	6420
	TGCTTACTGG	ATGACCAATT	AATATGATA	TGTGGGCGGA	CATGGTAATA	TGTGCATAAG	6480
	GGTAGGAGTA	GATGCCAATA	TAACAAGGTA	CTTCTATGAA	TACGATGCTG	ATGGCAACTT	6540
	TCAGACTGTT	TCTGTAAATG	ACAAAACCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
	CATTAACCTC	TTAAGCCATG	GGAAAGATGC	TCGTCCTTACT	CCTCTCCGAT	ATGACCTCCG	6660
80	AGACCCCATC	ACCAGATTAG	GAGRAAATCA	GTATAAAATG	GATGAAGATG	GCTTCTGTGAG	6720

	GCAGAGGGGA	AATGATATTT	TTGAATATAA	TTCTAATGGC	CTGCTGCAGA	AAGCCTACAA	6780
	TAAGGCTTCT	GGCTGGAGCT	TGCAGTATTA	CTATGATGGG	CTTGGGCGAC	GTGTCGCGAG	6840
	TAAGTCCAGC	CTAGGGGAGC	ACCTTCAGTT	CTTTGTGCGAC	GCGACCGCGA	ACCCATAAG	6900
5	AGTFACTCAT	TTGTACAACC	ACACAAGCTC	GGAGATTACA	TCTCTGTATT	ATGATCTCCA	6960
	AGGTACCTTT	ATTGCCATGG	AGTTAAGCAG	TGGTGAAGAA	TATATATGTAG	CCTGTGATAA	7020
	TACAGGTACC	CCACTAGCTG	TGTTCCAGCAG	CCGAGSTCAG	GTCTATAAAG	AGATACTATA	7080
	CACACCTTAT	GGCGATATCT	ATCATGACAC	TTACCTTGAC	TTTCAGGTCA	TAATTGGTPT	7140
	TCATGGAGGA	CTCTATGATT	TCCTTACTAA	ATTAGTGCAC	CTGGGGCAAA	GGGATTATGA	7200
10	TGTGTGTGCT	GGCAGATGGA	CAACGGCCTA	TCATCACATA	TGGAAACAGT	TGAACCTCCT	7260
	TCCTAAACCA	TTCAACCTCT	ACTCGTTTGA	AAATAACTAC	CCAGTTGGCA	AAATTCAAGA	7320
	TGTTGCAAG	TATACCACAG	ACATCAGAAG	TTGGTTGGAG	CTATTGGTIT	TCCAATTACA	7380
	CARTGTACTA	CCTGGATTTC	CCAAACCTGA	ATTAGAAAAA	TTAGAATTAA	CTTACGAGCT	7440
	TCFACGGCTT	CAGACAAAAA	CTCAAGAGTG	GGATCCTGGA	AAGACTATCC	TGGGCATTCA	7500
15	GTGTGAACCT	CAGAAACAGC	TCAGGAATTT	CATTTCCTTG	GACCAACTAC	CTATGACTCC	7560
	CCGATACAA	GATGGACGGT	GCCTTGAAGG	AGGGAAGCAA	CCAAGGTTTG	CTGCTGTCCC	7620
	TTCTGTTTTT	GGGAAAGGTA	TAAAATTTGC	CATCAAGGAT	GGCATAGTAA	CAGCTGATAT	7680
	TATAGAGGTA	GCCAAATGAAG	ATAGCAGGCG	GCTTGCTGCC	ATTCTCAATA	ATGCCCATTA	7740
	CCTGGAAAC	CTACATTTTA	CCATAGAGGG	GAGGGACACT	CACTACTTCA	TAAAGCTTTG	7800
20	GTCTCTGGAG	GAAGACCTGG	TGCTCATCGG	TAACTACTGG	GGGAGGCGGA	TTCTGGAGAA	7860
	TGGTGTCAAT	GTCACTGTGT	CCCAGATGAC	TTCTCTGTGT	AATGGGAGGA	CTAGACGGTT	7920
	TGCAGATATT	CAGCTCCAGC	ATGGAGCCCT	GTGCTTCAAC	ATCCGGTATG	GGCAACTGT	7980
	CGAAGAGGAA	AAGAATCACG	TGTTGGAGAT	TGCCAGACAG	CGCGCAGTGG	CCCAGGCTCG	8040
	GACTAAGGAA	CAAGAAGGCG	TGCAAGAGGG	GGAAGAGGGG	ATTAGGGCAT	GGACAGAAGG	8100
25	GGAAAAGCAG	CAGCTTTTGA	GCCTTGGGCG	GGTACAAGGT	TACGATGGGT	ATTTTGTTTT	8160
	GTCTGTGTAG	CAGTATTTAG	AACTTTCTGA	CAGTGCCAA	AAATPTCACT	TTATGAGACA	8220
	GAGCGAAATA	GGCAGAGAGT	AACAAAAATA	TCTCTGCCCT	TGCGTCACCA	AAGACTGCCT	8280
	GTMTTFAAAA	CATAAAATGG	TTTATTGTAT	TGTTTCTTA	GATCAGAAGT	CTGTATATGT	8340
	AAATATGGAG	GAAAAACATA	TCCAAGTCCC	TTTCAATGTG	ACGGAAGATG	GTATTTTAAT	8400
30	ATTGTTTGT	TAAACTCTTT	AAGAAATGAC	AGAGATTTTT	AGTTCTTGTG	TGGCAGTATT	8460
	CAAAATACCA	CAGTATGAAC	TCAAACAGCT	AAAAACAGTT	TTCAAGAAAG	ACCACTTTCA	8520
	ATTTGCGCAG	CCATGCAAT	GTTCCAATAT	CCAGAAAGAA	CCCAAGGTTT	TCTATCTCTA	8580
	TTGTGAGAAG	CAGTTTCATC	CTTAACTGTT	GGCAGAAGTT	ACGGGCTATT	TGAATAGGTG	8640
	GTGCAATAGT	ATCTGAAACT	TGCCCTTCGA	AAGACTGCCA	GCCTTTTGAC	GTPTTCCAGA	8700
35	TCGTGTATAG	GAAACTTAAA	AACAGGTGTA	AAATGTCTTC	AGCCACCATC	TCCTAGAGTG	8760
	AGGACCCAA	TGCCCTTCCT	TCTTGATAT	TCTCTCTGCG	TTGTTAAAGT	AAATGCCATA	8820
	TTGTGTGCT	GTGTTTGGC	GTGTGTTGGC	TGGGTTCTGT	CTACCATGCT	TCCCTGTGGG	8880
	TGTGGTAAAC	AGACTGTATA	GCCGCTATTT	GCTCGTGTGT	ACATGATACC	AAAGCAGCTG	8940
	GCCAGCGTGA	CCCTCTCTAC	ACGACCTGTT	TTGACTCAAT	TTTTTACTAA	AAGTTGTTC	9000
40	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAAT	TCTCAITTTAT	9060
	ATATAGGATG	TGTTTTGGTC	ATAGTTTCAC	ATTAGTGATT	CAGTATCTAT	ACACTGACCC	9120
	AATGGTTTTG	TGCACATGAA	CGGTAATTTA	CTTAAAAGTA	TGATTCTGGT	ACAAAAACAA	9180
	ACAAAAGCTT	TAGCAGGCTT	ACGTGTCTGG	GATGCCGATA	CATACATPAA	CTACTACTGC	9240
	AGAAATTCAT	AAGAGCCAAA	ACCTTAAAAA	AATAGACCTG	GTACTTAAAT	GAAAGTACTA	9300
45	AAGGGAAGAC	CAGCAACAA	ATCACAGCAG	TTGCTGCCAC	ATTGTTTCAG	CCCACCTAGA	9360
	TTTATCTTTC	AAATGTACAA	TTCTGTATTG	AACATCTCCC	AGCCATCTTC	AGGAAATCGA	9420
	ATCAAGTAAA	TCTCTTCCAA	CCGAAAACAT	TTCAACTAAC	TATAGAGAGG	CAGACTCATT	9480
	TTTACTAAAA	TAAATTTATAC	AGTTAGTTAT	TTTCGTTCTC	CGTACTTACC	CATTATCTTT	9540
	TATTTAATCG	TCTCTACTGC	CTAGGAAAAT	AACTATTTTC	CAGGACGGGT	TATTTGTTCT	9600
50	CGCATCATTT	AAAAATTGGA	GAAAGGTCAG	GATTAGTGTT	AATATCAGCT	GCAGTTTCTC	9660
	AATCTCTAGG	AATCTCTGAC	TAAACAAGC	CCCTTGGTGA	GCTGGAAGAT	TTGTGCCGAG	9720
	TGACAAAAG	ATAGTTTGTG	AAATGCTGTG	TAAATGTAA	TTACCACAAA	TGAAAAATACA	9780
	TGACAGCACA	ATGTGGCCCG	TAGAAAATTC	CCCTGAGCCA	GCTTCTGCAC	TTTCAATCAC	9840
	GAATCTGAAC	ATTTGCTATG	TCTGAAGGCA	AATTTATGAT	GGAATGTTAG	TTTGGATTCT	9900
55	TTCCAGATGC	TACTTAAATG	CAGTGTGGGG	TCATTGCGTT	GCTTTGCGAT	GACAGTTTCT	9960
	TTGAAAATAT	GAAAAGTCA	AAGCTCATGT	TAAGGTTTTT	CAAGAGTCTG	CCTCCTACTA	10020
	CACAAAGGAA	AGCAAGGGAA	AGGAAATGAC	CCTGGCAAA	AGTAGGGAAG	GGTGTATTCA	10080
	AACATTTTCT	TTTCAAAACC	TTCCGGTTAG	AATACCACTT	ACACATGTAT	TCTGAGAGAC	10140
	AGAATTCATG	AGGAACCTAT	CTCTCTTTAT	AATCGGAAAC	ACACCAGCTT	GATATATTGC	10200
60	TAAATCCATAC	TAAAATCATA	TTATTTGGGT	TTTCTGAAAT	CAGGCCTGTA	TTAATGGTAC	10260
	AGTATTTAT	CAGAATGGAA	TTCTAAAATT	ACTAACAAAC	TTGTTGAAAA	TTTGAATACC	10320
	TCCACACCAA	CCATAAAATG	GACCTTAAGT	TCCTAGAAC	TCTGATGTTT	TTTTAAATTA	10380
	ATGGAAAAAT	AAATTTGTGA	CTGTATATAG	AGAGTGCATT	CATAAATGTG	ATTATGTATT	10440
	TTATCACAAA	TCCAAAATGT	CAATATTAGA	GTCTATTTTG	CTTATATTTT	AAGCAATTAT	10500
65	ACGTTTTTGC	AAATTCATGA	TGATGTATCA	TTTTCAAACT	GCTTTAAATA	TCCATTAGAA	10560
	ACAAATATTT	GAAGCTTTTA	CTTAATAGTG	ATTACCTTGA	ACTGTGCATT	TCTAGTTTGT	10620
	AATACGTATT	TGGTTGGTTC	GTGCTTTAG	TTTGTTPAAG	TTACATTTGT	ATTATATTCA	10680
	GGAAATGCAC	TTTTTATTAC	TTACAGCTGT	GGTTTTTAATA	CTGCCTTGAA	CTATTATTAT	10740
	TCTTTTAC	ACTCCTTAAAG	CTTGAGGGAG	GAAAGAAAAA	AAAAACAAAA	CTACTAATCA	10800
70	GTAGTAAATC	GAGAGAAAC	ATTTTGGCAT	TTCTTAAGAA	GAAGATGGAG	ATATTGAGTA	10860
	TATCACTTCC	TATTCAGCTG	AATAGAAAGA	ATGCCTTCAT	TGACTTGCAG	TTCTGCAGTT	10920
	TAAATTTATG	AAAGAACAA	TCGTTTGCAT	TTCCGTATGA	AAGTAAAGC	ATTTTTTCAGA	10980
	GAAACATATG	AAATTTCTCAT	ACCCAGCAGA	CAGATGGCTG	ACACTGCACA	GCCACACACC	11040
	ATTCGAGTAA	GTTAAAGTGA	GAGCATAGTA	GTGAGACTCT	CCTATGAAGA	ACATTCTGGG	11100
75	CTGGAGGCG	GGAACTACTC	ATGTTTGT	CTTTTCTCTA	CTTAAGCCCA	TTTTTGTGTT	11160
	GCTTTTCTGT	TTTGTTTTGT	TTTCACTCTT	GCCTTACAGT	CTAGAGATCC	AAATGAAGTG	11220
	AAAAGTTCAA	AGTTTAAAC	ATTTAAATAT	GTTTACTTTT	AGTTGTCTAT	CTAATCGTTA	11280
	TTGATTAGAA	GCATGACTCC	TGAAGGAAAG	GGAAATAAAT	CTCAATTCAT	ACTAAGCTGC	11340
	AACAAAACAC	TTTTTACATA	TAAATAAGTA	TATGATTTAT	TTTTAACCCA	AAAAATGTAT	11400
80	AAAATAAGTG	TGTCTTTTAC	TGTCAATTTA	TCGAGAAGAT	CTATAATATA	TAGACTACAT	11460
	ATATATAATA	TATACAACAT	AGCCAAATGT	ATGAAAACCT	GACAAATGTAT	AAATTTGGAAT	11520

TCACATGCTA CCTATGTAGA CAGGTATGAA ATTAAAGTTAT AATTTTCATG AGACATTTTC 11580
 ATCACTGTTG ACACAGTTTC AAGGCATTCC ATCATGTTAT TTTGACTCTT TTCTTTTMTT 11640
 TTTTCCTTAA AATATATATT TTAAGTAGAC CAGGCCCCAC TATAATATCA CTTAAGAGAG 11700
 TCAGGGCAAA GTTTTTCAT TTATGAAGAT GTGTTTCATG AAGGGTGATT GTAATGGAGT 11760
 TCATTGGTAA TAGAAGCAAA AGTACAGTAA CGAAGTATTG AAAAGAAAAAT TTTGGAGACA 11820
 TTTGGAGCATA TTAATATATAG CTTGTGGAAA GACATAAGGC TACAGATGGA ATGGAACATT 11880
 CCTGTTTCTT TGAAGAAATT CACATACACA TAGCTGACCT GACTAGTACT TCAGCTCTTC 11940
 CACAGCCTTC TATAAAGGTT CTTTCTTCTG CAAAGAAAAA AAAACAAAAA AAAACAAAAA 12000
 AAAAAAAGC AAAAAAGCG CAAAAACAA AAAAAACAA AAAAGCAAG TAAATTTTAA 12060
 AATAACAGAA AACAAACAAC AAAAAAGAA TCAACCATAA ATAGTGACTA TTAATTTTCA 12120
 TGTGTCCTTC ATGTGAAGC TATTAAGGAC CAAATATACT ACTGTTTATA AGAAGAAATT 12180
 ACTTTCTAAA CAGTAAGTGA AAATACTTAG AGTTAAACTT GCTGTGGATT TGTCTTGGC 12240
 AGTTGTCATC TTACATTATT TGTCAAAGGA AATGTGTTTG GCAGTTAAAA ATCTTTCCCTT 12300
 AGATTTAGTG GTGGACTTTA ACCTCTTAAA TAAATGTTAG TATATCAGAT TGTGTCCTTG 12360
 AAAAAATATT TACTTGTATG AATCATGACA ACGTCTAAAT CTTTACTATT CTTCTGGCAA 12420
 AAGCATCAGT AAGAAAGAAG GCGAAAAAGA GAAGTATAGC CTTTATGTCA GAAAAACATT 12480
 CTTTTTAGCT GCTTACTTTC TCATGAAAAG TAAAGATGTT TACAGTGTAT GCCAAGTTT 12540
 CAGTTTCTGT ATACACACAG GTAGAGGTTT TAATCATATT GAAAAATGTT TTAATGTT 12600
 CTGAGCCACT TTGCTAGGAA ACAATAGGTT CCAATTTTGT ATTCTGCTC TCCTGTGCTG 12660
 AAAAGTGACT GGTACTGTGA CAGGTTTATG TTCTCTGGCT GCAGTTAAAT GGTCTTTTGC 12720
 ATTTTGCTCT GGCTTTTCAAG CCAGAAGCAT GCATTTTCTT ACAAGAGCAT CACAACAACA 12780
 TGTCTGTAAT ATTTAAAGTT AAACATTATG TGTGATATT TGAAGAAAAA GTACTTTGAA 12840
 TATTTTCAATT TTAAAAAATA AAATTGCCAA TGAAAAAAA

SEQ ID NO:230 PEZ2 Protein sequence:

Protein Accession #: NP_055068

1 11 21 31 41 51
 MEQTDCKPYQ PLPKVKHEMD LAYTSSSDES EDGRKPRQSY NSRETLEHYN QELRMNYSQ 60
 SRKRKEVEKS TQEMFECETS HTLCSGYQTD MHSVSRHGYQ LEMGSDVDTE TEGAASPDHA 120
 LRMWIRGMKS EHSSCLSSRA NSALSLTDTD HERKSDGENG FKFSPPCCDM BAQAGSTQDV 180
 QSSPHNQPTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTRSPQSPSA APAFPTSTQD 240
 SVHLHNSWVL NSNIPLETRH SLFKHSGSS AIFSAASQNY PLTSNTVYSP PPRELPRSTF 300
 SRPAFTFNPK YRCCNWKCTA LSATAITVTL ALLLAYVIAV HLPGLTWQLQ FVBGELYANG 360
 VSKGNRGTES MDITYSPIGG KVSDEKSEKV FQKGRALDIT EVDIGAQVMQ TTPPGLFWRF 420
 QITIHPIYVL KFNLSLAKDS LGGYGRINI PPTHQDFDV KLMDGKQLNK QDSKGSDDTQ 480
 HSPRNILITS LQETGPIEYM DQGPWYLAFY NDGKMBQVFL VLTATIEIMD DCSTNCNGNG 540
 ECISGHCHCF PGFLGSPDCAR DSCPVLCCGN GEYKKGHCVC RHQWKGPECD VPTEEQCIDPT 600
 CFHGCTCIMG VICVPGYKG EICEEEDCLD PMCSNHGICV KGECHCTSGT GMVNCETPLP 660
 VCQEQCSHGG TFLLDAGVCS CDPKWTGSDC STELCTMECG SHGVCSESGC QCEEGVWGPT 720
 CBERSCHSHC TEHQCKDKGK CECSPGWEGD HCTIAHYLDA VRDGCPLGFC GNGRCTLQDN 780
 GWHCVQCQGW SGGCGNVVME MLCGDNLNDND DGGLTDCVDP DCCQQSNCYI SPLCQGSDDP 840
 LDLIQSQSLT FSQHTSRLFY DRIKFLIGKD STHVIPPEVS FDSRRACVIR GQVVAIDGTP 900
 LVGVNVSPFL HSDYGFITSR QDGSFDLVAI GGISVILIFD RSPFLPEKRT LWLFWNQFIV 960
 VEKVTHQVRV SDPPSCDILN FISPNPIVLP SPLTSFGGSC PERGTIVPEL QVVQEEIPIP 1020
 SSFVRLSYLS SRPPGYKTLR RILLTHSTIP VGMKIVHLTV AVEGRITQKW FPAALNVYT 1080
 FAWNKTDIYG QKWGLAEAL VSVGYEYETC PDFILWEQRT VVLQGFEMDA SNLGDWLSNK 1140
 HHLILNQSGI IHKNGENEMF ISQPPVIST IMGNHQRVS ACTNCGPAH NNKLFPAPVAL 1200
 ASGPDGSVYV GDNFVRRIF PSGNSVSILE LSTSFAHKYY LAMPVSESL YLSDTNTKRV 1260
 YKLKSLVETK DLSKNFEVVA GTGDQCLPFD QSHCGDGGRA SEASLNSPRG ITVDRHGFYI 1320
 FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLEWPTDL AVNFMDSNLY 1380
 VLNNIVLQI SENRRVRIA GRPIHCQVPG IDHFLVSKVA IHSLESARA ISVSHSGLLF 1440
 IAETDERKVN RIQQVTNNGE TYIIAGAPTD CDCKIDPNCD CFSGDGGYAK DAKMKAPSSL 1500
 AVSPDGTLYV ADLGNVRIIT ISRNQAHLDN MNIYEIASPA DQELVQFTVN GTHLHTLNLI 1560
 TRDYVYNFTY NSEGDLAGIT SSNGNSVHIR RDAGGMPLWL VVPGGQVYWL TISSNGVLKR 1620
 VSAQGNYPAL MTPYGNLTGL ATKSNENGWT TVYEYDPEGH LTNATFTTGE VSSFHSDLEK 1680
 LTKVELDTSN RENVLMSTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSS 1740
 EPHILAGAVN PTLGKNISL PGEHNNALIE WRQRKEQNGK NVSAFERRLR AHNRLNLSID 1800
 FDHITRTGKI YDDHRKFTIR ILYDQTRPI LWSFVSRYNE VNITYSPSGL VTFIQRGTWN 1860
 EKMEYDQSGK IISRTWADGK TWSYTYLEKS VMLLLHSQRR YIFEYDQSDC LLSVTMPMSV 1920
 RSHLQTMLSV GYRNRYTTP DSSTSFIQDY SRDGRLLQTL HLTGTRRVLY KYTKQARLSE 1980
 VLYDTTQVTL TYEBSGVIK TIHLMDGFI CTIRYRQTGP LIGRQIFRFS BEGLVNARFD 2040
 YSYNNFRVTS MQAVINBTPL PIDLYRYVDV SGRTEQFGKF SVINYDLNQV ITTVMKHTK 2100
 IFSANGQVIE VQYBILKAI YWMTIQYDNV GRHGNMCIHV GVDANITRYF YEYDADGQLQ 2160
 TVSVNDKTQW RGSYDLNGDI NLLSHGKSAR LTPRYDLRD RITRLGEIQY KMDGDFLRQ 2220
 RGNDFEYNS NGLLKAYNK ASGWTVQYYY DGLGRRVASK SSLGQHLQFF VDATANPIRV 2280
 THLYNHTSSE ITSLYLDLQG HLIAMELSSG EEEYVACDNT GTPLAVFSSR GOVIKEILYT 2340
 PYGDIYHDYV PFDQVLIIGH GGLYDFLTKL VHLGQRDYDV VAGRWTAYH HIWKQLNLLP 2400
 KPFNLYSFEN NYVFGKIQDV AKYTTDIRSW LELFGFQLHN VLPGFPEKPEL ENLELYELL 2460
 RLQTKTQEMD PGKTIIGIQ ELQKQLRNF I LDQLPMTFPR YNDGRGLEGG KQPRFAAVPS 2520
 VFQKQKFAI KDGIVTADI GVANEDSRRL AAILNNAHYL ENLHFTIEGR DTHYFIKLS 2580
 LEEDLVLENG TGCRRILENG VNVTVSQMTS LLNGRTRREA DIQLQHGALC FNIRYGTTFE 2640
 EEKNHVLEIA RQRAVAQAWT KEQRRLEGE EGIRAWTEGE KQQLLSTGRV QGYDGYFVLS 2700
 VEQYLELSDS ANNIHFMRQS EIGRR

SEQ ID NO:231 PFD4 DNA SEQUENCE:

Nucleic Acid Accession #: NM_000441

Coding sequence:

225-2567 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
 CTGAGCCTTC CCGGTTCGGG AAAGGGGAAG AATGCGAGGAG GGGTAGGATT TCTTTCCTGA 60
 TAGGATCCGTG TGGGAAAGAC CGCAGCCTGT GTGTGTCCTT CCCTTCGACC AAGGTGCTCG 120
 TTGCTCCGTA AATAAAACGT CCCACTGCCT TCTGAGAGCG CTATAAAGGC AGCGGAAGGG 180
 TAGTCCCGGG GGCATTCCGG GCGGGGCGCG AGCAGAGACA GGTCTGGCA GCGCCAGGCG 240
 10 GCAGGTCCGA GCCCGCGCAG CTCGCCGAGT ACAGCTGCAG CTACATGGTG TCGCGGCCGG 300
 TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGCGG CCTGCAGGAG CGCAAGACGC 360
 TGGGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCCTT GGTGTGCTAA 420
 AGACTCTTGT GCCCATCTTG GAGTGGCTCC CCAAATACCG AGTCAAGGAA TGGCTGCTTA 480
 GTGACGTGAT TTCGGGAGTT AGTACTGGGC TAGTGGCCAC GGTGCAAGGG ATGGCATATG 540
 15 CCCTACTAGC TGCAGTTCTT GTCGGATATG GTCTCTACTC TGCTTTTTC CCTATCCTGA 600
 CATACTTTAT CTTTGGAAAC TCAAGACATA TCTCAGTTGG ACCTTTTCCA GTGGTGAGTT 660
 TAATGGTGGG ATCTGTTGTT CTGAGCATGG CCCCAGACGA ACATTTCTTC GTATCCAGCA 720
 GCAATGGAAC TGTATTAAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780
 TCCTGATTGC CAGTGCCTTG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840
 20 TGCAGATTGG ATTCTAGTGG AGGTACTTGG CAGATCCTTT GGTGTGTGGC TTCACAACAG 900
 CTGCTGCCTT CCAAGTGCTG GTCTCAGCAG TAAAGATTGT CCTCAATGTT TCAACCAAAA 960
 ACTACATGAG AGTCTCTCTC ATTATCTATA CGCTGGTTGA GATTTTTCAA AATATTGGTG 1020
 ATACCAATCT TGCTGATTTT ACTGCTGGAT TGCTCACCAT TGCTGCTGTG ATGGCAGTTA 1080
 AGGAATTAAG TGATCGGTTT AGACACAAAA TCCCAGTCCC TATTCTTATA GAAGTAATTG 1140
 25 TGACGATAAT TGCTACTGCC ATTTTCATATG GAGCCAACTT GGAACAAAAA TACAATGCTG 1200
 GCATTGTTAA ATCCATCCCA AGGGGGTTTT TGCTCCTGTA ACTTCCACCT GTGAGCTTGT 1260
 TCTCGGAGAT GCTGGCTGCA TCATTTTCCA TCCTGTGGGT GGCTTATGCT ATTGCAAGTG 1320
 CAGTAGGAAG AGTATATGCC ACCAAGTATG ATTACACCAT CGATGGGAAC CAGGAATTCA 1380
 TTGCCTTTGG GATCAGCAAC ATCTTCTCAG GATTCTTCTC TTGTTTGTGG GCCACCACTG 1440
 30 CTCTTTCCCG CACGGCCGCT CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500
 TCTCTGCTGC GATTGTGATG ATCGCCATTC TTGCCCTGGG GAAGCTTCTG GAACCCCTGC 1560
 AGAAGTCGGT CTTGGCAGCT GTTGTAAATG CCAACCTGAA AGGGATGTTT ATGCAGCTGT 1620
 GTGACATTC TCGTCTGTGG AGACAGAATA AGATTGATGC TGTATCTTGG GTGTTTACGT 1680
 35 GTATAGTGTG CATGTATCTG GGGCTGGATC TCGGTTTACT AGCTGGCCTT ATATTTGGAC 1740
 TGTGTAGTGT GGTCTCTGAG GTTCAGTTTC CTCTTGTGAA TGGCCTTGGA AGCATCCCTA 1800
 GCACAGATAT CTACAAAGAT ACCAAGAATT ACAAAACAT TGAAGAACCT CAAGGAGTGA 1860
 AGATTCCTAG ATTTTCCAGT CCTATTTCCT ATGGCAATGT CGATGGTTT AAAAAATGTA 1920
 TCAAGTCCAT AGTTGGATT GATGCCATTA GAGTATATAA TAAGAGGCTG AAAGCGCTGA 1980
 40 GGAAATACA GAAATTAATA AAAAGTGGAC AATTAAGAGC AACAAAGAA GGCATCATAA 2040
 GTGATGCTGT TTCAACAAGT AATGCTTTTG AGCCTGATGA GGATATTGAA GATCTGGAGG 2100
 AACTTGATAT CCCAACCAAT GAAATAGAGA TTCAAGTGA TTGGAACCTC GAGCTTCCAG 2160
 TCAAAATGAA CGTTPCCAAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220
 CTTTCTCGGA CGTTGTTGGA GTGAGATCAC TCGCGGTGAT TGTCAAAGAA TTCAAAGGAA 2280
 45 TTGATGTGAA TGTGATTTT GCATCACTTC AAGATTATGT GATAGAAAG CTGGAGCAAT 2340
 GCGGGTTCTT TGACGACAAC ATTAGAAAGG ACACATCTCT TTTGACGGTC CATGATGCTA 2400
 TACTCTATCT ACAGAACCAG GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTAGAAACGA 2460
 TCACCTCTAT TCAGGATTTG AAAGATACCC TTGAATTAAT AGAAACAGAG CTGACGGAAG 2520
 AAGAATCTGA TGTCCAGGAT GAGGCTATGC GTACACTTGC ATCCTGAAAG TGGGTTCGGG 2580
 50 AGGTCTCTAT GAGCAAGGAA TACAAGACAA AACTTCTCTA ATGCATTGAC TATTTCTTCA 2640
 GACTCAAAAC ACTCATCTCT TTTTCTATTA AGCCATGAAA AGAGAAGCAC TAAGACTGCT 2700
 TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCATGAATT 2760
 ATTACAGACA TTTGGCAGCG TCCAGGGTAA GCTGGTGTTA TAATACGCTG CTGATCTACA 2820
 TCACAGATT GCTAATAATG TTCACGTGGG CCCTGGCATA TCTCTGTGTA GTTAGAGTGA 2880
 55 GTGCTGACCC AACAGCCTCT GTGGTCAAGC GAGTCACGAA TGATTAACTA TAAAGAAAAA 2940
 TCAGTTTGTG ACTGACCTGG ATATCCATGA GCTGCACCTG TCACCATGTA AGGTCACATT 3000
 TAGTAAATGC TGAATATAAA TGATTAAATG ATTTATCAAT AAAAGCCTTT GAAATACTTT 3060
 TGGATAATAA ATTGGAGTTT TAAAAATGCA AATTTGCTTA GTATCTAATA ATGAAGTGTT 3120
 ATTACATATA GCCGGAATTG AGGATCTCTT TGATCCTGGA AATGGTTTAC CTAARAAGCTA 3180
 60 CAGAACCAGG CCAATATATT TTGAAATATT GATGCAGACA AATGAAATAA TAAAGAGATT 3240
 TTCATGGTTT ATAAAAATCT TTTTGTATAT GATAATATATC ATGATCACAA CTGAGATCAA 3300
 AAAAAATATAT GACAGATTAT TTTGTTTAAA AATGCAGTTT TAATATATCTT AGTCTATAGA 3360
 AATGATCAIT GCATGGAGGC ATGTATAGGT ATGATCTGTG TAAAATCTGA CATAAAAACA 3420
 GTGCTATTCT GAGTGAAAT TTTTGTGATG TGCTTACATA ACCATGGTGA TTAATAATGAG 3480
 65 TTTATATTTT TTCTCAAAAA TTTTAGCAGT GGTAAAGTA AGTAATCTTT AACTGAACCTC 3540
 TGACCACTTA AAAAAAATC TAAAAATTGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600
 ATTTTAAAG ACAAGCATT CTAATGAAC TCAATATAAA AACATTCATT TGGAAATGTAC 3660
 ATACTGAAA ATACAGGTTT TTTTGACCAA AAGTTTATAT ATCTTTTCTT TTTATTTATT 3720
 TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780
 70 GACTTTTCCC ATATATTTC CACTGGAGTG AATGAAGTTG TACTTCAATT CTAGAGAAAA 3840
 GPTATACCCA GGTCCCAAT TGAGAATGTC TTGCTTGATT GAAACGACA TCATCCCTTG 3900
 GTATACTCCA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTGT CACACTCAAG 3960
 TCCTGTCAGT ACCCTGCTCT AAAGATAGAA TGGCTTCTCT GTTTTCTTTC TGAATACAAA 4020
 CCAGAAACAA TGTCTCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTAAAT 4080
 CCTGAATCT GGTGTGTAAT CTGGTTACAG CATAACTAGG ATTATAATGC TGCCCTCATTT 4140
 75 TCACAGCACT ACTTCTTAT ATTGACAACA AATCATCTCG CTAAGAGAGT AATGTAGGCC 4200
 AGGCGCGGTG GCTCATGCTT GTAATCCAG CACTTTGGGA GGCCGAGGCG GGTGGATCAC 4260
 GAGGTGAGG GATGAGACG ATCCCTGGCTA ACATGGTAAA ACCCGTCTC TACTAAAAAT 4320
 AGAAAAAAG AAATAGCCTT AGCGTGGTGG CTGGCGGGCG CCTGTAGTCC CAGCTATTGT 4380
 80 GGAGGCTAAG GCAAGGAAT GCGGTGAACC CGGAGGCGGG AGCTTGCAGT GAGCCGAGGT 4440
 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATAA 4500

5
10
15
20
25
30

```

AAAAAAAAA AGAGTGAATG TAATAGTCTT GCAGAAAATG AATGAATACC TTTGTTCAAT 4560
AAAGGAATA TGCATTGCTC ACTTTTGTGA AGGAAATGCC AAAGTTACGT TTTACAACAA 4620
GGCTAGAGTT TGTAAATCTT GGGTTCAATT GTGATGACAT AAGTCAGCAA ACTGCGGGAA 4680
TACTGTCTCT TCTATGTATT TTGTGAATAG TAAGCATAAT TTTAGTTTGT TATTATCAAT 4740
GAAAATTTC A CTGAAATTA AAGCTGCCCT TTGTATATAT TTTAACCTAT AGGATAAGAT 4800
TCCAGTATG TATATGAGTT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAAATA 4860
TTTGACACAC TTTAAAAATA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGTCTCTT 4920
CTGAACAAAA

```

SEQ ID NO:232 PFD4 Protein sequence:

Protein Accession #: O43511

15
20
25
30

```

1      11      21      31      41      51
MAAPGGRSEP FQLPEYSCSY MVSRLPVYSEL AFQQQHERRL QERKTLRESL AKCCSCSRKR 60
AFGVLKTLPV ILEWLPKYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPGYGLYSA 120
FPFILTFFIF GTSRHISVGP FVVSLMVGVS VVLSMAPDEH FLVSSSNGTV LNTTMDTAA 180
RDTARVLIAS ALTLVLGLIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQLKIVL 240
NVSTKNYNGV LSIIYTLVEI FQNIQDITLA DFTAGLLTIV VCMAYKELND RFRHKIPVPI 300
PIEVIVTIIA TAIISYGANLE KYNAGIVKVS IPRGFLPPEL PPVSLFSEML AASFSLAVVA 360
YAIIVSVGVK YATKYDYTID GNQEFIAFGI SNIFSGFFSC FVATATLSRT AVQESTGGKT 420
QVAGIISAAI VMIAILALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWVFTCIYSI ILGLDLGLLA GLIFGLLTIV LRVQFPSWNG LGSIPSTDIV KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LKSGQLRAT 600
KNGIISDAVS TNNAFEDED IEDLELDIP TKEIEIQVDV NSELPVKVNV PKVPIHSLVL 660
DCGAIISPLDV VGVRSRLRIV KEFQRIDVNV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAILYLO NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEBELDV QDEAMRTLAS 780
QDEAMRTLAS

```

SEQ ID NO:233 PFH2 DNA SEQUENCE:

35
40

Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

40
45
50
55
60

```

1      11      21      31      41      51
CTGCGATCCC GCAGGCGCAG GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT 60
GGGCGTGCGC GCGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120
TGCTCCTGCT CTGTGTGCGC CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
TATGGGCGCA GTGGCAGGGA CGACGCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240
TGACTGGAGC CTCGAGTGGG ATTGGTGAGG AGCTGGCTTA CCAATGTCTT AACTAGGAG 300
TTTCTCTTGT GCTGTCAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
TAGAGAAATG CAATTATAAA GAAAAGATA TACTTGTTTT GCCCTTGAC CTGACCGACA 420
CTGTTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGGGAATG TCCCAGCGTT CTCTGTGCAT GGATACACAG TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTG CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTACTACT GAATAGCATC CTGGGTATCA 660
TATCTGTACC TCTTTCATTT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTITTTA 720
ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCCG 780
GACCTGTGCA ATCAAAATAT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
GCAATAATGG AGACCAATCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
TCAGCATGGC CAATGATTTG AAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCACAAAG ATGGGGAAGA 1020
AAAGGATGTA GAACTTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
AGACAAACA TGACTGAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
AGATTGCCAT GAATCTTGCA AA

```

65 SEQ ID NO:234 PFH2 Protein sequence:

Protein Accession #: NP_057113

70
75

```

1      11      21      31      41      51
MNWELLLWLL VICALLLLLV QLLRFLRADG DLTLLWAWEQ GRRPEWELTD MVVWVTGASS 60
GIGEELEYQL SKLGVSLVLS ARRVHELERV KRRCLENGNI KEKDILVLP DLDTTGSH EA 120
ATKAVLQEFQ RIDLLVNNNG MSQSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHEMER 180
KQKIVTVNS ILGIISVFLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGFVQSN 240
IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMARD LKEWWISEQP FLVTVYLWQY 300
MPTWAMNITN KMGKRLIENF KSGVDADSSY FKIFKTKHHD

```

SEQ ID NO:235 ACC5 DNA SEQUENCE

80
Nucleic Acid Accession #: NM_000450

Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 5 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
 GCCTGGTCTT ACACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAAGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
 TCCATATTGA GCTATTCACC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAAGAG CCAAGAACTG GGCTCCAGGT 300
 10 GAACCCAAAC ATAGGCCAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCTGTGA CCAATACATC CTGCAAGTGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 TACACTTGCA AGTGTACCC TGGCTTCAGT GGACTCAAAT GTGAGCAAAT TGTGAAGTGT 540
 ACAGCCCTGG AATCCCTCGA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC 600
 15 AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAAT TGTGTCCTC TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGGA 780
 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
 20 GCCCAGAGCC TTCAAGTGTAC CTCATCTGGG AATTTGGGACA ACGAGAAGCC AACGTGTAAG 900
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTC 960
 CCTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 TTGCAAGGAC CAGCCAGGTT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCA 1080
 25 GTTGTGAAAG CTTCCTAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCCTAGTG CTTCCTAGTG TTTCCGTTAT GGGTCCAGCT GTGAGTTCCT CTGTGAGCAG 1200
 GGTTCCTGCT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
 GAGAAGCCCA CAGTGAAGC GTGTGAGATG GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTCAATCCCC TATTTGGAGAA TTCACCTACA AGTCTCTCTG TGCTTCAGC 1380
 TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440
 30 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCGGGA 1500
 AAGATCAACA TGAGCTGACG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCCTGT 1560
 CTTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACTACCTTG TGAAGCTCCC ACTGAGTCCA ACATTCCTCT GTTAGCTGGA 1680
 CTTCCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCTCTCT GCTTCGGAAA 1740
 35 TGCTTACGGA AAGCAAAAGA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
 GGAAAGCTACC AAAAGCCTTC TTACATCCCT TAA

SEQ ID NO:236 ACC5 Protein sequence:

Protein Accession #: NP_000441

40

1 11 21 31 41 51
 45 MIAAQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKEBIEYLN 60
 SILSYSPSYI WIGIRKVNIV WVVGTQKPL TEEAKNWAPG EPNRQRKDED CVEIYIKREK 120
 DVGWMDNERC SKKKLALCYT AACTNTSCSG HGECEVETINN YTCKCDPFGS GLKCEQIVNC 180
 TALESPHEGS LVCSEPLNGF SYNSCSISC DRGYLFSSME TMQCMSSGEW SAPIACNVV 240
 50 ECDAVTNPAN GFVECFQNGP SFPWNTCTF DCEBGFELMG AQSLOCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSSS PAGEFTFKSS CNFTCEBGFH LQGPQVQECT TQGWTTQIIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSFRT GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420
 EKPTCEAVRC DAVHQPFKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 WTVEVPSQV VKCSLAVPG KINMSCSGEF VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 55 SGLLPTEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRL CLRKAKKFVP ASSQSLES 600
 GSYQKPSYIL

SEQ ID NO:237 PM28 DNA SEQUENCE

Nucleic Acid Accession #: N51002

Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

60

1 11 21 31 41 51
 60 ATGATGTGTG AAGTGATGCC CACGATTAAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60
 CAAAGCAGTG GCTCCGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120
 65 GAAAGGGATC GTCTCTTAGA CACCTTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180
 CAAAGACTTC AGGATGTCAAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTACAGC 240
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300
 CCGGAATTGT CTGCATCTGAC AAAAGAATTA AATGCCTGCA GGGAAACAAT TCTAGAAAAG 360
 70 GAAGAAGAAA TCCTCTGAAT TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
 TTGGAGTGCC TTGTGTACAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
 GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG 540
 TTTTGAGCAC ACAAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600
 AGAGTCTCTG CACTGGAAGA AGAAGTAGCT GCTGCTAATC AGGAGATTGT TGCTTTGCGT 660
 75 GAACAAAATG TTCATATACA AAGAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
 CATCTTGAAG GATGGAACCT TGGACAGAAA GTCCATGAGA AGCGTTTGTG CAATGGTTCT 780
 ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAAGTAC AAGAATTGCT TGAAAAGCAA 840
 AACTATGAAA TGCCCCAGAT GAAAGAACCT TTAGCAGCCC TTCTTCCCGG AGTGGGAGAG 900
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATTA AAACAGAAGA AATGAACACC 960
 80 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAGAATT 1020
 ACAACCCCTG AAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080

5 AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140
 10 AAAAAAGAGC AGTTACCAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGAGCCATG 1200
 15 AGAAAGGGCTG AAACCTTGCC TGAAGTAGAG GCTGAACCTGG CTCAGAGAAT TGCAGCCCTA 1260
 20 ACCAAGGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCTA 1320
 25 CTTGAAGAGA AGAATCAAGA ACTTCAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG 1380
 30 CATAACAAGA GATATTCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCCTA 1440
 35 CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAGAAA 1500
 40 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA 1560
 45 GAAATGAAA AGCTGAGATC TGAACCTGAC CAATTGAAA TGAGAACTGG CTCTTTAATT 1620
 50 GAACCCACAA TACCAAGAAG TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680
 55 TCCTTAGTGG ACAGCCAGTC TGATTACAGA ACAACTAAAG TAATAAGAAG ACCAAGGAGA 1740
 60 GGCCGCATGG GTGTGCGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800
 65 AATAGAACTC AACAGATTGG AGTACTAAGC AGCCACCCTT TTGAAAGTGA CACTGAAATG 1860
 70 TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTGTAGCT CAATGGATCT TCTCTCTCCA 1920
 75 AGTGGTCAAT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC 1980
 80 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040
 85 ATTGAAATA GAGTGCTAG TGTGAGCCTC GAAGGCTGGA ATTTGGCAAG GGTCCACCCA 2100
 90 GGTACCTCCA TTACTGCCTC TGTACAGCT TCATCGCTGG CCAGTTCATC TCCCCCAGT 2160
 95 GGACACTCAA CTCCAAGCT CACCCCTCGA AGCCCTGCCA GGAATATGGA TCGGATGGGA 2220
 100 GTCATGACAT TGCCAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCACT TGTGGAAGAA 2280
 105 GATGGTCCAG AGACAAAGC AACAAATAAA TGTGAAACTT CTCTCTCTCC TACCCTAGA 2340
 110 GCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
 115 TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTGTGATAGT CCAACAGCAG CCAAGACTCT 2460
 120 CPTCACAAG CCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTIGGTAAA 2520
 125 AAGAAAGAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG 2580
 130 GAGTCCCTGG GGTAGGCCAA ACTCGGAATC CAAGCTGAGA AGGATCGAAG ACTAAGAAA 2640
 135 AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGGATTAC CTTTTGCCCA GTGGGATGGG 2700
 140 CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
 145 TGCCGAGCCA ACGTGAAGAG TGGTGGCCTC ATGTCTGCTT TATCTGACAT TGAGATCCAG 2820
 150 AGAGAAATG GATTCAGCAA TCCACTGCAT CGCTTAAATC TTCGATTAGC AATCCAGGAG 2880
 155 ATGTTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAATCTCTTC AGGCAACGTT 2940
 160 TGGGTGACTC ATGAAGAAAT GGAAAACTT GCAGCTCCAG CAAAACGAA AGAATCTGAG 3000
 165 GAAGGAAGCT GGGCCAGTGG TCCGGTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
 170 CATGAGTGGG TTGGAATAGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
 175 TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCCGT 3180
 180 GTCCATTAAA AAATGGTGA TAGTTTCCAT CGAACAAAGT TACAATATGG AATTATGTGC 3240
 185 TTAAAGAGGT TGAATATTGA CAGAAAAGAA CTAGAAAAGG GACGGGAAGC AAGCCAACT 3300
 190 GAAATAAAG ACCTGTGTGT GTGGAGCAAT GACCGAATTA TTCGCTGGAT ACAAGCAATT 3360
 195 GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
 200 CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
 205 ACCCAGGCAA GGCAGATTCT TGAAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
 210 AGGCGACTGG ATGAAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600
 215 TTTCCTCCTC GTGAAGTACA TGGAAATCAGC ATGATGCTCG GTTCTCAGA AACATTACCA 3660
 220 GCTGGATTAA GGTAAACCAC AACCTCTGGG CAATCAAGAA AAATGACAAC AGATGTTGCT 3720
 225 TCATCAAGAC TGCAGAGGTT AGACAACTCC ACTGTTCCGA CATACTCATG TCTCGAGTAA 3780
 230 GCGGCCGCTT TAA

50 SEQ ID NO:238 PM28 Protein sequence:
 Protein Accession #: none found

55 1 11 21 31 41 51
 60 MMCEVMPITIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDTRL ETQESLSLAQ 60
 65 QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEI NACREQLLEK 120
 70 EEEISELKAE RNNTLLLEH LECLVSRHER SLRMTVVKRG AQSPSGVSSE VEVLKALKSL 180
 75 FEHHKALDEK VRERLKVSL RVSALEEEEL AANQEIVLR EQNVHIQRKM ASSEGSTESE 240
 80 HLEGMEPGQK VHEKRLSNGS IDSTDETSQI VELQELLEKQ NYEMAQMKER LAALSRLVGE 300
 85 VEQEAETARK DLIKTEEMNT KYQRDIRIAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360
 90 NDKLENELAN KEAILRQMBE KNRQLQERLE LAEQKLQQTIM RKAETLPEVE AELAQRIAAE 420
 95 TKAEERHGNL EERMRLHEGQ LEEKNQELQR ARQEKMNNEE HNKRLSDTVD RLLTESNERL 480
 100 QLHLKERMAA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRSELD QLKMRGTSLI 540
 105 EPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRRRR GRMGVRRDEP KVKSLGDHEW 600
 110 NRTQQIGVLS SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQDLAI 660
 115 NKEIRLIQEE KESTELRAEE IENRVAVSLS EGLNLARVHP GTSITASVTA SSLASSPPPS 720
 120 GHSTPKLTPR SPAREMDRMG VMTLPSDLRK HRRKIAVVEE DGREDKATIK CETSPPPTPR 780
 125 ALRMTHTLPS SPAREMDRMG VMTLPSDLRK HRRKIAVVEE DGREDKATIK CETSPPPTPR 840
 130 KEKARLGQLR GFMEETAAAO ESLGLKGLGT QAEKDRRLK KHELLEEAR KGLPFAQWDG 900
 135 PTVVAVLEW LGMPAWYVAA CRANVKSAGI MSALSDTEIQ REIGISNPLH RLKRLAIQE 960
 140 MVSLTSPAP PSTRTPSGNV WTHEEMENL AAPAKTKESE EGSWAQCPVF LQTLAYGDMN 1020
 145 HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMDVSFH RTSLOQYIMC 1080
 150 LKRLNYDRKE LERRREASH EIKDVLWNSN DRIIRWIQAI GLREYANNIL EGVHGSGLIA 1140
 155 LDENPDYSSL TLLLQIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200
 160 FPPREVHGIS MPPGSETLP AGFRLTTISG QSRKMTTDVA SSRLQRLDNS TVRTVSCLE

80 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 5 ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
 AAGGTTCCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
 TTTACAACATA TGGCTTTTATT AACCATATATG GAATTCCTAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCGCA TGAAGTGTCA ATATGTTTGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300
 10 GTTGCACTCG CAGATGGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420
 CAAGATGTGA TATTTAAAAA TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
 GATGATTCAT CACAGCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATC CACATCCTCG TGGTCATGCA 600
 CATTTCGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTTG 660
 15 TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAAGTGA AAAAATTCCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
 TATAAAATAT CGACAGACAC CCATCAGTTT TCTGTGACAG AAAGGGGAAC TATCATTAAC 840
 CATGCTGCAG CGAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTCTCTCT 900
 20 ATGCTGACAG TTAATGAGGA GCACATGCCA TTCTGGCAGT TTTTGTGAAG ACTCTGTGGT 960
 ATTGTTGGAG GAATCTTTTC AACCAACAGGC ATGTTACATG GAATTTGAAA ATTTATAGTT 1020
 GAAATAATTT GCTGTCTGTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTCTCTTTT 1080
 GAGGATGGCC ACACAGACAA CCACTTACCT CTTTATAGAA ATAATACACA TTTGA

25 SEQ ID NO:240 PQ14 Protein sequence:
 Protein Accession #: NP_057654

1 11 21 31 41 51
 30 MRRNRKKTLL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
 KYEYEVKDF SSKLRINIDI TVAMKQVVG ADVLDLAETM VASADGLVVE PIVFDLSPQQ 120
 KEWQRMQLLI QSRLEQEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180
 VAGNFHITVG KAIPIPRGHA HLAALVNHES YNFSHRIDHL SFGELVPAII NPLDGTAKIA 240
 35 IDHNQMFQYF IIVVPTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVTIEHMP FVQFFVRLCG IVGGIFSTMG MLHGIGKFTV EIIICRFRLG SYKPVNSVPF 360
 EDGHTDNHLP LLENNTH

SEQ ID NO:241 PBA7 DNA SEQUENCE

40 Nucleic Acid Accession#: AA219134
 Coding sequence: 24-1815 (underlined sequences correspond to start and stop codons)

AATTCGCCCT TGCTTAATTA AGCATGTTTA CCTTCTCTGC ATCTGTCACT GCTGCTGTCA 60
 GTGGCTCTCT GGTGGGTTAT GAAGTTGGGA TCATCTCTGG GGCTCTTCTT CAGATCAAAA 120
 45 CCTTATTAGC CCGAGCTGC CATGAGCAGG AAATGGTTGT GAGCTCCCTC GTCATTGGAG 180
 CCTCTCTTGC CTCACCTACC GGAGGGGTCC TGATAGACAG ATATGGAAGA AGGACAGCAA 240
 TCATCTTGTG ATCCTGCCTG CTGGACTCG GAAGCTTAGT CTGATCCTC AGTTTATCCT 300
 ACACGGTTCT TATAGTGGGA CGCATTGCCA TAGGGGTTTC CATCTCCCTC TCTTCCATTG 360
 CCACCTGTGT TTACATCGCA GAGATTGCTC CTCAACACAG AAGAGGCCCTT CTGTGTGTAC 420
 50 TGAATGAGCT GATGATTGTC ATCGGCATTG TTTCTGCCTA TATTTCAAAT TACGCATTGG 480
 CCAATGTTTT CCATGGCTGG AAGTACATGT TTGGTCTTGT GATTCCTCTG GGAGTTTTGC 540
 AAGCAATTGC AATGATTTTT CTCTCTCAA GCCCTCGGTT TCTGGTGATG AAAGGACAAG 600
 AGGGAGCTGC TAGCAAGGTT CTGGAAGGT TAAGAGCACT CTCAGATACA ACTGAGGAAC 660
 55 TCACGTGAT CAAATCTCTC CTGAAAGATG AATATCAGTA CAGTTTTTGG GATCTGTCTC 720
 GTTCAAAGA CAACATGCGG ACCCGAATAA TGATAGGACT AACACTAGTA TTTTGTGTAC 780
 AAATCACTGG CCAACCAAC ATATTGTCT ATGCATCAAC TGTTTTGAAG TCAGTTGGAT 840
 TTCAAAGCAA TGAGGCAGCT AGCCTCGCT CCACCTGGGT TGGAGTCGTC AAGGTCATTA 900
 GCACCATCCC TGCCACTCTT CTGTAGACC ATGTGCGCAG CAAAACATTC CTCTGCATTG 960
 60 GCTCTCTGT GATGGCAGCT TCGTTGGTGA CCATGGGCAT CGTAAATCTC AACATCCACA 1020
 TGAACCTTCA CCATATCTGC AGAAGCCACA ATTCTATCAA CAGTCTCTG GATGAGTCTG 1080
 TGATTTATGG ACCAGGAAAC CTGTCAACCA ACAACAATAC TCTCAGAGAC CACTTCAAAG 1140
 GGATTTCCTC CCATAGCAGA AGCTCACTCA TGCCCTCTAG AAATGATGTG GATAAGAGAG 1200
 GGGAGACGAC CTCAGCATCC TTGCTAAATG CTGGATTAAG CCACACTGAA TACCAGATAG 1260
 65 TCACAGACCC TGGGACGTC CCAGCTTTTT TGAAATGGCT GTCCTTAGCC AGCTTGCTTG 1320
 TTTATGTTGC TGCTTTTICA ATTGGTCTAG GACCAATGCC CTGGCTGGTG CTCAGCGAGA 1380
 TCTTCTCTGG TGGGATCAGA GGACGAGCCA TGGCTTTAAC TTCTAGCATG AACTGGGGCA 1440
 TCAATCTCCT CATCTCGCTG ACATTTTGA CTGTAACCTA TCTTATGGC CTGCCATGGG 1500
 TGTGCTTAT ATATACAAT ATGAGTCTAG ATCTTATTGG CCGCCATGG GTGTGCTTTA 1560
 70 TATATACAAT CATGAGTCTA GCATCCCTGC TTTTGTGTG TATGTTTATA CCTGAGACAA 1620
 AGGGATGCTC TTTGGAACAA ATATCAATGG AGCTAGCAAA AGTGAAGTAT GTGAAAAACA 1680
 ACAATTTGTT TATGAGTCAT CACCAAGAAG AATTAGTGCC AAAACAGCCT CAAAAAGAA 1740
 AACCCAGGA GCAGTCTTTG GAGTGTAACA AGCTGTGTGG TAGGGGCAA TCCAGGCAGC 1800
 TTTCTCCAGA GACCTAATGG CCTCAACACC TTCTGAACGT GGATAGTGCC AGAACACTTA 1860
 75 GGAGGGTGTG TTTGGACCAA TGCATAGTTG CGACTCTCTG GCTCTCTTTT CAGTGTCTAG 1920
 GAACTGGTTT TGAAGAGACA CTCTGAAATG ATAAAGACAG CCTTTAATCC CCTCTCTCMC 1980
 CAGAAGGAAC CTCAAAGGT AGATGAGTA CAAGGTCTTA AGTATCTCT TTTCTGAGC 2040
 AGGATATCAG GTTAAAAAAA AAAAGTTACT GGCTGGTTTA ATACTTTCTA CTTTCTTCAC 2100
 AGAGCAGCCT TTGAATAGAC TATGTCTAG TGAAGACATC AACCTCCGCG TTAAGCTATG 2160
 80 TATGTATGGA GTCCTGCTGC AGCTTTATTA TGCAGACACA CAAGTGGTCT GGACATGAGG 2220
 GTACAGTTTC TGCTACCAA GACACTACTT GCATGGATC TTACGCAAAA AAGAACCAGA 2280

ACACACAGTG TGGACAACTG CCCATATATT CTATCTAGAT TAGGAGAGGG TCCTGGCTAG 2340
 GATTTTAGTG GTAATTCTTA GTTACATTCA ACAAGTATAA AGATTATAGA GCTTATTTA 2400
 TGAACATAAA ACTATAATTT AATGCAAAAT ATCCTTTTAT GAATTTCATG TTAATAATTG 2460
 GAAATATTAA AATAATTCR CAATAGTTGA GAAAAATGAG CATTITTTTC CATTITTTAA 2520
 5 AAATGCATAG AAAAGACAA TTTAAAATCC TGGGACCATA TTTATTTAGA AGTAGCTGTT 2580
 AGTAAACAT TAGAAAAGGA GTCAGGCCAT TAGGTTATTT ATCCAAATCT CTAAGCAATT 2640
 AGGTGGAAGT TATTAAGTCA AGCCTAGAAA AGCTGCCTCC TTGTAAGGCT TTCATGACAA 2700
 TGATATAGTAA TCCACAGTGT CCAATTCCT ACACCTCTCA GGAATATCAC TACCTCAGGT 2760
 10 TACGGTACAC AGGCTATAAT TGATGATGAT GTTCAGATAA CTGAAGACAC AATAAATGAC 2820
 ATTCAGACAT CAGGAMAAWW CCCTCATGTT CTTTCTATG ATGGCCACCT GTACCAGCAA 2880
 CGTGGGTTTC ACCCACACAA CGATGAACTG TTCTCTTACT TCTCCAGTTG ATTTTAAAGA 2940
 CTTGTTAAGA GGTCTTACTA ATAAAAATTT GGTATGATAG AAAAWCCACA ATCAAAWCTT 3000
 GAACCAATA ACATATTTAA TTAATAAT TTAAGTGATG GAAGACACAC AAAAAACTTA 3060
 15 AAAGCACGAA CAACCTAACT TGA AAAAGAA TTTTAAATA TGATTAACCT GAAGAAAAGA 3120
 GAATCCTAAG AGCCAAAGCT CTTTTTAT TAGCTTGGAA TTTTCTTAT GGITCCTAAC 3180
 AAACGTGCCC AATGTTCAT AAGGAAACAT GATCTATTAC ATTCTTTAT AACAATGTGG 3240
 AGAGACTATA AACCTATGTA AGTAGTAAAA CTATATYAGA GACTCAGGAG ACTGACTAAA 3300
 AGGCTGGAT CTGCACTGTA TTATCTGTAT AAAAATTGGC AGGGGGAAGC TAAAAGGAAA 3360
 GGAGATTGGA GATTCCTAAT CTATCATGGT GTATTTCATA CGCAAAATCAG AGCATGCATT 3420
 20 GTTTTTTGT TTTGGAAAGA GAAGGGAAGT GTGTTCTGCC CCATGTTTCC TCCGTGTTT 3480
 ATAGTICAAA CTCTATATAT ACTTCAGGTA TTTTGTGTT AGCCCTTCAT TATAAATGGG 3540
 CAGGAAATG TTTATCAACC TAGCCAGTTT ATTACTAGTG ACCTTGACTT CAGTATCTTG 3600
 AGCATCTTCT TATATTTTCT TTTTATATC CTGAGTCTGT AACTAAACAA TTTTGTCTTC 3660
 AAATTTTAT CCAATATCCA TGGACCCACA CCAAAATCAAG CTCTTGATT TCAAAAAATA 3720
 25 AAAAGGGGGA AATACITACA ACTGTACAT ATATATTCAC AGTTTTTAT TATAAAAAAA 3780
 ATTTACAGTA CTTATGGAGA GCCAGCAGAA GACATCAGAG CACTCACTTC TTCCATCTT 3840
 TGTTAAGGTT AGCGAATTAC CCATGGACAC TGTTAGGTGA GGCTCAITTCG GCAGCCCTGA 3900
 AAACAAACCT GGTACACACT TCTTTACCCT CTCCTTCAG ATAAAGCACT TCGATTATCT 3960
 ATTGATCTGC CCACTTTTCA AGTCATGCGA ATACTAAAAA GGTTACATCA TCTGGATCTG 4020
 30 TACCTTGGCT ATATAAGCAT GTTTTCCCCC TATTCTATGT TTTTTTTTT GGTGAACATT 4080
 GAAAAACAGG AGGTGACTTA TTACTGTATA TAAAACTAA ATGAAAAATG TCAAGTCTTT 4140
 AAAACAGTGA GCTGTAACT CTTTCATGTA ATTTTATCT CTATGAATT GGCTATCTTA 4200
 CTGAATCTTA AATAAAGGA AATAAACACT TTTTTTTWAA AAAAAAGGAA AATAAARW 4260
 35 MWAAAAATCT CAATGAAATA TTTACAAGA AGGAAAAA

SEQ ID NO:242 PBA7 Protein sequence:

Protein Accession #: AAF91431

40 MFTFLSSVTA AVSGLLVGYE LGHSGALLQ IKILLALSCH EQEMVVSSLV IGALLASLTG 60
 GVLDTRYGRR TAILSSCLL GLGSLVLILS LSYTVLIVGR LAIGVISLS SIATCVYIAE 120
 IAPQHRRGLL VSLNELMIVI GILSAYISNY AFANVFHGWK YMFGLVPLG VLQAIAMYFL 180
 PPSRFLVMK GQEGAAASKVL GRLRLSDTT EELTVIKSSL KDEYQSFWD LFRSKDNMRT 240
 45 RIMIGLTLVF FVQITGQPNL LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPATLL 300
 VDHVGSKTEL CIGSSVMAAS LVTMGIVNLN IHMNFTHICR SHNSINQSLD ESIVYGPQNL 360
 STNNNTLRDH FKGISSHRSR SLMLPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
 AFLKWLSLAS LLVYVAAFSI GLGPMPLVLV SEIFPGGIRG RAMALTSSMN WGINLLISLT 480
 50 FLTVDLIGL PWVCFITIM SLDLIGLPWV CFYITMSLA SLLFVVMFIP ETKGCSLEQI 540
 SMELAKVNYV KNNICFMSHH QEELVPKQPQ KRKPQEQLE CNKLCGRGQS RQLSPET

SEQ ID NO:243 PAB4 DNA sequence:

Nucleic Acid Accession#: AA172056

Coding sequence: 121-339 (underlined sequences correspond to start and stop codons)

TTTAGCCACC AGAGGANTTC TCTTGAATA CCCCCAATCC ATCAGTATCT TGAATCATGC 60
 TGGATTTTGA AGAATCTTAA AGAAGCCATG TAAAGGGGGC TCTCTGGCCT TGAATAGTG 120
 60 ATGTTTTTTTA TACAGAAAGG AGAATGCAGA ATGGTCAGAC TATCATGCAC TGTTAAATTT 180
 GATTCAAGA AATTACAGGA AAACCTTCCA AAGTTCCATC TCACAGAANN TTATTTINCC 240
 AAGAATTCCA AGATAAGTIT AGITTTATGG AAGACTTTTA TGTGGTTTTT ACTCACTCTT 300
 CATCTCAGAC ATCGACAGAT GATTACATCA CTTATAGTTC TAGTAAATTT ATTAATATAA 360
 AACTCAGAGA CATTTCAATA TCCACATGTC TTACACCAT AGGCATAGAT TCAGTGTGAG 420
 65 CTATGACAAT TGA AAAATGAG CTGTTTGTG ATTTAAAGGT TTAATTTCT CTAACCAAAC 480
 TGCTIGATCC AGATGCAGGA CTGCAAATGT TAATATTGT TCTGGAAGAA CAATCAAATA 540
 AGACTTAAGA GGAAGGGGAA TGGCCCAAT CCACCTGAAA TTTTCTTA AAAAGTGTGC 600
 AGCCTACTAA ATCAGAAATGA AAATAGAAAGT ACAAGATTAT AAACAAAATG CAATCAAAC 660
 TTTCTTAAGC TTACCTAAAG TTATTCATC TGA AAAATTT AAGCAACTTT GTTCAACATT 720
 70 AAATTGACAA TCTAAACTAA CAAGTCTTT GAATTTATGC ATGGTAGTAA ACATTCTCTC 780
 TATTAACTTT ATTACCTAAG GCTAAACCTA AAATTTTAA GCAAAAATTAG AAAAAATGTC 840
 TTCATCATC AAAAAATAAA GTTGTGTACA TTTAGTATTT TCCCAATAAA ATTGGTCTGT 900
 CTTGGTTTTT TATTGTGAGA GTCTGTGCAA AATGTCTACT AAAATAAATT AGCACTAGAA 960
 ATTATTTCTA AATACCAA

SEQ ID NO:244 PBQ8 DNA SEQUENCE

Nucleic Acid Accession#: X51405

Coding sequence: 3-1721 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

5
10
15
20
25
30
35
40

```

| AAATGGCGTG | CCGGTCTCTC | CGCCGGCCCC | CTGCTCGCA | GTGGTTTCTC | CTGCAGCTCC | 60
| CCTGGGCTCC | GCGGCCAGTA | GTGCAGCCCG | TGGAGCCGCG | GCTTTGCCCG | TCTCCTCTGG | 120
| GTGGCCCCAG | TGCGCGGGCT | GACACTCATT | CAGCCGGGGA | AGGTGAGGCG | AGTAGAGGCT | 180
| GGTGCGGAAC | TTGCCGCCCC | CAGCAGCGCC | GCGGGGCTAA | GCCCAGGGCC | GGGCAGACAA | 240
| AAGAGGCGCG | CCGCTAGGA | AGGCACGGCC | GCGCGCGCGG | GAGCGCAGCG | ATGGCCGGGC | 300
| GAGGGGCGAG | CCGCTGCTG | GCTCTGTGCG | GGGCACTGGC | TGCTGCGGG | TGGCTCCTGG | 360
| GCGCCGAAGC | CCAGGAGCCC | GGGCGCCCCG | CGCGGGGCAT | GAGCGGGCGC | CGCGGGCTGC | 420
| AGCAAGAGGA | CGGCATCTCC | TTGAGTACC | ACCGCTACCC | CGAGCTGCGC | GAGGCGCTCG | 480
| TGTCCGTGTG | GCTGCAGTGC | ACCGCCATCA | GCAGGATTTA | CACGGTGGGG | CGCAGCTTCG | 540
| AGGGCCGGGA | GCTCTGGTC | ATCGAGCTGT | CCGACAACCC | TGGCGTCCAT | GAGCCTGGTG | 600
| AGCCTGAATT | TAAATACATT | GGGAAATATG | ATGGGAATGA | GGCTGTGTGA | CGAGAAGTGC | 660
| TCATTTTCTT | GGGCCAGTAC | CTATGCAACG | AATACCAGAA | GGGGAACGAG | ACAATTGTCA | 720
| ACCTGATCCA | CAGTACCCGC | ATTCACATCA | TGCTTCCCT | GAACCCAGAT | GGCTTTGAGA | 780
| AGGCAGCGTC | TCAGCTGGT | GAACCAAGG | ACTGGTTGT | GGGTCGAAGC | AATGCCCAGG | 840
| GAATAGATCT | GAACCGGAAC | TTCCAGACC | TGGATAGGAT | AGTGACGTG | AATGAGAAAG | 900
| AAGGTGGTCC | AAATAATCAT | CTGTTGAAAA | ATATGAAGAA | AATTGTGGAT | CAAAACACAA | 960
| AGCTTGTCTG | TGAGACCAAG | GCTGTCAATC | ATTGGATTAT | GGATATTCCT | TTTGTGCTTT | 1020
| CTGCCAATCT | CCATGGAGGA | GACCTTGTGG | CCAATTATCC | ATATGATGAG | ACGCGGAGTG | 1080
| GTAGTGCTCA | CGAATACAGC | TCTCCCCAG | ATGACGCCAT | TTCCCAAAGC | TTGGCCCGGG | 1140
| CATACTCTTC | TTTCAACCCG | GCCATGTCTG | ACCCAATCG | GCCACCATGT | CGCAAGAATG | 1200
| ATGATGACAG | CAGCTTTGTA | GATGGAACCA | CCAACGGTGG | TGCTTGGTAC | AGCGTACCTG | 1260
| GAGGGATGCA | AGACTTCAAT | TACCTTAGCA | GCAACTGTTT | TGAGATCACC | GTGGAGCTTA | 1320
| GCTGTGAGAA | GTTCCCACT | GAAGAGACTC | TGAAGACCTA | CTGGGAGGAT | AACAACAACT | 1380
| CCTCATATG | CTACCTTGAG | CAGATACACC | GAGGAGTTAA | AGGATTGTCT | CGAGACCTTC | 1440
| AAGGTAACCC | AATTGCGAAT | GCCACCATCT | CCGTGGAAAG | AATAGACCAC | GATGTTACAT | 1500
| CCGCAAGGA | TGGTGATTAC | TGGGATTGCG | TTATACCTGG | AACTATATAA | CTTACAGCCT | 1560
| CAGCTCCAGC | CTATCTGGCA | ATAAACAAAG | AAGTGGCAGT | TCCTTACAGC | CCTGCTGCTG | 1620
| GGGTGTGATT | TGAATGGAG | TCATTTTCTG | AAAGGAAAGA | AGAGGAGAAG | GAAGAATTGA | 1680
| TGGAAATGGT | GAAATGATG | TCAGAAACTT | TAAATTTTAA | AAAAGGCTTC | TAGTTAGCTG | 1740
| CTTTAAATCT | ATCTATATAA | TGTAGTAGTA | TGTAAATGTT | TCTTTTCTTT | AGATTTTGTG | 1800
| CAGTTAATAC | TTAACATTTA | TTTATTTTCT | AATCAATTTA | ATATTAAATCA | ACTTTCCTTA | 1860
| AAATAAATAG | CCTCTTAGGT | AAAAAATATA | GAACTTGATA | TATTTCAATC | TCTTATATAG | 1920
| TATTCAATTT | CCTACCTATA | TTACACAAAA | AAGTATAGAA | AAGATTTAAG | TAAATTTGCC | 1980
| ATCTAGGCT | TAAATGCAAT | ATTCTGGTGA | TTATTTACAA | TGCAGAAATT | TTTGAGTAAT | 2040
| TCTAGCTTTC | AAAAATTAGT | GAAGTCTCTT | TACTGTAAAT | GGTGACAATG | TCACATAATG | 2100
| AATGCTATTG | AAAAGGTAA | CAGATACAGC | TCGGAGTTGT | GAGCACTCTA | CTGCAAGACT | 2160
| TAAATAGTTC | AGTATAAATT | GTCTTTTCTT | TCTGTGCTG | ACTAACTATA | AGCATGATCT | 2220
| TGTTAATGCA | TTTTGTATGG | GAAGAAAAGG | TACATGTTTA | CAAAGAGGTT | TTTGAAAAGG | 2280
| AATAAAATCT | GACTTCTTGC | TTGTACATAT | AGGAGCAATA | CTATTATATF | ATGTAGTCCG | 2340
| TTAACACTAC | TTAAGATTTT | AGGGTTTCT | CTGGTTGTA | GAGTGGCCCA | GAATTGCATT | 2400
| CTGAATGAAT | AAAGGTTAAA | AAAAAATCCC | CAGTGAAGAA | AAA

```

SEQ ID NO:245 PBQ8 Protein sequence

Protein Accession#: P16870

45
50
55

```

MAGRGGGALL ALCGALAACG WLLGAEAEQEP GAPAAGMRRR RRLQQEDGIS FEYHRYPELR 60
EALVSVWLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEFKYI GNMHIGNEAVG 120
RELLIFLAQY LCNEVYQKNE TIVNLIHSTR IHIMPSLNPD GFKAASQPG ELKDWVFGVRS 180
NAQGDILNRN FPLDRIYVY NEKEGGPNNH LLKNMKKIVD QNTKLAPETK AVIHWMIDIP 240
FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSPDDAIFQS LARAYSSFN AMSDENRPPC 300
RKNDDSSSFV DGTINGGAWY SVPGGMQDFN YLSSNCFEIT VELSCEKFPF EETLKTYWED 360
NKNLSLYLE QHHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSAKDGDY WRLLIPGNYK 420
LTASAFGYLA ITKKVAVPYS PAAGVDFELE SFSEKKEEEK HELMEVWKMM SETLNF

```

SEQ ID NO:246 PBV4 DNA sequence

Nucleic Acid Accession#: AF038966

Coding sequence:

91-1107 (underlined sequence corresponds to start and stop codon)

60
65
70
75
80

```

1 11 21 31 41 51
| | | | |
| GGGGCGACGT | GAGCGCGCAG | GGGGGCGGGG | GCCTCGCCTC | GTCTCTCTCT | CTGCGCCTGG | 60
| GTCCGGTGGG | TGACGCCGAG | AGCCAGAGAG | ATGTCGGATT | TCGACAGTAA | CCCGTTTGGC | 120
| GACCCGGATC | TCAACAATCC | CTTCAAGGAT | CCATCAGTTA | CACAAGTGAC | AAGAAATGTT | 180
| CCACCAGGAC | TTAGTGAATA | TAATCCATTC | TCGGATTCTA | GAACACCTCC | ACCAGGCGGT | 240
| GTGAAGATGC | CTAATGTACC | CAATACACAA | CCAGCATAAA | TGAAACCAAC | AGAGGAACAT | 300
| CCAGCTTATA | CACAGATTGC | AAAGGAACAT | GCATTGGCCC | AAGCTGAAGT | TCTTAAGCGC | 360
| CAAGAAGAAC | TAGAAAGAAA | AGCCGCAGAA | TTGATCGTGC | GGGAACGAGA | AATGCAAAAC | 420
| CTCAGTCAAC | ATGGTAGAAA | AAATATTTGG | CCACCTCTCT | CTAGCAATTT | TCCTTCGGGA | 480
| CCTTGTCTCT | ATCAGGAATT | TTCTGTAGAC | ATTCTGTAGT | AATTCACAAA | GACAGTAAAG | 540
| CTTATGTAAT | ACTTGTGGAT | GTTCCATGCA | GTACACTGT | TTCTAAATAT | CTTGCGATGC | 600
| TTGGCTTGGT | TTTGTGTGTA | TTCTGCAAGA | GCGGTTGATT | TTGGATTGAG | TATCCTGTGG | 660
| TTCTTGCTTT | TTACTCTTTG | TTCAATTGTC | TGTGTGTACA | GACCACTTTA | TGGAGCTTTC | 720
| AGGAGTGACA | GTTCATTTAG | ATCTTTGTA | TTCTTCTTCC | TCTATATTTG | TCAGTTTGGT | 780
| GTACATGTAC | TCCAAGCTGC | AGGATTTCAT | AACTGGGGCA | ATTTGGGTTG | GATTTCATCC | 840
| CTTACTGGTC | TCAACCAAAA | TATTCCTGTT | GGAATCATGA | TGATAATCAT | AGCAGCACTT | 900
| TTACAGCAT | CAGCAGTCAT | CTCAGTAGTT | ATGTTCAAAA | AAGTACATGG | ACTATATCGC | 960
| ACAACAGGTG | CTAGTTTGA | GAAGGCCCAA | CAGGAGTTTG | CAACAGGTGT | GATGTCCAAC | 1020
| AAAACTGTCC | AGACCGCAGC | TGCAAAATGCA | GCTTCAACTG | CAGCATCTAG | TGCAGCTCAG | 1080

```

5
10
15

```

AATGCTTTCA AGGCTAACCA GATTTAAGAA TCTTCAAACA ATACACTGTT ACCTTTTGAC 1140
TGTACCTTTT TCTCCAGTTA CTGTATTCTA CAAATATTTT TATGTTCAAA ACACACAGTA 1200
CAGACAGCAT GGATATTTC TGTTCACFIG TGCATGGGCT AAAACCAGGA AAACCTCCTT 1260
GTCTTATTAC TTTACCTAAT AGTTCTTCAA TATTTTCAGTG CCCCTTGCG AGAAAAATAT 1320
ACATGCTAAA TAAATATTCT CCATATTTT GGGGATGAC ATTCAGTGAA TTATTTTCA 1380
GGTGACCCAC TGAATTTTAA TATGGTACT TATGATTAAA AACGCATTTA ATACTAACTG 1440
CAGTAGTTCT TTTAGAGATC TTTAGAGATA AGGATTCAC ATTGGAAAAG TAAACCATGT 1500
TTCATTCTCT TTTCCCTATT TATATTGAAA GAAATAGGCC AGCAGAGACT TAGGGATTTT 1560
AAATGGCTT GCTTTTATG TGTTCAGTC ACCAGTGAAG AGCCTATGT CATTTGTAG 1620
TAGATAATGT AAAATTTGTC ATCTTTTCT TTTCTTTT TTAGAATAGC TGATATTTT 1680
ATAACATCT CTAAATTTGCA TGGGCACCAC ATTTCTTATA TTAAGAAGT TAGTGTTTT 1740
GCTTCGTAC TGTATTGGT TGTAGGATTC AGGGTTAAT GGAATCACAG AAATGATAT 1800
CTGCAAGAT TCTTTTAAA TAAAAAGTT GGGGTGCAA TATAAGAAG TTATATAATA 1860
TGCAGTACAT TATCCAAAG AGAAGGTAGT TAATGCAGTA GAAAGTAGT GTAATAATTC 1920
CTTTT

```

SEQ ID NO: 247 PB4 Protein sequence:

20
25

```

Protein Accession #:
MSDFDSNPFA DPDLNNPFKD PSVTQVTRNV PPLDEYNPF SDSRTPPGG VKMPNVPNTQ 60
PAIMKPTTEH PAYTQIAKEH ALAQALLKR QEELERKAAE LDRREREMQN LSQHGRKNW 120
PPLSNFPVG PCFYQESVD IPVEFQKTVK LMYLWMFHA VTLFLNIFGC LAWFCVDSAR 180
AVDFGLSLW FLLFTPCSFV CWYRPLYGAF RSDSSFRFFV FFFVYICQFA VHLQAAGFH 240
NWGNCGWISS LTGNNQIPV GIMMILAAL FTASAVISLV MFKKVHGLYR TTGASFEKAQ 300
QEFATGVMSN KTVQTAANA ASTAASSAAQ NAFKGNQI

```

SEQ ID NO: 248 PBH2 DNA sequence

30

```

Nucleic Acid Accession#: none found
Coding sequence: 1-613 (underlined sequence corresponds to start and stop codon)

```

35
40
45

```

ATGAGAGACA ATAAATCGTG TGCTTTTTC ATGGGAAAGT TAAATGTTT TTTGAAGGC 60
ACAGTAATAG CAGGCTATT AGTGTGTTGCC ACTACCTGCA TCATCATCT GGCTGTAGCT 120
AGTGCACATC AATTTCCTAA AAGTCTTCT CACCCTCACA GGACTGCTCT ACATCTGGCC 180
TCTGCCAATG GAAATTCAGA AGTAGTAAAA CTCCTGCTGG ACAGACGATG TCAACTTAAT 240
ATCCTTGACA AAAAAAGAG GACAGCTCTG ACAAAGGCCG TACAATGCCA GGAAGATGAA 300
TGTGCGTTAA TGTTGCTGGA ACATGGCACT GATCCGAATA TTCCAGATGA GTATGGAAAT 360
ACCGCTCTAC ACTATGCTAT CTACAATGAA GATAAATTA TGGCCAAAGC ACTGCTCTTA 420
TACGGTGCTG ATATCGAATC AAAAAACAAG CATGGCCTCA CACCCTGTT ACTTGGTGA 480
CATGAGCAAA AACAGCAAGT GGTGAAATTT TTAATCAAGA AAAAAGCAAA TTAAATGCA 540
CTGGATAGAT ATGGAAGGTG TGTGACCTTG GGAACGTTAT TTACCACCAA ATATGTTGTC 600
ATATATGAAA AGTAG

```

SEQ ID NO: 249 PBH2 Protein sequence:

50

```

Protein Accession #: none found
MRDNKSCAFF MGKLNVCFEF TVIAGYSVFA TTCIHLAVA SALQFPKSS HPHRTALHLA 60
SANGNSEVFF LLLDRRCQLN ILDNKKRTAL TKAVQCQDE CALMLEHGT DPNIPDEYGN 120
TALHYAIYNE DKLMAKALL YGADIESKNK HGLTPLLLGV HEQKQVVKF LIKKKANLNA 180
LDRYGRCVTL GTLFTTKYVV IYEK

```

SEQ ID NO: 250 PB1 DNA sequence

60
65
70
75

```

ATGGTGATCA TCTATCTTC TTTCTGCAAT TATTACATGG AGTTCTACAG AGAAGAGCTT 60
CCCCACATTG ACTATTTGAT TGACATTCAG TTTGCAACAG GAAAGGTTAC TCAGCCGGGA 120
GAGGACACTT CCTACCATCA ATGCGCTCAG CTGGAAGCCA GAGACGAAGG CACCGACAGT 180
TTATTATTAA ACAATGGCAG CAGCGCCACG CTGAAGACAC GAACGCGCTG TTATGGAACC 240
CCCAGAGGTC TCCCCCATCG TAGCCTGCTC CAGCCGACTC CGCCACATG TAAACGAAG 300
ATCAGGAGCA GATTTGAAGA ATTACAAAGT GAATGGTGC CAGTCAGCAT GTCAGAGACA 360
GACCACATAG CCTCTACTTC CTCTGATAAA AATGTTGGGA AAACACCTGA ATTAAGGAA 420
GACTCATGCA ACTTGTTC TGGCAATGAA AGCAGCAAAT TAGAAAATGA GTCCAACTA 480
TGTCAATTA ACACGTGATA AACTTTATGT CAACCTAATG AGCATAATA TCGAATTGAA 540
GCCCAGGAAA ATTATATTCC AGATCATGGT GGAGGTGAGG ATTCTGTGTC CAAAACAGAC 600
ACAGGCTCAG AAAATCTG ACAAATAGCT AATTTTCTA GTGAAATTT TGCTAAACAT 660
ATTTCAAAAA CAAATGAAAC AGAACAGAAA GTAACACAAA TATTGGTGGA ATTAAGGTCA 720
TCTACATTTC CAGAAATCAG TAATGAAAA ACTIATTCAG AAAGCCCTTA TGATACAGAC 780
TGCACCAAGA AATTATTTC AAAAAATAAG AGCGTTTCAG CATCAGAGGA TTTGTTGGAA 840
GAAATAGAAT CTGAGCTCTT ATCTACGGAG TTGCAGAAC ATCGAGTACC AAATGGAATG 900
AATAAGGGAG AACATGCATT AGTTCTGTTT GAAAAGTGTG TGCAAGATA ATATTTCAG 960
CAGGAACATA TCATAAAAAA GTTAATTAAA GAAAATAAGA AGCATCAGGA GCTCTTCGTA 1020
GACATTGTT CAGAAAAAGA CAATTTAAGA GAAGAATAA AGAAAGAACT AGAAACTGAG 1080
AAGCAGCATA TGAACACAA TAAACAGTTA GAATCAAGAA TAGAAGAACT TAATAAGAA 1140
GTAAAGCTT CCAGAGATCA ACTAATAGCT CAAGACGTTA CAGCTAAAAA TGCAGTTCAG 1200

```

CAGTTACACA AAGAGATGGC CCAACGGATG GAACAGGCCA ACAAGAAATG TGAAGAGGCA 1260
 CGCCAAAGAA AAGAAGCAAT GGTAAATGAAA TATGTAAGAG GTGAGAAGGA ATCTTTAGAT 1320
 CTTCGAAAGG AAAAAGAGAC ACTTGAGAAA AAACCTTAGAG ATGCAAAATA GGAACCTGAG 1380
 AAAAACTA ACAAATTAAT GCAGCTTTCT CAGGAGAAAG GACGGTTGCA CCAGCTGTAT 1440
 5 GAAACTAAGG AAGGCGAAAC GACTAGACTC ATCAGAGAAA TAGACAAATT AAAGGAAGAC 1500
 ATTAACCTCT ACGTCATCAA AGTAAAGTGG GCACAAAACA AATTAAGAGC TGAATGGAT 1560
 TCACACAAGG AAACCAAGAA TAAACTCAAA GAAACAACAA CAAAATTAAC ACAAGCAAG 1620
 GAAGAAGCAG ATCAGATACG AAAAACTGT CAGGATATGA TAAAAACATA TCAGGAGTCA 1680
 10 GAAGAAATTA AATCAATGA GCITGATGCA AAGCTTAGAG TCACAAAAGG AGAAGCTTGA 1740
 AAACAAATGC AAGAAAAATC TGACCAGCTA GAGATGCATC ATGCCAAAAT AAAGGAACTA 1800
 GAAGATCTGA AGAGAACATT TAAGGAGGGT ATGGATGAGT TAAGAACACT GAGAACAAAG 1860
 GTGAAATGTC TAGAAGATGA ACGATTAAGA ACAGAAGATG AATTATCAAA ATATAAGGAA 1920
 ATTATTAATC GCCAAAAAGC TGAAATTCAG AATTTATTGG ACAAGGTGAA AACTGCAGAT 1980
 15 CAGCTACAGG AGCAGCTTCA AAGAGGTAAG CAAGAAATITG AAAATTTGAA AGAAGAAGTG 2040
 GAAAGCTTAT ATCTTTGAT TAATGACCTA CAAAAGAGCA TCGAAGGCAG TAGGAAAAGA 2100
 GAATCTGAGC TGCTGTGTTT TACAGAAAGG CTCAGTAGTA AGAATGCACA GCTTCAGTCT 2160
 GAATCCAATT CTTTGCAGTC ACAATTTGAT AAAGTTTCT GTAGTGAAAG TCAGTTACAA 2220
 AGCCAGTGTG AAAAAATGAA ACAGACAAAT ATTAATTTGG AAAGTAGGTT GTTGAAAGAG 2280
 20 GAAGAACTGC GAAAAGAGGA AGTCCAAACT CTGCAAGCTG AACTCGCTTG TAGACAAACA 2340
 GAAGTTAAAG CATTGAGTAC CCAGGTAGAA GAATTAAGAG ATGAGTTAGT AACTCAGAGA 2400
 CGTAAACATG CCTCTAGTAT CAAGGATCTC ACCAAACAAC TTCAGCAAGC ACGAAGAAA 2460
 TTAGATCAGG TTGAGAGTGG AAGCTATGAC AAAGAAGTCA GCAGCATGGG AAGTCGTTCT 2520
 AGTTTCATCAG GGTCCCTGAA TGCTCGAAGC AGTGCAGAGG ATCGATCTCC AGAAATACT 2580
 25 GGGTCCCTCAG TAGCTGTGGA TAACTTTCCA CAAGTAGATA AGGCCATGTT GATTGAGAGA 2640
 ATAGTTAGGC TGCAAAAAGC ACATGCCCGG AAAAAATGAA AGATAGAATT TATGGAGGAC 2700
 CACATCAAAAC AACTGGTGGA AGAAATTAGG AAAAAACAA AAATAATTCA AAGTTATATT 2760
 TTACGAGAAG AATCAGGCAC ACTTCTTCA GAGGCATCTG ATTTTAACAA AGTTCATTTA 2820
 AGTAGACGGG GTGGCATCAT GGCATCTTTA TATACATCCC ATCCAGCTGA CAATGGATTA 2880
 ACATGGAGC TCTCTTTGGA AATCAACCGA AAATTACAGG CTGTTTTGGA GGATACGTTA 2940
 30 CTAATAAATA TTACTTTGAA GGAATACTA CAAACACTTG GAACAGAAAT AGAACGTCTT 3000
 ATTAACACCC AGCATGAACT AGAACAGAGG ACAAAGAAAA CCTAAAAACA GCCTCTTGCT 3060
 CAGTAAAGAG ACAAAGCCA CACAGGAGTA GGTGCCACTG ACCTCTATTG TTGGAGACTT 3120
 TGTTCACATT TTTGTTTCA CCAGTAAAAA TATGTTTTG CTTCATCTGT ACACAAAAAA 3180
 35 ATACCTTTT ACAATTGAA TGCATTGCTG TATATACTGT AAGACTGAAA GCTTTGATGA 3240
 AATTGTTTT TGTATGGTGC AATATGACAG CCTGTCTTGG AATCTAAACA ACTTAATTG 3300
 CTTGTATTCA TAAGAAGTGT TGAACATTAC AAGGCTTTT AT

40 Protein Accession #: SEQ ID NO:251 PB.J1 Protein sequence:
 NP_060487

45 MVIYLSFCN YMEFYREL PHIDYLDIQ FATGKVTQPG EDTSYHQCAQ LEARDEGTDS 60
 LLLNNGSSAT LKTRTRCYGT PRGLPHRSLL QTPPTCKTK IRSRFEELQS ELVPVSMSET 120
 DHIASTSDK NVGKTPELKE DSCNLFSGNE SSKLENESKL LSLNTDKTLC QPNEHNNRIE 180
 AQENYIPDHG GGEDSCKATD TGSENSEQIA NFPSGNFAKH ISKTNETQK VTQILVELRS 240
 50 STFPESANEK TYSESPYDID CTKKFISKIK SVSASEDLLE EIESELLSTE FAEHRVPNGM 300
 NKGEHALVLF EKCVDQKYLO QEHUUKLIK ENKKHQELFV DICSEKDNLR EELKKRTETE 360
 KQHMNTIKQL ESRIELNKE VKASRDQLIA QDVTAKNAVQ QLHKEMAQRM EQANKKCEEA 420
 ROKEAMVMK YVRGEKESLD LRKEKETLEK KLRDANKLE KNTNKKIKLS QEKGRHLQLY 480
 ETKEGETRL IREIDKLKED INSHVIKVKW AQNKLKAEMD SHKETDKLK ETTTKLTQAK 540
 55 EADQIRKNC QDMIKTYQES EIKSNELDA KLRVTKGELE KQMQEKSDQL EMHHAKIKEL 600
 EDLKRITFEG MDELRLTRTK VKCLEDERLR TEDELSKYKE INNRQKAEIQ NLLDKVKTAD 660
 QLQELQQRKQ QEHENLKEBV ESLNSLINDL OKDIEGSRKR ESELLLFTER LTSKNAQLQS 720
 ESNSLQSQFD KVSSESQLO SQCEQMKQTN INLESRLKE EELRKEEVQT LQELACRQT 780
 EVKALSTQVE ELKDELVTOR RKHASSIKDL TKQLQARRK LDQVESGSYD KEVSSMGSRS 840
 SSSGSLNARS SAEDRSPENT GSSVAVDNFP QVDKAMLIER IVRLQKAHAR KNEKIEFMED 900
 HIKQLVEEIR KTKTKIYSYI LREESGLTSS EASDFNKVHL SRRGIMASL YTSHPADNGL 960
 60 TLELSLEINR KLQAVLEDTL LKNITLKENL QTLGTEIERL IKHQHELEQR TKKT

65 SEQ ID NO:252 PB.J6 DNA sequence
 Nucleic Acid Accession#: D83760
 Coding sequence: 56-1459 (underlined sequence corresponds to start and stop codon)

65 1 11 21 31 41 51
 TTGCCGTGAA GGGCTGTGCG GTTCCCGTGC GCGCCGGAGC CTGCTGTGCG CTCTTATGCA 60
 CTCACCAACC CCATCATGCT CCCTCTTCTC CTTCACCAAG CCCGCACTGA AGAGACTGCT 120
 70 AGGCTGGAAG CAAGGAGATG AAGAGGAAAA GTGGGCAGAG AAGGCACTGG ACTCTCTAGT 180
 GAAGAAGTTA AAGAAGAAGA AGGAGGCAAT GGACGAGCTG GAGAGGGCTC TCAGCTGCC 240
 GGGCAGACCC AGCAAAATGCC TCACGATTCC CCGCTCCCTG GACGGGCGGC TGCAGTGTGC 300
 CCACCGCAAG GGCCTGCCCC ATGTGATTTA CTGTGCGCTG TGGCGCTGCG CGGATCTGCA 360
 GTCCCAACAC GAGCTGAAGC CGCTGGAGTG CTGTGAGTTC CCATTTGGCT CCAAGCAGAA 420
 AGAAGTGTGC ATTAACCTTT ACCACTACCG CCGGGTGGAG ACTCCAGTAC TGCCTCTGT 480
 75 GCTCGTGCCA AGACACAGTG AATATAACCC CCAGCTCAGC CTCTGGCCA AGTTCGCGAG 540
 CGCCTCCCTG CACAGTGAGC CACTCATGCC ACACAACGCC ACCTATCCCT ACTCTTTCCA 600
 GCAGCTCCG TGCTCTGCAC TCCTCTCCCT ACCCAGCCAC GCGTTCTCCC AGTCCCGCTG 660
 CACGGCCAGC TACCTCACT CCACAGGAAG TCCTTCTGAG CCAGAGAGTC CCTATCAACA 720
 CTCAGTTGAC ACACCACCCC TGCCCTATCA TGCCACAGAA GCCTCTGAGA CCCAGAGTGG 780

5 CCAACCTGTA GATGCCACAG CTGATAGACA TGTAGTGCTA TCGATACCAA ATGGAGACTT 840
 TCGACCAAGTT TGTACGAGG AGCCCCAGCA CTGGTGCTCG GTGCGCTACT ATGAAC TGAA 900
 CAACCCGAGTT GGGGAGACAT TCCAGGCTTC CTCCCGAAGT GTGCTCATAG ATGGGTTTAC 960
 CGACCCCTTCA AATAACAGGA ACAGATTCTG TCTTGGACTT CTTTCTAATG TAAACAGAAA 1020
 CTCACACGATA GAAAATACCA GGAGACATAT AGGAAAGGGT GTGCACCTGT ACTACGTCGG 1080
 GGGAGAGGTG TATGCCGAGT GCGTGAGTGA CAGCAGCATC TTTGTGCAGA GCCGGAAC TG 1140
 CAACTATCAA CACGGCTTCC ACCCAGCTAC CGTCTGCAAG ATCCCGACGG GCTGCAGCCT 1200
 CAAGGTCTTC AACCAACGAG TCTTCGCTCA GCTCCTGGCC CAGTCAGTTC ACCACGGCTT 1260
 10 TGAAGTCGTG TATGAAC TGA CCAAGATGTG TACTATCCGG ATGAGTTTGT TTAAGGGTTG 1320
 GGGTGCTGAG TATCATCGCC AGGATGTGAC CAGCAGCCCG TGCTGGATTG AGATTCTATCT 1380
 TCATGGGCCA CTGCAAGTGG TGGACAAAGT TCTGACTCAG ATGGGCTCTC CACATAACCC 1440
 CATTTCTTCA GTGTCTTAAC AGTCATGTCT TAAGCTGCAT TTCCATAGGA T

15 **SEQ ID NO:253 PBj6 Protein sequence:**
 Protein Accession #: NP_005896

20 MHSTPISSL FSFSPAVKR LLGWKQGDDE EKWA EKAVDS LVKKLKKKKG AMDELERALS 60
 CPGQPSKCVT IPRSLDGR LQ VSHRKG LPHV IYCRVWRWPD LQSHHE LKPL ECCEFFPGSK 120
 25 KQEV CINPYH YRRVETPVLP PVLVPRHSEY NPQLSLLAKF RSASLHSEPL MPHINATYPD 180
 FQQPSPCALP PSPSHAFSQS PCTASYPHSP GSPSESPY QHSVDTPLP YHATEASETQ 240
 SGQPV DATAD RHVVLSPNG DFRPV CYEEP QHWCSVAYYE LNNRVGETFQ ASSRSLVDG 300
 FTDPSNNRRN FCLGLLSNVN RNSTIENTRR HIGKGVHLYY VGEVYAE CV SDSSIFVQSR 360
 NCNYQHGFHP ATYCKIPSGC SLKVFNQLF AQLLAQSVHH GFVVYELTK MCTIRMSFVK 420
 GWGA EYHRQD VSTPCWIEI HLHGFLQWLD KVL TQMGSFPH NPISSVS

30 **SEQ ID NO:254 PBj8 DNA sequence**
 Nucleic Acid Accession#: AB04684
 Coding sequence: 472-4377 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
 | | | | | |
 TGCAGGTTTG CAGGGTCTGA GATTACTTGG GCTTTTCCTG CTTTTCCTT TTGCTTAAGG 60
 GATGGACAAG GAGCTGAGAT TTATGACCTT TATTAGAGAA AAAAATGTGC CTTCCTAGGG 120
 TGGGGACACT TGGTTGATGC AGTCTCTCTC TCTCTTTCTC GGTGTTTATA ACAAACAAA 180
 ACCAAAATGA ACTGAGGGGT TTGTAATGGT AGTTTGTTTG TTGCTGGAGA ATGCTACTTT 240
 GCATGCTTTT TTTCTCTTGC AGGGTATGTT CTGTCTTGTG CTTTTCCTTT TAGAAGCTAC 300
 40 TAAAGGGTGT TGGGGATGCT TCTGACTATT ATGAAGGCCA AAAGGCCGTG TGAAGCTGGG 360
 TGCTTTTAACT CCTTTCCTAT TTGCTGAGAA TGCAGCCGTG TGACAGTAAC TGAACATTGG 420
 TCTAAAGTCT TTCCAAAAGG TCAAGGTTCA CAAGAATATC TGCTCAAAAT AATGACCATG 480
 GGGGATATGA AGACCCGAGA CTTTGATGAC CTCCGCGCAG CATTTGACAT CCCAGATATG 540
 GTCGATCTCT AAGCAGCTAT TGAGTCTGGA CACGATGACC ATGAAGGCCA CATGAAGCAG 600
 45 AATGCTCAGC GAGAGGATGA CTCCACGCGA CCATCATCTT CTGATGTGGG TGTCAGCGTT 660
 ATCGTCAAGA ATGTTTCGGA CATTGACTCT TCCGAGGGCG GGGAGAAAGA CGGCCACAAC 720
 CCCACTGGCA ATGGCTTACA TAATGGGTTT CTACACGATC CTTCCTTGA CAGTTACAGT 780
 AAAGATGGAG CAAGTCTCTT GAAAGGAGAT GTGCTGCGCT CTGAGGTGAC ACTGAAAGAC 840
 TCGACATTTA GCCAGTTTAA CCCGATCTCC AGTGCTGAAG AGTTTGATGA CGACGAGAAG 900
 50 ATTGAGGTGG ATGACCCCCC TGACAAGGAG GACATGCGAT CAAGCTTCAG GTCGAATGTG 960
 TTGACGGGGT CGGCTCCCCA GCAGGACTAC GATAAGCTGA AGGCACTCGG AGGGGAAAAA 1020
 TCCAGCAAAA CTGACTCTCT TACGTCAGGC AATGTGGAGA AAAACAAAGC TGTTAAGAGA 1080
 GAAACAGAAG CCAATCTCTAT AAACCTGAGT GTTTATGAAC CTTTAAAGT CAGAAAAGCA 1140
 GAGGATAAAT TGAAGGAAAG CTCTGACAAG GTGCTGGAAA ACAGAGTCTC AGATGGGAAG 1200
 55 CTGAGCTCGG AGAAGATGA CACGAGCTC CCCAGCGTTG CGCATCAAA GACAAAGTCG 1260
 TCCTCCAAGC TCTCGTCTCG CATCGCTGCC ATCGCGGCTC TCAGCGCTAA AAAGCGCGCT 1320
 TCAGACTCTC GCAAGGAACC AGTGGCCAAT TCGAGGGAAT CCTCCCGGTT ACCAAAGAA 1380
 GTAAATGACA GTCCGAGAGC CGCTGACAAG TCTCTCTGAA CCCAGAACTC CATCGACGGG 1440
 ACCAAAAAAC CATCCCTGAA GCAACCGGAT AGTCCAGAA GCATCTCAAG TGAGAACAGC 1500
 60 AGCAAAAGGAT CCCCCTCTCT TCCCGCAGGG TCCACACCAG CAATCCCAA AGTCCGCATA 1560
 AAAACCATTA AGACATCTTC TGGGGAAATC AAGAGAACAG TGACAGGGT ATTGCCAGAA 1620
 GTGGATCTTG ACTCTGGAAG GAAACCTTCC GAGCAGACAG CGTCCGTGAT GGCCTCTGTG 1680
 ACATCCCTTC TGTCGTCTCC AGCATCAGCC GCCGTCTTTT CCTCTCCCC CAGGCGCCT 1740
 CTCCAGTCTG CGGTCTGTGAC CAATGCAATT TCCCCTGCAG AGCTCACCCC CAACAGGTC 1800
 65 ACAATCAAGC CTGTGGCTAC TGCTTTCTCT CCAGTGTCTG CTGTGAAGAC GGCAGGATCC 1860
 CAAGTCATTA ATTTGAAGCT CGCTAAACAAC ACCACGGTGA AAGCCACGGT CATATCTGCT 1920
 GCCTCTGTCC AGAGTGCCAG CAGCGCCATC ATTAAGAGCTG CCAACGCCAT CCAGCAGCAA 1980
 ACTGTCTGTG TGCCGGCATC CAGCCTGGCC AATGCCAAAC TCGTGCCAAA GACTGTGCAC 2040
 CTTGCCAACC TTAACCTTTT GCCTCAGGGT GCCCAGGCCA CCTCTGAAC CCGCCAAGTG 2100
 70 CTAACCAAAAC CTCAGCAACA AATAAAGCAG GCAATAATCA ATGCAGCAGC CTGCAACACC 2160
 CCCAAAAAGG TGCTCTGAGT CCAGGTGGTG TCGTCTTTCG AGAGTCTGTG GTTGGGAAGT 2220
 TTCAACAAAG TGCTGAGCAG TGTCAATCCA GTCCCTGTTT ACATCCCAA CCTCAGTCTC 2280
 CCGCCCAATG CAGGGATCAC GTTACCGACG CGTGGGTACA AGTGCTTGA GTGTGGGGAC 2340
 TCCTTTGTCAC TTGAAAAGAG TCTGACCCAG CACTACGACA GACGGAGCGT GCGCATCGAA 2400
 75 GTAAAGTGCA ACATGTTGAC AAAGAACCTC GTTTTPTTACA ACAAATGCAG CCTCCTTTCC 2460
 CATGCCCGTG GGCATAAGGA GAAAGGGGTG GTAATGCAAT GCTCCCACTT AATTTTAAAG 2520
 CCAGTCCAG CAGATCAAT GATAGTTTCT CCGTCAAGCA ATACTTCCAC TTCACTTTCC 2580
 ACTCTTCAGA GCCCTGTGGG AGCTGGCACA CACACTGTCA CAAAAATICA GTCTGGCATA 2640
 ACTGGGACCT TCATATCGGC TCCTTCAAGC ACTCCCATCA CCCCAGCCAT GCCCTTAGAT 2700
 80 GAAGACCCCT CCAAACTGTG TAGACATAGT CTAATAAGTT TGGAGTGTA TGAAGTCTTC 2760
 CAGGACGAGA CATCACTGCG TACACATTTT CAGCAGGCTG CAGATACGAG TGGACAAAAG 2820

5 ACTTGCACCTA TCTGCCAGAT GCTGCTTCCT AACCAGTGCA GTTATGCATC ACACCAGAGA 2880
 ATCCATCAGC ACAAATCTCC CTACACCTGC CCTGAGTGTG GGGCCATCTG CAGGTCGGTG 2940
 CACTTCCAGA CCCACGTCCAC CAAGAAGTGT CTGCACATCA CGAGGAGAGT TGGTTTTCGA 3000
 TGTGTGCATT GCAATGTTGT GTACTCTGAT GTGGCTGCTC TGAAGTCTCA CATTCAAGGT 3060
 TCTCACTGTG AAGTCTTCTA CAAGTGTCTT ATTTGTCCAA TGGCGTTTAA GTCTGCCCCA 3120
 AGCACACATT CCCACGCTTA CACACAGCAT CCTGGCATCA AGATAGGAGA ACCAAAAATA 3180
 ATATATAAGT GTTCCATGTG CGACACTGTG TTCACCTGCG AAACCTTGCT GTATCGCCAC 3240
 TTTGACCAAC ACATTGAAAA CCAGAAGGTG TCTGTTTTCA AGTGTCCAGA CTGTTCTCTT 3300
 TTATATGCAC AGAAGCAACT TATGATGGAC CATATCAAGT CTATGCATGG AACATTGAAA 3360
 10 AGTATTGAAG GGCCTCCAAA CTTGGGTATA AACTTGCCCT TGAGCATTAAG GCCTGCAACT 3420
 CAAAATTGAG CAAATCAGAA CAAAGAGGAC ACCAAATCCA TGAATGGGAA AGAGAAATTG 3480
 GAAAAGAAAT CTCCATCTCC TGTGAAAAAA TCAATGGAAA CCAAGAAAGT GGCCAGTCTT 3540
 GGGTGGACGT GTTGGGAGTG TGACTGCCTG TTCATGCAGA GAGATGTGTA CATATCCAC 3600
 GTGAGGAAGG AGCAGGGGAA GCAAAATGAAG AAACACCCCT GCCGCCAGTG TGACAAGTCT 3660
 15 TTCACTCGT TTGCGGCTG GTGCCGGCAC AACCAGATCA AGCACAAGG CATCAGGAAA 3720
 GTGTACGCTT GCTCGCACTG CCCAGACTCC AGACGTACCT TTACCAAAACG TTTGATGCTG 3780
 GAGAAGCAGC TCCAGCTGAT GCATGGCATC AAGGACCCCT ACCTGAAAGA AATGACAGAT 3840
 GCCACCAATG AGGAGGAAAC AGAAATAAAA GAAGACACTA AGGTCCCCAG TCCCAAGCGG 3900
 AAGTTGAAG AACCACTTCT GGAGTTTCAAG CCTCCCGAG GAGCAATCAC TCAACCACTG 3960
 20 AAAAAAGCTG AATCAATGT TTTTAAGGTT CACAAGTGTG CCGTGTGTGG CTCACCACT 4020
 GAAAACCTGC TGCATTTCCA CGAACACATC CCTCAGCACA AATCGGATGG TTCTTCTTAC 4080
 CAGTGCCTGG AGTGTGGCTT CTGCTACACG TCTCAGCTCT CTCTGTCCAG GCACCTCTTC 4140
 ATCGTACACA AGTTAAAGGA ACCTCAGCCA GTGTCCAAGC AAAATGGGGC TGGGGAGAGT 4200
 AACCAACAGG AGAACAACCC CAGCCACGAG GATGAATCCC CTGATGGCGC CGTGTGAGAC 4260
 25 AGAAAGTGCA AAGTCTGCGC AAAAACTTTT GAACTGAAG CTGCCCTTAA TACTCACATG 4320
 CGGACACAGC GCATGGCCCTT CATCAATCC AAAAGGATGA GCTCAGCCGA GAAATAGCCA 4380
 CAGATGCTCC ATGAGGAAAA TCCCTGTCCA CATTTGAATA AAAAAAGCAT TTTTGTATCA 4440
 AAGTTTGCAG TATAATAGAG TTAACAGTAC TGCTAGGCTT GTTGCAATAT ATTCTCTTTC 4500
 30 AATGTACCTT CCTTACCTCT GTCGTATATA TCCTCGATAA GTATTAAAC AGTATTGAG 4560
 TTTAAAAGAG TTTGTATATA TTTAAATGAA TAACTTTTTA TACTCTTTGT TACATGTTTG 4620
 TATCAGTATT TAGTGGAAAA CCATTTGAGT TGTTTTGGGT TAGAATTTT CTTTGTGTAC 4680
 TGTTTCTTTA AAACAGAGTT CTTAGTAACA GGGCAGTTTC CTGAATTCAA ATAAACCAAT 4740
 35 TTGTATGTTT GATTTTGAAT TGGGTTAACT AATTACAGGC TAAATTAATG CCTTTTGTAG 4800
 TGTTTTAAAT TTTTAGAATT CACTACATAA ATTGTAAGTA ATTGTGGGTC TCAAAAACAC 4860
 TAGGAACCTT TAAGTGTCTT AGCACTTCTT CGATGTGCTT GCCCTGAGGG AGTGAGTTCA 4920
 CATTTGAGAC AACTGCTACT CAGTGTGGAC GTGCCCTTGT CTTCAGGCCA TGCCGAAGGG 4980
 TGTTTAAAGC AGTCTTGAGC GTCGCTCCTT TCCAGCCCGT GGATAAAAC TGAAGCTAGG 5040
 40 AATCTAATAA GGAATGCTGA TTTCTTCACT TCCATTTTGA GGAATGGGGA AGGCTATTCT 5100
 AAAGAAAAAA ATGGGATTGT TTTTCTCGGC AGATCTGCRA GGCTGGCTTT AAGAGCACAA 5160
 GGAGGGAAAG TAACGAAAGG GCTGGACTAC TATAAAAGTT ACAAATACGT AGTTAGACCA 5220
 ATAGATTTAT ATAGTCAGGT TTTTGTCTAT TAATTTATTA ACTAACTATT ACAGAAACAC 5280
 AGCTAAGAAAT ATCAAGTATT TCTCTGGCTC TTGACAGAAA AAAATCAGTT GACTTAACCC 5340
 45 TTTGCTGTCA AAAGAGTTGG CGTTTCTCTT TCTGGGTGCT ACTGCCAAC GTTATGGTAT 5400
 TTAGAGTCGG GATGCACAAC TTCAACCAAC GACTTATCAA TGCAGCCGCC TGTGTATTGC 5460
 AATTGGCCGT TACCTTAAGC ACTGAGCCAC CCGGGTTTAG TTCAGCCAT TCAAGAAAGTA 5520
 TATTTAAGCT CGGTAGTTCT GCTTTATTAA AATGAGCAG AGGTACTCTT CTGTCCCTTC 5580
 CGTTTATAGT TCTCTGAGAG AGTTCTATT TTTGGTTTGT TTTTGTGTTT TCTTTTGCAT 5640
 TTTGTATCTT GTATTATATC CTGAACATGT TTTGTACCTT TTTTTTTTTT TTTTFTTTAA 5700
 50 GAAAAGGAAT TCTTTTGTGT ATATATAGAT ACTTGATGTA TATACTGTAG TCAATGTTGC 5760
 GTTCTTCAAA AGGTCTTGCT GCTGTGAGGT GTTATGCAT CCATCCATCA TAACTGTATG 5820
 AAACACATTT CATATGTAAA TAAACGTGGG ACATTTG

55 Protein Accession #: SEQ ID NO:255 PBJ8 Protein sequence:
 BAB13455

MKTPDFDDLL AAFDIPDMVD PKAAIESGHD DHESHMKQNA HGEDDSHAPS SSDVGVSVIV 60
 KNVRNIDSS EGEKDGHNPT GNGLHNGFLT ASSLDSYSKD GAKSLKGDVP ASEVTLKDST 120
 60 FSQFSPISSA EEFDDDEKIE VDDPPDKEDM RSSFRSNVLT GSAQQDYDK LKALGGENSS 180
 KTGSTSGNV EKNKAVKRET EASSINLSVY EPFKVRKABD KLESSDKVL ENRVLDGKLS 240
 SEKNDTSLPS VAPSKTKSS KLSSCIAALA ALSAKKAASD SCKEPVANSR ESSPLKEVN 300
 DSPRAADKSP EQNLIDGDK KPSLKQPDSP RSISSENSSK GSPSPAGST PAIPKVRKLT 360
 IKTSSGEIKR TVRVLPEDV LDGKKPSEQ TASVMASVTS LLSPASAAV LSSPPRAPLQ 420
 SAVVTNAVSP AELTPKQVTT KPVATAFLPV SAVKTAGSQV INLKLANNIT VKATVISAAS 480
 65 VQSASSAIK AANAQQQTV VVPASSLANA KLVPKTVHLA NLNLLPQGAQ ATSELRQVLT 540
 KPQQQIKQAI INAAASQPPK KVSRRVQVSS LQSSVVEAFN KVLSSVNPVP VYIPNLSPPA 600
 NAGITLPTRG YKCLECGDSF ALEKSLTQHY DRRSVRIEVT CNHCTKNLVE YNKCSLLSHA 660
 RGHEKEGVVV QCSHLILKPV PADQMIVSPS SNTSSTSTL QSPVVGAGTHT VTKIQSGITG 720
 70 TVISAPSSPT ITPAMPLDED PSKLCRHSK CLECNVFDQ ETSLATHFQ AADTSQGKTC 780
 TICQMLFPNQ CSYASHQRH QHKSPTYCPE CGAICRSVHF QTHVTKNCLH YTRRVGFRVC 840
 HCNVVYSDVA ALKSHIQGSH CEVFFYKCPIC PMAFKSPST HSHAYTQHPG IKIGEPKHY 900
 KCSMCDTVFT LQILLYRHFD QHIENQKVSF FKCPDCSLY AQKQLMMDHI KSMHGTLSI 960
 EGPNPLGNL PLSIKPATQN SANQKEDTK SMNGKEKLEK KSPSPVKKSM ETKKVASPGW 1020
 75 TCWEDCLFM QRDVYISHVR KEHGKQMKKH PCRQCDKSF SSSHLSCRHNR IKHKGIRKVV 1080
 ACSHPDSRR TTFKRLHGIK HVQLMHGIK PDLKEMTDAT NEHETEIKED TKVPSPKRKL 1140
 EEPVLEFRFP RGAITQLKK LKINVKVHK CAVCGFTTEN LLQFHEHIP HKSDGSSYQC 1200
 RECGLCYTSH VSLSRHLFIV HKLKEPQPV KQNGAGEDNQ QENKPSHEDE SPDGAVSDRK 1260
 CKVCAKTFT EALNTHMRT HGMATIKSKR MSSAEK

SEQ ID NO:256 PBM1 DNA sequence

Nucleic Acid Accession#: AF111847

Coding sequence: 58-1608 (underlined sequence corresponds to start and stop codon)

5 1 11 21 31 41 51
 | | | | | |
 TTTTCGTCGA CTCCTACCGG TTGGCTGGGC CAGCTGCGCC GCGGCTCACA GCTGACGATG 60
 GGGGACCCCA GCAAGCAGGA CATCTTGACC ATCTTCAAGC GCCTCCGCTC GGTGCCCACT 120
 AACCAAGGTGT GTTTTGATTG TGGTGCCAAA AATCCCAGCT GGGCAAGCAT AACCTATGGA 180
 GTGTTCCTTT GCATTGATTG CTCAGGGTCC CACCGGTAC TTGGTGTTC CTTGAGTTT 240
 ATTGCATCTA CAGAGTTGGA TTCCAACATG TCATGGTTTC AGTTGCGATG CATGCAAGTC 300
 GGAGGAAACG CTAGTGATC TTCCCTTTT CATCAACATG GGTGTTCAC CAATGACACC 360
 AATGCCAAGT ACAACAGTCG TGCTGCTCAG CTCTATAGGG AGAAAATCAA ATCGCTCGCC 420
 TCTCAAGCAA CACGGAAGCA TGGCACTGAT CTGTGGCTTG ATAGTTGTGT GGTTCACCT 480
 15 TTGTCCCTCT CACCAAAGGA GGAAGATTTT TTTGCTCTC ACCTTTCTCC TGAGGTGAGT 540
 GACACAGCGT GGGCATCAGC AATAGCAGAA CCATCTTCTT TAACATCAAG GCCTGTGGAA 600
 ACCACTTTGG AAAATAATGA AGGTGGACAA GAGCAAGGAC CAAGTGGA AGGTCTTAAT 660
 GTACCAACAA AGGCTACTTT AGAGGTATCC TCTATCATAA AAAAGAAACC AATCAAGCT 720
 20 AAAAAAGGCC TTGGGGCCAA AAAAGGAAGT TTGGGAGCTC AGAACTGGC AAACACATGC 780
 TTTAATGAAA TTGAAAACA AGCTCAAGCT GCGGATAAAA TGAAGGAGCA GGAAGACCTG 840
 GCCAAGGTGG TATCTAAGAA AGAATCAATT GTTTCATCAT TACGATTAGC CTATAAGGAT 900
 CTTGAATATC AAATGAAGAA AGACGAAAG ATGAACATTA GTGGCAAAA AATGTGTGAC 960
 TCAGACAGAG TCGCATGCGG ATTTGGAAAT TGCAGAAGTG TTATTTCACA TTCAGTCACT 1020
 25 TCAGATATGC AGACCATAGA GCAGGAATCA CCCATTATGG CAAAACCAAG AAAAAAGTAT 1080
 AATGATGACA GTGACGATTC ATATTTTACT TCCAGCTCAA GTTACTTTGA CGAGCCAGTG 1140
 GAGTTAAGGA CAGGTTCTTT CTCTAGCTGG GATGACAGTT CAGATTCTTA TTGGAAAAA 1200
 GAGACACAGA AAGATACTGA AACAGTTCTG AAAACCCAG GCTATTTCAGA CAGACCTACT 1260
 GCTCGCCGCA AGCCAGATTA TGAGCCAGTT GAAAATACAG ATGAGGCCCA GAAGAAGTTT 1320
 30 GGCAATGTA AGGCCATTPC ATCAGATATG TATTTTGGAA GACAAATCCA GGCTGATTAT 1380
 GAGACACAGG CCCGCCTAGA GAGGCTGTGG GCAAGTTCCCT CCATAAGCTC GGCTGATCTG 1440
 TTCGAGGAGC CGAGGAAGCA GCCAGCAGGG AACTACAGCC TGTCAGTGT GCTGCCCAAC 1500
 GCCCCGACA TGGCGCAGTT CAAGCAGGGA GTGAGATCGG TTGCTGAAA ACTCTCCGTC 1560
 TTTGCTAATG GAGTCGTGAC TTCAATTCAG GATCGCTACG GTTCTTAATA CTGAAGTCAT 1620
 35 GATGTGTATT TCCTGGAGAA ATTCTCTTTT AAATGAACAA GTAAACACAT CTAGGCCGGC 1680
 AGTGAAGTCC AGATAGTTT GCAGATTGTT TTGCTACTTT TTCATATGTT ATATGTTTCT 1740
 GATTTTAAAT ATTTCTTTTG AGAAATTCG AGTTCTGATG TAGGAGCTTT CCTGTGATTT 1800
 CTGTTTCAGG TTCCTTCTG TCACACCCCT CTTTGGCGTC TCTGTGTATA TCCTTGCTTT 1860
 ATTTTCTTGG AACCTTTGAT TTCAACACTG AGGGCCTGGA GACCTCGGCT CCTCCTGCTC 1920
 40 CTGAACCCAG AGGCTTCTG TGGGGGAGGA GGAGAGGTCT CCATGTGACA CATGGGCTCA 1980
 GGGCTGCCAG AATCAGCGGA TGCTGGATGG GCCTGCAGAA ACAACACTCA CCACACACAC 2040
 TTCCTTCAAA AGACCAAAAG TGACTGGTGT CTCGTGTGAC AGATTGCTTC ATTTATGTTT 2100
 CTACATAGTA AGGTGACTGC CAAATAATAT TTGAAGTCAT CTGCTCTTT GTAAATTAAT 2160
 TTATATGACC TATAAATTTA AAAATGTTT TCAGTGAGTG CTTTAAACAA ACTTAAGCTT 2220
 45 CTGCCCTGCC AAGGGAATTA ATGTTATCTT GTGAAAGGTG TTGCTGTTTG AATTGATGAG 2280
 AAATGAAGA TGAGAACTCC CTAAGAGTTC TCATAATAAA TCATCTCATC ACAATCAAT 2340
 ACGGTATACA GAGTTAAAGT GGAATGAGGT AAGAAGATAC AGCTACAGAA AATAGTTGCG 2400
 TGTATGGGAG AACAGTCATT GTAATTGGGT AGTTTGTGTA ATAAATATTT TTAATCTTGG 2460
 CTTTTCAGAA ATTACCGAAT GTGTATAAAC AAATAAGAA AATAATTTA GCTGTGTTT 2520
 50 AGACACGATT AGAATATATT GTTCAGCACA GTAAATATA TTTGAAATTT GATAAGCCAA 2580
 AAATGTGTTT TTGAATGAAT ATTTTGTGAA TCTTCTTAA AAGCTCAAT TTGTAGACTT 2640
 CTAAATAGAA TAAACACTTG CAGCAGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2700
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760

SEQ ID NO:257 PBM1 Protein sequence:
 PBM1 Protein sequence: CAB76901

60 MGDPSKQDIL TIFKRLRSVP TNKVCDFCGA KNPSWASITY GVFLCIDCSG SHRSLGVHLS 60
 FIRSTELDSN WSWFQLRCMQ VGGNASASSF FHQHGCTND INAKYNSRAA QLYREKIKSL 120
 ASQATRKHGT DLWLDSCVVP PLSPPKKEED FFASHVSPEV SDTAWASALA EPSLTSRPV 180
 ETTLENNEGG QEQQPSVEGL NVPTKATLEV SSIKKKPNQ AKKGLGAKKG SLGAOKLANT 240
 CFNEIEKQQA AADKMKEQED LAKVVSKEES IVSSLRLAYK DLEIQMKKDE KMNISGKKNV 300
 65 DSDRLGMFGF NCRSVISHSV TSDMQTIEQE SPIMAKPRKK YNDDSDSYF TSSSYFDEP 360
 VELRSSFSF WDDSDSYWK KETSKDTETV LKTTGYSDRP TARRKPDYEP VENTDEAQKK 420
 FGNVKAISSD MYFGRQSQAD YETRARLERL SASSSISSAD LFEEPRKQPA GNYSLSSVLP 480
 NAPDMAQFKQ GVRVSAGKLS VFANGVVTSI QDRYGS

SEQ ID NO:258 PBM4 DNA sequence

Nucleic Acid Accession#: D30891

Coding sequence: 1-4032 (underlined sequence corresponds to start and stop codon)

75 ATGGATACTG TCATGAAGCA GACACATGCT GACACACCTG TTGATCATTG TCTATCTGGC 60
 ATAAGAAAGT GTAGCAGCAC CTTTAAGCTT AAAAGTGAAG TCAACAAGCA TGAAACAGCC 120
 CTGAAATGCG AGAATCCAAA TTGAACAAT AAAGAATGTT GTTTCACCTT TACGTTGAAT 180
 GGAAACTCCA GAAATTAGA CCGTAGTGTG TTTACAGCAT ATGGTAAACC CAGCGAGAGT 240
 ATCTACTACG CCCTGAGTGC TAATGACTAT TTCAGTGAAA GGATAAAGAA TCAGTTTAAT 300
 80 AAGAACATTA TTGTTATGA AGAAAAGACA ATAGATGGAC ATATAAATT AGGAATGCCT 360
 CTAAGTGGCC TGCCATAGTA TTCTCATTTT AAAATTACAT TTGGTCAAAG AAAGAGTAGC 420

AAAGAAGATG GACACATATT ACGCCAATGT GAAAAATCCAA ACATGGAATG CATTCTTTTT 480
 CATGTTGTTG CTATAGGAAG GACAAGAAAG AAGATTGTTA AGATCAACGA ACTTCATGAA 540
 AAAGGAAGTA AACTTTGTAT TTATGCCTTG AAGGGTGAGA CTATGGAAGG AGCCTTATGC 600
 AAGGATGGCC GTTTTCGGTC TGACATAGGT GAATTIGAAT GGAAACTAAA GGAAGGTCA 660
 5 AAGAAAAATT ATGGAAAACA GTCCATGGTG GATGAAGTAT CTGGAAAAAGT CTTAGAAATG 720
 GACATTTCAA AAAAAAAGC ATTACAACAG AAAGATATCC ATAAAAAAT TAAACAGAAT 780
 GAAAGTGGCA CTGTGAAAT TAATCACCAG AGTCTGATAC AGTCTAAGAA AAAAGTCCAC 840
 AAACCAAAGA AAGATGGAGA GACCAAAGAT GTAGAACACA GCAGAGAGCA AATTCTCCCA 900
 CCTCAGGATC TAAGCCATTA TATTAAAGAT AAAACTCGCC AGACAATTCC CAGGATTAGA 960
 10 AATTATTACT TTTGTAGTTT GCCCGAAAA TATAGGCAAA TAAACTCACA AGTTAGACGG 1020
 AGGCCGATC TGGGTAGGCG GTATGCTATT AATCTGGATG TCCAAAAGGA GGCAATTAA 1080
 CTCTTAAAGA ATTATCAAAC GTTGAATGAA GCCATAATGC ATCAGTATCC GAATTTTAAA 1140
 GAGGAGGCAC AGTGGGTAAG AAAATATTTT CGGGAAGAAC AAAAGAGAAT GAATCTTTCA 1200
 CCAGCTAAGC AATTCAACAT ATATAAAAG GACTTCGGAA AAATGACTGC AAATCTGTT 1260
 15 TCAGTTGCAAC CTTGCGAACA GCTTACATAT TATAGCAAGT CAGTTGGGTT CATGCAATGG 1320
 GACATAATG GAAACACAGG TAATGCTACT TGCTTTGTCT TCAATGGTGG TTATATTTTC 1380
 ACCTGTGAGT ATGTGTGATA TCTTATGGTG GGTAAAAACA CACATCCAAG TTTGTGGCCA 1440
 GATATAATTA GCAAAATGTC GAAGGTAACC TTCACCTATA CAGAGTTCTG CCTACTCCT 1500
 GACAAATGGT TTTCCATTGA GCCATGGCTT AAAGTGTCCA ATGAAAAATCT AGATTATGCC 1560
 20 ATTTTAAAG TTTGAGTAA TGGAAATGCG TTTCCTCCAG GACTATGGCG ACAGATTICT 1620
 CCTCAACCAT CTACTGGTTT GATTATTATA ATTGGTCACT CTGAAGGCCA GATCAAGAAA 1680
 ATAGATGGTT GTACTGTGAT TCTCTAAAC GAACGATGTA AAAAATATCC AAACGATTGT 1740
 CAAGATGGGT TGTAGATCT CTATGATACC ACCAGTAATG TATACTGTAT GTTTACCCAA 1800
 AGAAGTTTCC TATCAGAGGT TTGGAACACA CACACGCTTA GTTATGATAC TTGTTTCTCT 1860
 25 GATGGTCTCT CAGGCTCCCC AGTGTTTAAT GCATCTGGCA AATTGGTTGC TTTGCATACC 1920
 TTTGGGCTTT TTTATCAACG AGGATTTAAT GTGCATGCCC TTATTGAATT TGGTTATTCT 1980
 ATGGATTCTA TTCTTTGTGA TATTAATAAG ACAATGAGA GCTTGTATAA ATCATTAAAT 2040
 GATGAGAAAC TTGAGACTTA CGATGAAGAG AAAGCCCGGC CCAGGCCAGC CTACCGGCGA 2100
 CTAGGATGCT TTGCTTTTCG CTCTCGCTTT CCAATACTCG GGACTGGGGA AACCGGGAGA 2160
 30 ATAGAAGCAG GCAAGGACCG CCGTGGGCAC GGGTCACTG AGACAGGGTC CTGCTCGCGG 2220
 CGTCAAGGAG GAGCGCTGTG GTGTGCCCA GCGCAGCCAA TCGGCTTCG AAGTAGCTGG 2280
 AGCTCTGGAG CCTTTGCTTC CTCAAAATAG AGCGGGAATC GCGTTGAGCG CTGGATTCCA 2340
 GGCCGAGTGC TGGCGAGGCG CGCAGTCTCT AAAGAGCAAC AGAATAATTG CAGTACTTCT 2400
 35 CTAATGAGGA TGGAGTCTAG AGGAGACCCA AGAGCCACAA CTAATACCCA GGCTCAAAGA 2460
 TTCCATTAC CTAAGAAAAA TCCAGAAGAC CAGACCATGC CCAAAATAG GACAATATAT 2520
 GTTACCTTGA AGCGTGTGAG AAAAGAGATA GAAACTCACC AAGGCCAAGA AATGCTTTGTG 2580
 CGTGGCAGAG AAGGAATCAA AGAGTACATA AACCTTGGA TGGCCCTCAG TTGTTTCCCT 2640
 GAAGGTGGCC AGTGGTCTAT TACATTTTCC CAAAGTAAAA GTAAGCAGAA GGAAGATAAC 2700
 40 CACATATTG CAGGCGAGGA CAAAGCATCG ACTGAATGTG TCAAATTTTA CATTATGCA 2760
 ATTGGAATTG GGAAGGTGAA AAGAAGGATT GTTAAATGTG GGAAGCTTCA CAAAAAGGGG 2820
 CGCAAACTCT GTGTTTATGC TTCAAAGGA GAAACCATCA AGGATGCACT GTGCAAGGAT 2880
 GGCAGATTTC TTCTTTCTTG GGAGATGAT GATTGGAAC TCATTGAAAA CAATGACACC 2940
 ATTTTAGAAA GCACCCAGCC AGTTGATGAA TTAGAAGGCA GATACTTTCA GGTGAGGTT 3000
 GAGAAAAAGAA TGGTCCCGAG TGCAGCAGCT TCTCAGAATC CTGAGTCAGA GAAAAGAAAC 3060
 45 ACCTGTGTG TGAGAGAAAC AATCGTGGCT CAGTACCCCA GTTTGAAAAG AGAAAGTGAA 3120
 AAAATCTGT AAAACTTCAA GAAAAAATG AAAGTAAAAA ATGGGGAAAC ATTATTGAA 3180
 TTGCATAGAA CAACGTTTGG GAAAGTAACA AAAAATTTCT CTTCGATTAA AGTAGTGAAA 3240
 CTCTTTGTAT GTCTCAGTGA CTCAGTTGGG TACTTATTCT GGGACAGTGC AACTACGGGT 3300
 50 TACGCCACT GCTTTGTATT TAAAGGATTG TTCAATTTAA CTGTCTGCGA TGTAATAGAT 3360
 AGCATTGTGG GAGACGGAAT AGAGCCAAGT AAGTGGGCAA CCAATATTGG TCAATGTGTA 3420
 AGGGTGACAT TTGGTTATGA AGAGCTAAAA GACAAGGAAA CAAACTACTT TTTTGTGAA 3480
 CCTTGGTTG AGTACATAAA TGAAGAGCTT GACTATGCTG TCTTGAAACT GAAGGAAAAAT 3540
 GGACAACAAG TACCTATGGA ACTATATAAT GGAATTACTC CTGTGCCACT TAGTGGGTTG 3600
 55 ATACATATA TTGGCCATCC ATATGGAGAA AAAAAAGCAGA TTGATGCTTG TGCTGTGATC 3660
 CCTCAGGGTC AGCGAGCAAA GAAATGTCAG GAACGTGTTT AGTCTAAAAA AGCAGAAAGT 3720
 CCAGAGTATG TCCATATGTA TACTCAAAGA AGTTTCCAGA AAATAGTTCA CAACCTGAT 3780
 GTGATTACCT ATGACACTGA ATTTTCTTT GGGGCTTCCG GCTCCCTGT GTTTGATTCA 3840
 AAAGGTTTCA TTGTTGGCAT GCATGCTGCT GGCTTTGCTT ATACTTACCA AATGAGACT 3900
 60 CGTAGTATCA TTGAGTTTGG CTCTACCATG GAATCCATCC TCCTTGATAT TAAGCAAAGA 3960
 CATAAACCAT GGTATGAAGA AGTATTGTA AATCAGCAGG ATGTAGAAAT GATGAGTGAT 4020
 GAGGACTTGT GAGAATTGAG TCTACTGGAT TTAAGGGAAT GGCTTATGGA GTTGTTATT 4080
 CGTAGGCATT GAAAATGGTT TTCTAAACTC CAAAATGGTC ATCTTATCAA TAATAATAAT 4140
 ATTGACCATT TCCTATCTGC CAGGCATTTT TCTAAGCACA TGAAGAAAT AGTCTAACA 4200
 65 ACACATGAG ATGGACTATA ACTTGGCCAA ATTTTCTTT TTTTGTAGAC TGAGTCTCAC 4260
 TCTGTCCCT GGGCTGGAGT ACAGTGGTGC GATCTCAGCT CACTGCAACT TCCACCTCCC 4320
 AGGTTCAAGC GATTCTTATG CCTCAGTCTC CTGAGCAGCT GGGATTACAG GCAACGCCA 4380
 CCACACCCAG CTAATTTTTT TTTTCTTTT TGTATTTTA GTAGAGACAG GGTTCACCA 4440
 TGTGTGTCAG GCGGGTCTCG AACTCCTGAC CTCGTGATCC ACCTGCCTCG GCGTTCCAAA 4500
 70 GTGCTGGGAT TACAAGTTTG AGCCACTGCA CCTGCTAAC TTGCCCTATT TTAAGTCAA 4560
 GCAATGGGAA GAATAACAAG ATTATATAGT AATCAGTTTC ATGACACTAA AAGTCATATA 4620
 GTCATAGGGT TTTTTCATCT TTATATCTT TGCCTAAAT CATTTGTAC AGTGCAGGAA 4680
 CCAAACTTG TTATCTCAT GATTCCTAC ATCTGACATA AGGAAAGTAA GTGCTCAGAA 4740
 AAATGTGCAG GTCAATAAGT TGCAAAAGT GGGGCTGCAA TTAATGCTAA CATAAGAGCT 4800
 75 AAATGCTTGA TTAGAATGA TCTCAAAACC TTTTAGAATT TCAAAATCT TCATATTACT 4860
 GAAACTGCG GAATATATGG GTCTGAAAT TCAGAAGATG ATAGTCACTC TTCCCATATT 4920
 TATAGGCTAT TAAGGCAAGG GATATCTTAA ACATCATATT ACTTTATTTA GATTCTACT 4980
 ACTCCAATTA TTAATGTTAT GTATTTCTCA TTGTTTACT TCTTCATGGT ATTATGAAGA 5040
 CTATATAGAT GATTCACCA AGCCTGCAAA TCTCCCTCT GTGGAATTCC ACTGGACCCA 5100
 ATCTGTTTTC CATTTCATT GCAATACTAC TAAAGCCATA CAATATCAAG CACCTCCTCT 5160

CTAGGTCCAG GGAATATCAC AGAAGAAGCA GGCATGTAAG ATTTTAAGGA CTGGTTTCGA 5220
 GGGGTGAGT GTAGGAAAAC AGCCTGTGTC ATTGTAAGAG TGATGTACCC TTGAAGAGCA 5280
 GCTGGCATGA TGACTGCTGT TTGACTCCTG CATACCAAGA TATTCTGCAG CAATGTCTTT 5340
 AAACAGTGCC GGTAGTACAG ATAACCCCTC ATAAAGATGC TTATCTAACC TCCCCAGTGT 5400
 TCAGGTGTTT CACAAGAAAAG TCTGAGATAT GACTAGTAC ACGTTTTGCC AAAAAATGCTT 5460
 GTTATATAAA GGGTACTTTT GGGAGGGTGA GTGCCGCCAT TTAGTGGCTG CTAGAAACAT 5520
 TGCTTCTGTT TGTAAGTTCC TATTAATGT TCTTCTGAG AAAAAAAAAA A

SEQ ID NO:259 PBM4 Protein sequence:
 PBM4 Protein sequence: BAB67788

MDTVMKQTHA DTPVDHCLSG IRKCSSTFKL KSEVKNHETA LEMQNPNLNN KECCFTFTLN 60
 GNSRKLDRSV FTAYGKPSES IYSALSANDY FSERIKNQFN KNIIVYEKT IDGHINLGMP 120
 LKCLPSDSHF KITFGQKSS KEDGHILRQC ENPNMECILF HVVAIGRTRK KIVKINELHE 180
 KGSKLCTIYAL KGETIEGALC KDGRFRSDIG EFEWKLKEGH KKIYQKQSMV DEVSGKVLEM 240
 DISKKKALQQ KDIHKKKIQN ESATDEINHQ SLIQSKKKVH KPKKDGETKD VEHSREQILP 300
 PQDLSHYIKD KTRQTPRIR NYYFCSLPRK YRQINSQVRR RPHLGRRYAI NLDVQKEAIN 360
 LLKNYQTLNE AIMHQYPNFK EEAQWVRKYF REEQKRMNLS PAKQFNYYKK DFGKMTANSV 420
 SVATCEQLTY YKSVGFMQW DNNNGTGNAT CFVFNNGYIF TCRHVVHLMV GKNTHPSLWP 480
 DIISKCAKVT FYTFECPPT DNWFSIEPWL KVSNNELDYA ILKLKENGNA FPPGLWRQIS 540
 PQPSTGLIYL IGHPEGQIKK IDGCTVIPLN ERLKKYPNDQ QDGLVDLYDT TSNVYCMFTQ 600
 RSFLSEVWNT HTLSYDTCSF DGSSGSPVFN ASGKLVALHT FGLFYQRFEN VHALIEFGYS 660
 MDSILCDIKK TNESLYKSLN DEKLETYDEE KARPRPAYRR LGCFRFRSRF PILGTGETGR 720
 IEAGKDRRGH GVSEITGCSR RQGGALWVSP AQPIGFRSSW SSGAFASNT SGNCOVERWIP 780
 GRVLARRAVS KEQQNNCSTS LMRMESRGDP RATINTQAGR FHSPKKNPED QTMPQNRITY 840
 VTLKAVRKEI ETHQGQEMLV RGTGKIKEYI NLGMPLSCFP EGGQVVITFS QSKSKQKEDN 900
 HIFGRQDKAS TECVKFYIHA IGIGKCKRRI VKCGKLHKKG RKLVCYAFKG ETIKDALCKD 960
 GRFLSFLEND DWKLIENNDT ILESTQPVDE LEGRYFQVEV EKRMVPSAAA SQNPSEKERN 1020
 TCVLRQIIVA QYPSLKRSE KIHENFKKKM KVKNGEILFE LHRITFGKVT KNSSSIKVVK 1080
 LRVRLSDSVG YLFWDSATTG YATCFVFKGL FLTCRHVID SIVGDGIEPS KWATIHQCV 1140
 RVTFGYEELK DKETNYFFVE PWFEIHNEEL DYAVLKLKEN GQQVPMELYN GITPVPLSGL 1200
 IHIGHPYGE KKQIDACAVI PQGQRAKKCQ ERVQSKKAE PEYVHMYQR SFQKIVHNPD 1260
 VITYDTEHFF GASGSPVFDG KGLVAMHAA GFAYTYQNET RSIEFGSTM ESILLDIKQR 1320
 HKPWYEEYFV NQQDVEEMSD EDL

SEQ ID NO:260 PBQ1 DNA sequence
 Nucleic Acid Accession#: NM_015642
 Coding sequence: 489-2489 (underlined sequence corresponds to start and stop codon)

	1	11	21	31	41	51	
45	ACATTTCAAA	AAAAATACAT	AGACTGATGT	TTCAGACTTG	TGCAGCATAA	GCCTACAGGG	60
	TACGAAGAA	GAACTCTGAG	AATGTTTGA	GAATGTTTCA	TCATTACTAA	CAGGATATTTC	120
	CTCATGACAT	TGCTGTCTGA	TCTTTGACCA	TCAGTCTGTG	ACCTGCCCTT	TCTCTTTTACA	180
	TGCAGCGCT	CTCTGCTCCC	TGCCCCAATG	AACATCTGCA	CTAGGCCCAA	GCCTTGGAGT	240
50	AAATTACCTG	AAGAGTGACA	CCATTGATTT	TGAAACTACT	GAAGAAACCC	AAGACAGCTG	300
	AAAACCGAA	GGCATCTGAG	GAGAATGAGA	TACTCTAGCC	GGGTGGATCC	AGCGCCAGC	360
	CGGGCCTTCC	CTGGCTGAAC	TTTGAAGCTG	TTTGTCTCC	AGACCCAGCC	CTCATCCACT	420
	CAACACATTC	ACTGACAAAC	TCTCACGCTC	ACACCGGCTC	ATCTGATTGT	GACATCAGTT	480
	GCAAGGGGAT	GACCCGAGCG	ATTCACAGCA	TCAACCTTCA	CAACTTCAGC	AATTCCGTGC	540
55	TCGAGACCTT	CAACAGAGCAG	CGCAACCGTG	GCCACTTCTG	TGACGTAAACG	GTGCGCATCC	600
	ACGGGAGCAT	GCTGCGCGCA	CACCGCTGCG	TGCTGGCAGC	CGGCAGCCCC	TTCTTCCAGG	660
	ACAAACTGCT	GCTTGGCTAC	AGCGACATCG	AGATCCCGTC	GGTGGTGTC	GTGCACTCAG	720
	TGCAAAAGCT	CATTGACTTC	ATGTACAGCG	CGCTGCTACG	GGTCTCGCAG	TCGGAAGCTC	780
	TGCAGATCCT	CACGGCCGCC	AGCATCCTGC	AGATCAAAAC	AGTCATCGAC	GAGTGCAGCG	840
60	GCATCGTGTC	ACAGAACGTG	GGCGATGTGT	TCCCGGGGAT	CCAGGACTCG	GGCCAGGACA	900
	CGCCCGGGGG	CACCTCCGAG	TCAGGCACGT	CAGGCCAGAG	CAGCGACACG	GAGTCGGGCT	960
	ACCTGCAGAG	CCACCCACAG	CACAGCGTGG	ACAGGATCTA	CTCGGCACCT	TACGCGTGCT	1020
	CCATGCAGAA	TGGCAGCGGC	GAGCGCTCTT	TTTACAGCGG	CGCAGTGGTC	AGCCACCACG	1080
	AGACTGCGCT	CGGCCTGCC	CGCGACCACC	ACATGGGAAG	CCCCAGCTGG	ATCACACGCA	1140
	TCCATGAGCG	CTCGCAGCAG	ATGGAGCGCT	ACCTGTCCAC	CACCCCGCAG	ACCCAGCACT	1200
65	GCCGCAAGCA	GCCCCGGCCT	GTGCGCATCC	AGACCTAGT	GGGCAACATC	CACATCAAGC	1260
	AGGAGATGGA	GGACGATTAC	GACTACTACG	GGCAGCAAAG	GGTGCAGATC	CTGGAACGCA	1320
	ACGAATCCGA	GGAGTGCACG	GAAGACACAG	ACCAGGCCGA	GGGCACCGAG	AGTGAGCCCA	1380
	AAGGTGAAG	CTTGCAGTCG	GGCGTCAGCT	CCTCCATAGG	CACCGAGCCT	GACTCGGTGG	1440
	AGCAGCAGTT	TGGGCTTGGG	GCGGCGCGGG	ACAGCCAGGC	TGAACCCACC	CAACCCGAGC	1500
70	AGGCTGCAGA	AGCCCCCGCT	GAGGTTGGTC	CGCAGACAAA	CCAGCTAGAA	ACAGGTGCTT	1560
	CCTCTCCGGA	GAGAAGCAAT	GAAGTGGAGA	TGGACAGCAC	TGTTATCACT	GTGACCAACA	1620
	GCTCCGACAA	GAGCGTCTTA	CAACAGCCTT	CGGTCAACAC	GTCCATCGGG	CAGCCATTGC	1680
	CAAGTACCCA	GCTCTACTTA	CGCCAGACAG	AAACCCCTAC	CAGCAACCTG	AGGATGCCCTC	1740
	TGACCTTGAC	CAGCAACACG	CAGGTCAATTG	GCACAGCTGG	CAACACCTAC	CTGCCAGCCC	1800
75	TCTTCACTAC	CCAGCCCCGG	GGCAGTGGCC	CCAAGCCTTT	CCTCTTCAGC	CTGCCACAGC	1860
	CCCTGGCAGG	CCAGCAGACC	CAGTTTGTGA	CAGTGTCCCA	GCCCGGCTTG	TCGACCTTTA	1920
	CTGCACAGCT	GCGACCGCCA	CAGCCCCCTGG	CCTCATCCCG	AGGCCACAGC	ACAGCCAGTG	1980
	GGCAAGCGGA	AAAAAGGCTT	TATGAGTGCA	CTCTCTGCAA	CAAGACTTTC	ACCGCCAAAC	2040
	AGAACTACGT	CAAGCACATG	TTCTGTACACA	CAGGTGAGAA	GCCCCACCAA	TGCAGCATCT	2100
80	GTTGGCGCTC	CTTCTCTTAA	AAGGATTACC	TTATCAAGCA	CATGGTGACA	CACACAGGAG	2160

5 TGAGGGCATA CCAGTGTAGT ATCTGCAACA AGCGCTTCAC CCAGAAGAGC TCCCTCAACG 2220
 TGCACATGCG CCTCCACCGG GGAGAGAAGT CCTACGAGTG CTACATCTGC AAAAAGAAAGT 2280
 TCCTCTACAA GACCTCCTG GAGCGACACG TGGCCCTGCA CAGTGCCAGC AATGGGACCC 2340
 CCCTGCGAGG CACACCCCA GGTGCCCGCG CTGGCCCGCC AGGCGTGGTG GCCTGCACGG 2400
 AGGGGACCAC TTACGTCTGC TCCGCTGCGC CAGCAAAGTT TGACCAAAATC GAGCAGTTCA 2460
 ACGACCACAT GAGGATGCAT GTGTCTGACG GATAAGTAGT ATCTTTCTCT CTTCCTTATG 2520
 AACAAACAA AACAAACAA AAAAACAAC AAACAAAAA GCTATGGCAC TAGAATTAA 2580
 10 GAAATGTTTT GGTTCATTT TTAATTTCTG TTTTGTGTTT TGTTCGTTT CATTTGTAC 2640
 TACATGAAGA ACTGTTTTT CCCTGCTGGT ACATTTACATT TCCGGAGGCT TGGGTGAATA 2700
 ATAGTTTTCC CAGTCTCCCT CGGATGGTGG CCTTAAGGCC TGGTAGTGCT TCAAGAGGTC 2760
 CACTGGTTGG ATCTCTAGCT ACTGGCCTCT AAATACAACC CTCTTTTACA AAAAAAAA 2820
 AAAAAAAA

15 SEQ ID NO:261 PBQ1 Protein sequence:

PBQ1 Protein sequence: NP_056457

20 MTERIHSINL HNFNSVLET LNEQRNRGHF CDVTVRIHGS MLRAHRCVLA AGSPFFQDKL 60
 LLGYSDIEHP SVVSQSVQK LIDFMYSGVL RVSQSEALQI LTAASILQIK TVIDECTRIV 120
 SQNVGDVFPF IQDSGQDTPK GTPESGTSGQ SSDTESGYLQ SHPQHSVDRI YSALYACSMQ 180
 NGSERSFYS GAVVSHHETA LGLPRDHHME DPSWITRIHE RSQQMERYLS TTPETHCRK 240
 QPRPVRIQTL VGNIIHQEM EDDYDYYGQQ RVQILERNES EECTEDTDQA EGTESEPKGE 300
 SFDSGVSSSI GTEPDSVEQQ FPGGAARDSQ AEPTQPEQAA EAPAEGGPQT NQLETGASSP 360
 25 ERSNEVEMDS TVITVSNSSD KSVLQPSVN TSIQOPLPT QLYLRQTETL TSNLRMPLTL 420
 TSNTQVIGTA GNTYLPALFT TQPAAGSPKP FLFSLPOPLA GQQTQFVTVS QPGLSTFTAQ 480
 LPAPQPLASS AGHSTASGQG EKKPYECILC NKIFTAKQNY VKHMFVHTGE KPHQCSICWR 540
 SFLSKDYLIK HMVTHTGVR A YQCSICNKR F TQKSLNVHM RLHRGEKSYE CYICKKKFSH 600
 KTLLEHVAL HSASNGTPPA GTPPGARAGP PGVVACTEGT TYVCSVCPAK FDQIEQFNDH 660
 30 MRMHVSDG

35 SEQ ID NO: 262 PBQ6 DNA sequence

Nucleic Acid Accession#: A1654187

Coding sequence: 1-912 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
 | | | | |
 40 ATGGTGAAG AGGAAACAGG CATATCTTAC ATGGTGGCAG ACAAGGGACA CCCTTCTACA 60
 AACTCTACCA CTTCCTGCGC GTCGTTTCGA CCATATAAAA ACGACCTATG CGAACTGCGT 120
 CGGAAAACCTC CCTCAGCATG TAAAACGAAG ATCAGGAGCA GATTTGAAGA ATTACAAAGT 180
 GAATTGGTGC CAGTCAGCAT GTCAGAGACA GACCACATAG CCTCTACTTC CTCTGATAAA 240
 AAATGTPGGGA AAACACCTGA ATTAAGGAA GACTCATGCA ACTTGTGTTT TGGCAATGAA 300
 AGCAGCAAAAT TAGAAATGA GTCCAAACTA TTGTCAATTAA ACACGTGATAA AACTTTATGT 360
 CAACCTAAATG AGCATAATAA TCGAATTGAA GCCCAGGAAA ATTATATTCC AGATCATGGT 420
 45 GGAGGTGAGG ATCTCTGTGC CAAAACAGAC ACAGGCTCAG AAAATTCCTGA ACAAATAGCT 480
 AATTTTCCTA GTGGAATTTT TGCTAAACAT ATTTCAAAA CAAATGAAC AGAACAGAAA 540
 GTAACACAAA TATTGTTGGA ATTAAGGTCA TCTACATTTC CAGAACTCAG TAATGAAAAG 600
 ACTTATTCAG AAAGCCCTTA TGATACAGAC TGACACCAAGA AATTATTTTC AAAAAATAAG 660
 50 AGCGTTTCAG CATCAGAGGA TTTGTTGGA GAAATAGAAT CTGAGCTCTT ATCTACGGAG 720
 TTTGCAGAAC ATCAGATACC AAATGGAATG AATAAGGGAG AACATGCATT AGTTCTGTTT 780
 TTTTGCAGTG TGCAAGATAA ATATTGTCAG CAGGAACATA TCATAAAAAA GGCCAGACTT 840
 GGTCTCTGTT ATTTGCCATC AAGAACCTCA ATTGACACGT TAATTCGGTT TATCCCAAT 900
 TTATATAGAT AA

55 SEQ ID NO:263 PBQ6 Protein sequence:

Protein Accession #: NP_060170

60 MEPKEATGKE NMVTKKKNLA FLRSRLYMLE RRKTDTVVES SVSGDHSGLT RRSQSDRTEY 60
 NQKLQEKMTF QGECVAETL TPEEEHMKR MMAKREKIK ELIQTEKDYLDLELCVREV 120
 VQPLRNKKT DRLVDLSLFSN IESVHQISAK LSLLEEATT DVEPAMQVIG EVHLQIKGPL 180
 EDIYKIYCYH HDEAHSILES YEKEELKEH LSHCIQSLK

65 SEQ ID NO:264 PBQ7 DNA sequence

Nucleic Acid Accession#: NM_014323

Coding sequence: 662-2725 (underlined sequence corresponds to start and stop codon)

70 1 11 21 31 41 51
 | | | | |
 GGGCCTACTC TGCCGCGGCC GCGCGCGGCC CGCTCCAGCC GCGCGCGCGC CCGCCACCGC 60
 CCTCCAGGCT CGGGAGACCG GCGCGCGCCA CCGCCCGCGT GCGCGCGCGC CCGCGCGCGC 120
 CTTCGCTTTC GCGCTTTGTT TCTCCGCTC CCGCGCGCCC GCGCGCGCTC GCGCTTTGTA 180
 75 GGGGACGAGC GCGCGCGCCC CAGCGGGGCC GGGAAAAGCG GCGCGCGCGC GCGCGCGCTG 240
 CGCGCGCGAC CCTCCTTCT CTTCCCGCG TGCCTGTCCT CTCTTGGCT GCGCGCGCGC 300
 GCCGCTTGGC GGGCGGGAGG GGAGGTGGCA GGCCTGTTT CAGGAGGGGC GCACCTCTTC 360
 GCTCGCGCAC CCCCCGGGAA GGTAGACCGG GAAGGGGAGG CCGCGCGCGC GAGAGGAGAG 420
 AGTGGCGCGC AGTCCAGCGA GGGCGGGGCT TGGCTATGTG GGGGGTGGT CACCCCGCAG 480
 80 TCTAGACAGT CTAGTCCGGG CTGGGGGCGT GTACACTCGG GCGACCTGCG AGACTACAGA 540
 GCCTCGGGCC GGCACGTGTG GGGAGGTGTG ACACGTCTGC TGCCTCCGCG TTCTCGCTGC 600

	TGAGGGGAAG	GGAGGGGGCG	GGCAGGTGCA	CGCGCCGGGC	TAGTGGGAGG	GGGCGGCGGC	660
	CATGGAGCGG	GTGAACGACG	CTTCGTGCGG	CCCGTCTGGC	TGCTACACAT	ACCAGGTGAG	720
	CAGACACAGC	ACCGAGATGC	TGCACMACCT	GAACACAGCAG	CGCAAAACG	CGCGGCGCTT	780
5	CTGCGACGTG	CTCTTGGCGG	TAGGCGACGA	GAGCTTCCCA	GCACACCGCG	CCGTGCTGGC	840
	CGCCTGCAGC	GAGTACTTTG	AGTCGGTGT	CAGCGCCAG	TTGGGCGACG	CGCGAGCTGC	900
	GGACGGGGGT	CCGGCTGATG	TAGGGGGCGC	GACGGCAGCA	CCAGGCGGCG	GGGCGGGGG	960
	CAGCCGGGAG	CTGCAGATGC	ACACTATCAG	CTCCAAGGTA	TTTGGGGACA	TTCTGGACTT	1020
	CGCCTACACT	TCCCGCATCG	TGGTGGCTT	GGAGAGCTTT	CCCCAACTCA	TGACGGCCGC	1080
10	CAAGTTCCTG	CTGATGAGGT	CGGTATATCGA	GATCTGCCAG	GAAGTCATCA	AACAGTCCAA	1140
	CGTACAGATC	CTGGTACCCC	CTGCCCGCGC	CGATATAATG	CTCTTTCGCC	CCCCTGGGAC	1200
	CTCGGACTTG	GGCTTCCTCT	TGGACATGAC	CAACGGGGCA	GCCTTGGCAG	CCAACAGCAA	1260
	TGGCATCGCC	GGCAGCATGC	AGCCAGAGGA	GGAGGCAGCT	CGGGCGGCTG	GTGCAGCCAT	1320
	TGCAGGCCAA	GCCTCTTTGC	CTGTGTATCC	TGGGGTGGAC	CGCTTGCCCA	TGGTGGCTGG	1380
15	ACCCCTATCC	CCCCAACTGC	TGACTTCCCC	ATTCCTCCAGT	GTGGCATCCA	GTGCCCCCTC	1440
	CCTGACTTGC	AAGCGAGGCC	GGGGCCGCCC	AAGGAAGGCC	AACCTGCTGG	ACTCAATGTT	1500
	TGGGTCCCA	GGGGCCCTGA	GGGAGGCAGG	CATCCTTCCA	TGCGGTCTAT	GTGTAAGGT	1560
	GTTCATGTAT	GCCAAACCGG	TCCGGCAGCA	CGAGGCCAG	CACGGTGTCA	CCAGCTTCCA	1620
	GCTGGGCTAC	ATCGACCTTC	CTCCTCCGAG	GCTGGGTGAG	AATGGGCTAC	CCATCTCTGA	1680
20	AGACCCCGAC	GGCCCCGAA	AGAGGAGCCG	GACCAAGGAG	CAGGTGGCTT	GTGAGATCTG	1740
	CGGCAAGATC	TTCCGTGATG	TGTATCATCT	TAACCGGCAC	AAGCTGTCCC	ACTCTGGGA	1800
	GAAGCCCTAC	TCCTGCCCTG	TGTGTGGGTT	CGGGTTCAG	AGAAAAGACC	GCATGTCTTA	1860
	CCATGTGCGG	TCCCATGATG	GGTCCGTGGG	CAAGCCTTAC	ATCTGCCAGA	GCTGTGGGAA	1920
	AGGCTTCTCC	AGGCTGATC	ACTTGAACGG	ACATATCAAG	CAGGTGCACA	CTTCTGAGCG	1980
25	GCCTCACAA	TGTCAGACCT	GCAATGCTTC	TTTTCGCCAC	CGAGACCGTC	TGCGCTCCA	2040
	CCTGGCCTGT	CATGAAGACA	AGGTGCCCTG	CCAGGTGTGT	GGGAAGTACT	TGCGGGCAGC	2100
	ATACATGGCA	GACCACCTGA	AGAAGCACAG	CGAGGGGCC	AGCAACTTCT	GCAGTATCTG	2160
	TAACCCAGGT	TTCTCTCTGT	CCTCTACTT	AAAGGTCAT	GTTAAACACC	ACCACGCTGT	2220
	TCCCTTCTCC	CAGGTCTCCA	GGCACCAGGA	GCCATCCTG	AATGGGGGAG	CAGCGTTCCA	2280
30	CTGCGCCAGG	ACCTATGGCA	ACAAAGAAGG	CCAGAAATGC	TCACATCAGG	ATCCGATPGA	2340
	GAGCTCTGAC	TCCTATGGTG	ACCTCTCAGA	TGCCAGCGAC	CTGAAGACGC	CAGAGAAGCA	2400
	GAGTGGCAAT	GGCTCTTCT	CCTGCGACAT	GGCAGTCCCC	AAAAACAAAA	TGGAGTCTGA	2460
	TGGGGAGAAG	AAGTACCAT	GCCCTGAATG	TGGGAGCTTC	TTCCGCTCTA	AGTCTACTT	2520
	GAACAAACAC	ATCCAGAAGG	TGCAATGCTC	GGCTCTCGGG	GGCCCTCTGG	GGGACCTGGG	2580
35	CCCTGCCCC	GGCTCACCTT	TCTCTCCTCA	GCAGAACATG	TCTCTCTCTG	AGTCTTCTGG	2640
	GTTCAGATG	GTTCAGTCGG	CATTTGCCCTC	ATCTTTAGTA	GATCTCTGAG	TTGACCAAGCA	2700
	GCCCATGGGG	CTGAAGGGA	AATGAGGCAG	CTGCTGTGTC	CCACACGAAA	CAACCATCTG	2760
	GGGACTGCTG	GGAATGCTGT	TGAATGCGGA	GGGAAGTGAT	GTTTGGGTTT	TGTAGCTGAG	2820
	AGATTTTAT	TCATTTTAA	CTGCCCCCA	ACCCCACTCC	AACTCTCTCT	CCACCACCA	2880
40	TTCTCCCAAT	GGTCTTTAGA	AATAGATTTT	CATCTGATAT	TCTGCAGAAA	TATCAATGAG	2940
	ACTTGTATG	GGACAGGGG	AGAAAACACT	ACATAGGCCT	CCAAGGCAAA	ACCAGTCCCA	3000
	GTTCCTTTAA	TGGGAAGAAG	CTGGAATTCC	TGGTGTCTAA	TTCTTAGTGA	CCCCAATCTT	3060
	ATACCCAAAT	CTATGATATT	CTGGGACCTC	AGTGATTTTG	GTCCCTCTCC	ACTTCTCTAG	3120
	TTCTGTCATC	TCCCTTCCCA	TATCTTTCAA	AAGAACCACA	CTAGGGTCTC	CACCTACTTA	3180
45	TACAAATGGA	ATGCCCAACT	GTTTTAAAGG	AAGCCAGAAG	CATCCCATGG	ACCATGGGGT	3240
	GAGTGTCTC	CAAGAGCCCC	CTGAGCTCAG	CCCTCTGCT	GGAGGGCTCC	AGACCTTTCT	3300
	GAGCCCTGCT	TGGAGGCGAG	CATTTTCACT	GCTAGGACAA	GCTCAGCTGT	TGAGGACACC	3360
	CCCAACCCAA	ATTTTCACTC	TTACGTGATT	TTAACCATTC	AACATGCTGT	TGGGTTTAA	3420
	TTCTCTAAT	ATATATTATA	TTGTTATAT	TTTTTAGGAC	CAGTTGTAGT	GAATTGCTAC	3480
50	TGAAAGCTAT	CCAGGTGAT	ACAGAGCTCT	TTGTAACCCG	CAGTCACACA	TTAGGGTTAG	3540
	TATTAACCTT	TGTTTATGAT	TACCATAATT	AACTTGGCTA	GTTGATTGTT	TGAAGTCTAT	3600
	GGAGAAATGA	GTTTTATGCA	AAATTTTAAA	AAATGCCAGT	CTGGTCAGGG	AAGTAGGGGG	3660
	TTTCAATGCT	TTGGGAACCC	AGGAAGGTGG	GACAGCCGGC	AGGTAGGGAC	ATTGTGTACC	3720
	TCAGTTGTGT	CACATGTGAG	CAAGCCAGG	TTGACCTTGT	GATGTGAATT	GATCTGATCA	3780
55	GACTGTATTA	AAAATGTTAG	TACATTACTC	TA			

SEQ ID NO:265 *PBY7 Protein sequence:*

Protein Accession #: NP_114439

60	MERVNDASCG	PSGCYTYQVS	RHSTEMLHNL	NQQRKNGGRF	CDVLLRVGDE	SFPAHRAVLA	60
	ACSEYFESVF	SAQLGDGGAA	DGGPADVGGA	TAAPGGGAGG	SRELEMHTIS	SKVFGDILDF	120
	AYTSRIVVRL	ESFPELMTAA	KFLLMRSVIE	ICQEVIKQSN	VQILVPPARA	DMLEFRPPGT	180
	SDLGFLDMT	NGAALAANSN	GIAGSMQPEE	EAARAAGAAI	AGQASLPVLP	GVDRLPMVAG	240
65	PLSPQLLTSP	PPSVASSAPP	LTGKRGRGRP	RKANLLDSMF	GSPGGLREAG	ILPCGLCGKV	300
	FTDANRLRQH	EAQHGVTSIQ	LGYYDLPPPR	LGENGLPISE	DPDGPGRKRSR	TRKQVACEIC	360
	GKIFRDVYHL	NRHKLSHSGE	KPYSCPVCGL	RFKRKDRMSY	HVRSHDGSVG	KPYICQSCGK	420
	GFSRPDLHNG	HIKQVHTSER	PHKQCTCNAS	FATRDRLRSH	LACHEDKVPC	QVCGKYLRAA	480
	YMADHLKKHS	EGPSNFCIS	NREGQKCSHQ	DPIESSDSYG	DLSDASDLKT	PEKQSANGSF	540
70	SCDMAVPKNK	MESDGEKKYP	CPECGSFFRS	KSYLNKHIQK	VHVRALGGPL	GDLGPALGSP	600
	FSPQQNMSLL	ESFGQIVQS	AFASSLVDPE	VDQQPMGPEG	K		

SEQ ID NO:266 *PBY9 DNA sequence*

Nucleic Acid Accession#: NM_012429

Coding sequence: 174-1385 (underlined sequence corresponds to start and stop codon)

	1	11	21	31	41	51	
80	CCCTACTCCG	CCTCTCGGGA	TCCTTTAAGA	GGCGGGGCTT	GGCTGCCAGC	TCCGCGGCCC	60
	GGGCAAAAGG	CTGGGACTTT	ACTCCGGGTG	GCAGCGAGGA	CGAGTCTGTG	CTCCATCAGC	120

5 TGCCGCACCC GCCGCCCTCCC GCCCCCAAAC CCCATCCCCG CGGTTGAGCC ACGATGAGCG 180
 GCAGAGTCCG CGATCTGAGC CCCAGGCAGA AGGAGGCATT GGCCAAAGTTT CGGGAGAAATG 240
 TCCAGGATGT GCTGCCGGCC CTGCCGAATC CAGATGACTA TTTTCTCCTG CGPTGGCTCC 300
 GAGCCAGAAG CTTCGACCTG CAGAAGTCCG AGGCCATGCT CCGGAAGCAT GTGGAGTTC 360
 GAAAGCAAAA GGACATTGAC AACATCATTA GCTGGCAGCC TCCAGAGGTG ATCCAACAGT 420
 ATCTGTCAAG GGTATATGT GGCATGACCC TGGATGGCTG CCCAGTCTGG TACGACATAA 480
 TTGGACCTCT GGATGCCAAG GGTCTGCTGT TCTCAGCCTC CAAACAGGAC CTGCTGAGGA 540
 CCAAGATGCG GGAGTGTGAG CTGCTTCTGC AAGAGTGTGC CCACCAGACC ACAAGTPTGG 600
 10 GGAGGAGGT GGAGACCATC ACCATAATTT ATGACTGCGA GGGGCTTGGC CTCAGGATC 660
 TCTGGAGCC TGTCTGGAG GCCTATGGAG AGTTTCTCTG CATGTTTGAG GAAAATTATC 720
 CCGAAACACT GAAGCGTCTT TTTGTTGTTA AAGCCCCCAA ACTGTTTCTT GTGGCCTATA 780
 ACCTCATCAA ACCCTTCTCT AGTGAGGACA CTGTAAGAA GATCATGGTC CTGGGAGCAA 840
 ATTGGAGGA GGTTTTACTG AAACATATCA GCCCTGACCA GGTCCCTGTG GAGTATGGGG 900
 GCACCATGAC TGACCTTGAT GGAACCCCA AGTGCAAAATC CAAGATCAAC TACGGGGGTG 960
 15 ACATCCCCAG GAATATTTAT GTGCGAGACC AGGTGAAACA GCAGTATGAA CACAGCGTGC 1020
 AGATTTCCTG TGGCTCCTCC CACCAAGTGG AGTATGAGAT CCTCTTCCCT GGCTGTGTCC 1080
 TCAGGTGCGA GTTTATGTCA GATGGAGCGG ATGTTGGTTT TGGGATTTTC CTGAAGACCA 1140
 AGATGGGAGA GAGGCAGCGG GCAGGGGAGA TGACAGAGGT GCTGCCCAAC CAGAGGTACA 1200
 ACTCCACCT GGTCCCTGAA GATGGGACCC TCACCTGACG TGATCTTGGC ATCTATGTCC 1260
 20 TGCGGTTTGA CAACACCTAC AGCTTCATTC ATGCCAAGAA GGTCAATTTT ACTGTGGAGG 1320
 TCCTGCTTCC AGACAAAGCC TCAGAAGAGA AGATGAAACA GCTGGGGGCA GGCACCCCGA 1380
 AATAACACCT TCTCCTATAG CAGGCCTGGC CCCCTCAGTG TCTCCTGTG AATTCTTACC 1440
 CCTGTAGCA GTCATTTTCG CACAACCCCTG AAGCCCAAAG AAACCTGGGT GGAGGACAGA 1500
 25 CCTCAGGAGC TTTTCATTTCA GTTAGGCAGA GGAAGAGCGA CTCAGTGGG TCTCCGTGTC 1560
 TATCAATAC CTAAGGAGTC CCCAGGAGCT GGTGGCCAT CGTGATAGGA TCTGTCTGTC 1620
 CTGTAACTG CTGCAACTTC ACCTGTCCAG GGACAGCGAA GCTGGGGGTG GCGGGGGGCA 1680
 TGTACACAG GGTGGCAGCA GGGAAAAAA TTAGAAAAAG GTGAAAGATT GGGACTTAAC 1740
 ACTTCAGGGA AGTCAGCTGC CGGGGAGAAA CTGCTTCTTA AATGAACACA TAAGTTTAGA 1800
 30 TCGCAATGAG GAGTAGCAGG GTAGCTGGTT GCTAGAGTTA CGGTGGGGAT CAGAACTCT 1860
 TCCAAACATT TTAGCACTGA GGCTGGGGTA GCTTTTGGCT TTTCCAGGT CTCAGGAGGT 1920
 GGCTGAGTC AGCACACATC TTCCCACTCG GTAGACAGGC TGGCCTCTCC CTCACCTTGA 1980
 GACTTTGGCA ACTCTGGGC CACACGGCCT GCCTCTTTGA TTAATATGA TTGTCAGTGA 2040
 CTCAGAGCTT CCTGGGACTT CGGGTACCCA CCCGCTGTTC TCCATGCAA CAAAGCGCCA 2100
 35 GGGAAATGAC CCACAGGGAT CGCAGCTGCA GGGAGGGCCA GGGAGGTTGG GGGTGGGAGT 2160
 GAATGCTAAA AGCAGATCGT CCAGTGCCCT TTTAGTGTCT ACCGGCTCT CACCAAGCAG 2220
 TCCTCCATGT GAGCAACCCC GAGACAAAAA TGCTAAGTGG GATCAAGAGA GCAGCACTCG 2280
 GAGAGGGTGT TTGCCAGTCT GAGTGTCCCG CGGTGCCCGC CAACCCGCTT CTGACTGAC 2340
 CTGAGCAAGG TCTTACTAAG CAGTCCCATC TCTGTGGGAG GCATGCAACG CGTGCAGGGA 2400
 40 GTTCAGGTGC CGGTCCGGCT AGCCAGGCCT GGAGGCCCCC CAGGCAGGAG GCCGCCCAAA 2460
 GGGGGGGCG GGTCTGCGCA GACTAGGGGC TGGGGGGCGC CACAGAGGCC CTCGAAACCA 2520
 CAGCCCTTAC CCCAATCCCA CGAGCCCCGC CAACGAACCA CAGGTGCTGG GCTTTAGAGA 2580
 ACATGGGAAG GCGGCCCCAG ACCTGGCGGG AACGCCCTTC CCTCAGAGCC AGGCCCGGGC 2640
 CCCGTCTGGG AAGCTCATCT TCGAAGCTG AGGGAGCTCA GGGCAAGGC CAGGCTAGCG 2700
 45 CGGACCGGAA GGGGCCAGG CTGCACGGGC CTCTGCCAGA ACGCTCAGGA CATCCCGGCC 2760
 TGGGTTTACA ACGCTGTAG GAAAATTAA CAATGAATAA AGCAACGCTC AGTCCGCA

SEQ ID NO:267 PB9 Protein sequence:

Protein Accession #: NP_036561

50 MSGRVGLDSP RQKEALAKFR ENVQDVLPAL PNPDDYFLLR WLRARSFDLQ KSEAMLRKHV 60
 EFRKQKDDN IISWQPEVI QQYLSGGMCG YDLGCPVWY DIHPLDAKG LLFSASKQDL 120
 LRTKMRECEL LLQECARHT KLGRKVETIT IYDCEGLGL KHLWKPAVEA YGEFLCMFEE 180
 55 NYPETLKRFL VVKAPKLPV AYNLIKPLS EDRKKIMVL GANWKEVLLK HISPQVVPVE 240
 YGGTMDPPD NPKCKSKIN YGGDPRKYV RDQVKQYEH SVQISRSSH QVEYEILFP 300
 CVLRWQFMSD GADVGFIFL KTKMGERQRA GEMTEVLPNQ RYNHSLVPED GTLTCDSPGI 360
 YVLRFDNTYS FIHAKKVNFT VEVLLPKAS EEKMKQLGAG TPK

SEQ ID NO:268 PBH8 DNA sequence

Nucleic Acid Accession #: XM_009756

Coding sequence: 301-1440 (underlined sequence corresponds to start and stop codon)

65 1 11 21 31 41 51
 GTGGGACAG CCGAGCCCGC CCGGGCCCCT GGACGGCGTC GCCAAGGAGC TGGGATCGCA 60
 CTGTCTGCAG ACTTTGGATG GATTGTGTTT TGTGGTAGCA TCTGATGGCA AAATCATGTA 120
 TATATCCGAG ACCGCTCTCT TCCATTTAGG CTTATCCAG GTGGAGCTCA CGGGCACAG 180
 70 TATTTATGAA TACATCCATC CTCTGACCA CGATGAGATG ACCGCTGTCC TCACGGCCCA 240
 CCAGCCGCTG CACCACACC TGCTCCAAGG TATGAGATAG AGAGGTCTGT CTTTCTTGA 300
 ATGAAATGTG TCTTTGGCAA AAGGAACGCG GGCTTGACCT GCAGCGGATA CAAGGTCAATC 360
 CACTGCACTG GCTACTTGAA GATCAGGCAG TATATGCTGG ACATGTCCCT GTACGACTCC 420
 TGCTACCAAG TGTGGGGGCT GGTGGCCGTG GGCCAGTCGC TGCCACCCAG TGCCATCACC 480
 GAGATCAAGC TGTACAGTAA CATGTTTCATG TTCAGGGCCA GCCTTGACCT GAAGCTGATA 540
 75 TTCCTGGATT CCAGGGTGAC CGAGGTGACG GGGTACGAG CCGAGGACCT GATCGAGAAG 600
 ACCCTATACC ATCAGCTGCA CGGCTGCGAC GTGTTCACCC TCCGCTACGC ACACCACTTC 660
 CTGTTGGTGA AGGGCCAGGT CACCAACCAAG TACTACCGGC TGCTGTCCAA GCGGGGGCGC 720
 TGGGTGTGGG TGCAAGACTA CGCCACCGTG GTGCACAACA GCGCTCTGTC CCGGGCCCCA 780
 TGCATCTGTA GTGTCAATTA TGTACTCAGC GAGATTGAAT ACAAGGAAC TACGCTGTCC 840
 80 CTGGAGCAGG TGTCCACTGC CAAGTCCAG GACTCCCTGA GACCGCCTT GTCTACCTCA 900

5 CAAGAACTA GGAAATTAGT GAAACCCAAA AATACCAAGA TGAAGACAAA GCTGAGAACA 960
 AACCCATTACC CCCACAGCA ATACAGCTCG TTCCAAATGG ACAAACTGGA ATGCGGCCAG 1020
 CTCGGAAACT GGAGAGCCAG TCCCTCTGCA AGCGCTGCTG CTCCTCCAGA ACTGCAGCCC 1080
 CACTCAGAAA GCAGTGACCT TCTGTACAG CCATCTTACA GCCTGCCCTT CTCCTACCAT 1140
 TACGGACACT TCCTCTGGA CTCTCACGTC TTCAGCAGCA AAAAGCCAAT GTTGCCGGCC 1200
 AAGTTCGGGC AGCCCCAAGG ATCCCTTGTG GAGGTGGCAC GCTTTTCTCT GAGCACACTG 1260
 CCAGCCAGCG GTGAATGCCA GTGGCATTAT GCCAACCCCC TAGTGCCTAG CAGCTCGTCT 1320
 CCAGCTAAAA ATCTCCAGA GCCACCGGCG AACACTGCTA GGCACAGCCT GGTGCCAAGC 1380
 TACGAAGGCA AGCAGATGTC CTCTGCGGAG ATACCGCCAG CTCGCCAGGA CGCAGACTGA 1440
 10 CTCTGTGTTG CTGCTGAGC CAAC

SEQ ID NO:269 PBH8 Protein sequence:

Protein Accession #: NP_005060

15 MKEKSKNAK TRREKENGFE YELAKLLPLP SAITSQLDKA SIIRLTTSYL KMRAVFPPEGL 60
 GDAWQPSRA GPLDGVAKEL GSHLLQLLDG FVFVVASDGL IMYISETASV HLGLSQVELT 120
 20 GNSIYEYIHP SDHDEMTAVL TAHQPLHHHL LQEYIERSF FLRMKCVLAK RNAGLTCSGY 180
 KVIHCSGYLK IRQYMLDMSL YDSCYQIVGL VAVGQSLPPS AITEIKLYSN MFMFRASLDL 240
 KLIFLDSRVT EYTGYPEQDL IEKTLYHHVH GCDVFHLRYA HHLLEVKGQV TTKYRLLSK 300
 RGGWVWVQSY ATVVHNSRSS RPHCIVSVNY VLTEIEYKEL QLSLBQVSTA KSQDSWR TAL 360
 STSQETRLKV KPNKTKMKT LRTNPYPQQ YSSFQMDKLE CGQLGNWRAS PPASAAAPPE 420
 LQPHSESDLL LYTPSYSLPF SYHYGHFPLD SHVFSSKKPM LPAKFGQPQ SPCEVARFFL 480
 25 STLPAHGECQ WHYANPLVPS SSSPAKNPPE PPANTARHSL VPSYEAPAAA VRRFGEDTAP 540
 PSFPCSGHYR EEPALGPAKA ARQAARDGAR LALARAAPEC CAPPTPEAFG APAQLPFVLL 600
 NYHRVLARRG PLGGAAPAAS GLACAPGGPE AATGALRLRH PPSAATSPPG APLPHYLGAS 660
 VIITNGR

SEQ ID NO:270 PBJ9 DNA sequence:

Nucleic Acid Accession#: AA760894

GGCACGAGGA GAAGATGTGG CTGTCTCATG CTGTGACTCT GCCATGGTTG TGAGGCCTCC 60
 CCAGCCATGT GGAAGCTGTT TCAGGTGCTG GTTCCATGGC TCCTCCTGAG CCGAAAAATA 120
 35 GGAAACTCCA TAGACTCTGT CCACTGGAAC TCGTTCCTCAT CTACCTCCA CTCTATCCAG 180
 GGTGATGGAT CTCTGCAGTA AGTGGAAAGAG TTCTTCATGG CCCCCAAGGT TATATCCATC 240
 TAGAACTTCA GCACGTAATT TCATCTGGAA ATAGTGCCTT TGTGGATATA AGTTAGGTAA 300
 AACTGAAGAT GAGATCATA TGGATTAGGA TGGGATCTAA ATCCAATGAA AATGTCTTCA 360
 TAAAAAACAG GAAAGAACCC ATAGAAACAC AAGGAAGAAG GTCATGTGAA GATGGAGGCA 420
 40 GAGATTGGAG GGATGCGAGC ACCGGCCCGG GAATGCCAGC AGCCACCCAG AAGCTGGAAG 480
 GAAATAGGGG ATTCTCTCTC AGAACCTTGA GAGAGRACAT GGTCTCTGTA ACAGCTTGAT 540
 TTTGGACTTG CCCATAGCTT GTATACTCTT ACTTTGGATA CAATTTTATC CAACTTGGC 600
 TAAACAGTTT CTCAGCCTAT GGAAAAATTA AAATGGAGAA GATTCAACTC GATTCCTACA 660
 GATTCAAAGC AAGAAATATG TGGGAACATA GGAGGAGACC AAGAAAGCCT AAAAAAGCA 720
 45 AAAATATGAA GTGAACATGT TGGTAGCTTT AAGATGTTTA GTGTAGCTGC AGGCACCCTA 780
 TACACATGAA AACCCCCAAG GGGAAATCCCC ATATCACAGT GTAGTGTGAT ATTGACATT 840
 YGTGATCATY TAGAGATGTA CAGAAAAGGT GAATCTGTGT TCTGTATATT CTGCCTAAGG 900
 CAAAGAAATG TTTAGCTCTC TTAAAAATAG TTCCATAATT TTTTAAATAA AGCTTTGCTT 960
 50 GAAAACTGTA AGCTTCCCAT ATCTGGAGCA TTTCACITTA AATATTTGGA TAAATATGTT 1020
 ATCTTCTTAC TTGGACATTT CATGTGTTTA GGGATTGTYT TYTAAATTCT TCCTAATTA 1080
 TATAGCTGCT AACACTTCCC GCAGAGCTAA ACCATTACAG ANTATGAAAT AAAGACCTTA 1140
 TTGATTTGAA CTTAAAAAAA AAAAMAMAAA AAAAAAAAAA AAAAAAAAAA GA

SEQ ID NO:271 PBQ4 DNA sequence

Nucleic Acid Accession#: AA149579

Coding sequence: 1-1363 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 60 ATGGAATCAA TCTCTATGAT GGGAAAGCCCT AAGAGCCCTA GTGAAACTTG TTTACCTAAT 60
 GGCATAAATG GTATCAAGA TGC AAGGAAG GTCACGTAG GTGTGATTGG AAGTGGAGAT 120
 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
 AGAAATCCTA AGTTTGCTTC TGAATTTTCT CCTCATGTGG TAGATGTCAC TCATCATGAA 240
 GATGCTCTCA CAAAAACAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300
 65 CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CARTAACATG 360
 AGGATAAAC AGTACCAGA ATCCAATGCT GAATATTTGG CTTCATTATT CCCAGATTCT 420
 TTGATTGTCA AAGGATTTAA TGTGTCTCA GCTTGGGCAC TTCAGTAGG ACCTAAGGAT 480
 GCCAGCCGGC AGGTTTATAT ATGCAGCAAC AATATTC AAG CGGACAACA GGTATTTGAA 540
 CTGTGCCGCC AGTTGAATTT CATTCCTCAT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600
 70 ATTGAAATTT TACCCCTACG ACTCTTTACT CTCTGGAGAG GGCCAGTGGT GGTAGCTATA 660
 AGCTTGGCCA CATTTTTCTT CCTTTATFCC TTGTCTAGAG ATGTGATTTA TCCATATGCT 720
 AGAAACCAAC AAGGTGACTT TTACAAATTT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
 ATAGTTGCCA TTAATTTGCT CTCCCTAGTA TACCTCGCAG GTCTTCTGGC AGCTGCTTAT 840
 CAACCTTATT ACGGCACCAA GTATAGGAGA TTTCACCTT GGTGGAAC CTGGTTACAG 900
 75 TGTAGAAAAC AGCTTGGATT ACTAAGTTT TTCTTCGCTA TGGTCCATGT TGCCTACAGC 960
 CTCTGCTTAC CGATGAGAAG GTACAGAGAGA TATTGTGTTT TCAACATGGC TTATCAGCAG 1020
 GTTCATGCAA ATATTGAAA CTCTTGGAA GAGGAAGAAG TTTGGAGAA TGAATGTAT 1080
 ATCTCTTTG GCATAATGAG CCTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTTA TTCAGTCTAC ACTTGATAT 1200

GTGCGCTCTGCG TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAAACG AGCTTTTGTAG 1260
 GAAGAGTACT ACAGATTTTA TACACCACCA AACTTTGTTT TTGCTCTTGT TTTGCCCTCA 1320
 ATGTGAATTC TGGATTTTTT GCAGCTTTGC AGATACCCAG ACTGA

5

SEQ ID NO:272 PBQ4 Protein sequence:
 Protein Accession #: none

10 1 11 21 31 41 51
 MESISMMGSP KSLSETCLPN GINGIKDARK VTVGVIGSGD FAKSLTIRLI RCGYHVIVGS 60
 RNKFFASEFF PHVVDVTHHE DALTKTNIIF VAIHREHYTS LWDLRHLLVG KILIDVSNM 120
 RINQYPESNA EYLASLFPDS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQVIE 180
 LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGPFVVVAI SLATFFFLYS FVRDVIHPYA 240
 15 RNQSQDFYKI PIETVNTLPI IVAITLLSLV YLAGLLAAAY QLYYGFKYRR FPFWLETWLQ 300
 CRKQLGLLSF FFAMVHVAYS LCLPMRRSER YLFLNMAVQQ VHANIENSWN EEEVWRIEMY 360
 ISFGIMSLGL LSLLAVTSIP SVSNALNWR FSIQSTLGY VALLISTFHV LIYGWKRAFE 420
 EEEYRFYTPP NFVLAIVLPS IVILDLLQLC RYPD

20

SEQ ID NO:273 PBQ5 DNA SEQUENCE

Nucleic Acid Accession#: NM_001973
 Coding sequence: 150-1445 (underlined sequence corresponds to start and stop codon)

25 1 11 21 31 41 51
 CCGCCGCCCTT CTACTCCGCC GCGGGGGTCC CAGCGGCTGC CGCGCCGTCC TCGAGTTTCC 60
 AGCGTGAGGA GAGGCTGAGG GCGGAGAGG CGCATCGTGT TCGAGGCGGA GACCGAGGGG 120
 GAGCCCGCGG CGCGGCGTCC CTCATTGCTA TGGACAGTGC TATCACCTGT TGGCAGTTCC 180
 30 TTCTTCAGCT CCTGCGAAG CCTCAGAAC AGCAGATGAT CTGTTGGACC TCTAATGATG 240
 GGCAGTTTAA GCTTTTTCAG GCAGAAGAGG TGGCTCGTCT CTGGGGGATT CGCAAGAACA 300
 AGCCTAACAT GAATATGAC AACTTCAGCC GAGCCCTCAG ATACTATTAT GTAAAGAATA 360
 TCATCAAAAA AGTGAATGGT CAGAAGTTTG TGTACAAGTT TGTCTCTTAT CCAGAGATTT 420
 TGAACATGGA TCCAATGACA GTGGGCAGGA TTGAGGGTGA CTGTGAAAGT TTAACCTTCA 480
 GTGAAGTCAG CAGCAGTTCC AAAGATGTGG AGAATGGAGG GAAAGATAAA CCACCTCAGC 540
 35 CTGGTGCCAA GACCTCTAGC CGCAATGACT ACATACACTC TGGCTTATAT TCTTCATTTA 600
 CTCTCAACTC TTTGAATGCC TCCAATGTAA AGCTTTTCAA ATTGATAAAG ACTGAGAATC 660
 CAGCCGAGAA ACTGGCAGAG AAAAAATCTC CTCAGGAGCC CACACCATCT GTCATCAAAAT 720
 TTGTACACGAC ACCTTCCAAA AAGCCACCAG TTGAACCTGT TGCTGCCACC ATTTCAAATTG 780
 40 GCCCAAGTAT TTCTCCATCT TCAGAAGAAA CTATCCAAGC TTTGGAGACA TTGGTTTCCC 840
 CAAAACGTCC TTCCCTGGAA GCCCAACCT CTGCCTCTAA CGTAATGACT GCTTTTCCCA 900
 CCACAGCACG CATTTCTGTC ATACCCCTTT TGCAGGAACC TCCCAGAAAC CTTTCACCCAC 960
 CACTGAGTTC TCACCCAGAC ATCGACACAG ACATGTGATC AGTGGCTTCT CAGCCAATGG 1020
 AACTTCCAGA GAATTTGTCT CTGGAGCCTA AAGACCAGGA TTCAGTCTTG CTAGAAAAGG 1080
 45 ACAAAGTAAA TAAVTCATCA AGATCCAAGA AACCCAAAGG GTTAGGACTG GCACCCACCC 1140
 TTGTGATCAC GAGCAGTGAT CCAAGCCAC TGGGAATACT GAGCCCATCT CTCCCTACAG 1200
 CTTCTCTTAC ACCAGCATTT TTTTCACAGA CACCATCAT ACTGACTCCA AGCCCTTTCG 1260
 TCTCCAGTAT CCACTTCTGG AGTACTCTCA GTCCCTGTTC TCCCTTAAGT CCAGCCAGAC 1320
 TGAAGGTGCG TAACACACTT TTCCAGTTTC CTTCTGTACT GAACAGTCAT GGGCCATTCA 1380
 50 CTCTGTCTGG GCTGGATGGA CCTTCCACCC CTGGCCCAT TTTCCACAGC CTACAGAAGA 1440
 CATTAACATAT GCATCTGTGG AATGAGAGAA CCGAGGAACG AAGAAACAGA CATTCACAT 1500
 GATTGCAATT GAAGTGAGCA ATTGATAGTT TCACAATGCT GATAATAGAC TATTTGTGAT 1560
 TTTGCCATTC CCCATGAAA ACATCTTTT AGGATTTCTCT TTGAATAGGA CTCAGTTTGG 1620
 ACTATATGTA TAAAAATGCC TTAATTGGAG TCTAACTCC ACCTCCCTCT GTCTTTTCCT 1680
 55 TTTCTTTTTC TTTCTTCTCT TCTTCTTTA AAAATATTTT GAGCTTTGTG 1740
 CTGAAGAAGT TTTTGGTGGG CTTTAGTGAC TGTGCTTTGC AAAAGCAATT AAGAACAAG 1800
 TTACTCCTTC TGGCTATTGG GACCTTTGG CCAGGAAAAA TTATGCTTAG AATCTATTAT 1860
 TTAAGAAGT ATTTGTGAAA TGAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1920
 AAAAAAAA AAA

60

SEQ ID NO:274 PBQ5 Protein sequence:
 Protein Accession #: NP_001964

65 MDSAITLWQF LLOLLQKPN KHMICWTSND GQFKLLQAE VARIWGIRKN KPNMNYDKLS 60
 RALRYYYVKN IIKVNGQKF VYKFVYPEI LNMDPMTVGR IEGDCESLNF SEVSSSKDV 120
 ENGGKDKPPQ PGAKTSSRND YHSGLYSSF TLNSLNSSNV KLFKLIKTE PAEKLAEEKS 180
 PQEPTPSVIK FVTTPSKPP VEPVAATISI GPSISPSSEE TIQALETLS PKLPSLEAPT 240
 SASNVMTAFA TTPNISIPP LQEPPTPSP PLSSHPDIDT DIDSVASQPM ELPENLSLEP 300
 70 KDQDSVLEK DKVNNSSRSR KPKGLGLAPT LVITSSDFSP LGILSPSLPT ASLTPAFESQ 360
 TPILTPSPL LSSIHFWSTL SPVAPLSPAR LQGANTLFQF PSVLNSHGFF TSLGLDGPST 420
 PGFSPDLQK T

75

SEQ ID NO:275 PB3 DNA SEQUENCE

Nucleic Acid Accession#: AB040921
 Coding sequence: 131-2560 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

5 AATCAGGAAC AGATCATATA TTGACCGAGA TTCTGAGTAT CTCTTGCAAG AAAATGAACC 60
 AGATGGAAGT TTAGACCAAA AATTTATTTGGA AGATTTACAA AAGAAAAAA ATGACCTTCG 120
 GTATATTTGAA ATCCAGCATT TCAGAGAAAA GCTGCCTTCG TATGGAATGC AAAAGGAATT 180
 GGTAATTTTA ATTGATAACC ATCAGGTAAC AGTAATAAGT GGTGAAACTG GTTGTGGCAA 240
 AACCRCTCAA GTTACTCAGT TCATTTTGGG TAACCTACAT GAAAGAGGAA AAGGATCTGC 300
 TTGCAGAAATA GTTTGTACTC AGCCAAGAAG AATTAGTGCC ATTTTCAGTTG CGGAAAGAGT 360
 AGCTGCAGAA AGGGCAGAAT CTGTGCGCAG TGGTAATAGT ACTGGATATC AAATTCGTC 420
 CCAGAGTCGG TTGCCAAGGA AACAGGGTTC TATCTTATAC TGTACAACAG GAATCATCCT 480
 10 TCAGTGGCTC CAGTCAGACC CGTATTTGTC CAGTGTTAGT CATATCGTAC TTGATGAAT 540
 CCATGAAAGA AATCTGCAGT CAGATGTTTT AATGACTGTT GTTAAAGACC TTCTCAATTT 600
 TCGATCTGAC TTGAAAGTAA TATTGATGAG TGCACATTTG AATGCAGAAA AGTTTTCAGA 660
 ATATTTTGGT AACTGTCCAA TGATACATAT ACCTGGTTTT ACCTTTCGGG TTGTGGARTA 720
 TCTTTTGGAA GATGTAATTG AAAAAATAAG GTATGTTCCA GAACAAAAAG AACACAGATC 780
 15 CCAGTTTAAG AGGGGTTTCA TGCAAGGGCA TGTAATAGTA CAAGAAAAAG AAGAAAAAGA 840
 AGCAATATAT AAAGAAGCTT GGCCAGATTA TGTAAGGGAA CTGCCAAGAA GGTATCTGTC 900
 AAGTACTGTA GATGTTATAG AAATGATGGA GGATGATAAA GTTGATCTGA ATTTGATTGT 960
 TGCCCTCATC CGATACATTTG TTTTGGAAAG AGAGGATGGT GCGATACTGG TCTTCTGCC 1020
 AGGCTGGGAC AATATCAGCA CTTTACATGA TCTCTTGATG TCACAAGTAA TGTTTAAATC 1080
 20 AGATAAATTT TTAATTTATC CTTTACATTC ACTGATGCCT ACAGTTAACC AGACACAGGT 1140
 GTTTAAAAAG ACCCTTCCTG GTGTTCCGAA AATAGTAATT GCTACCAACA TTGCGGAGAC 1200
 TAGCATTTAC ATGATGATG TGCTTTTATGT GATAGATGGA GGAAAAATAA AAGAGACGCA 1260
 TTTTGATACT CAGAACATA TCAGTACAA GTCCGCTGAG TGGGTAGTA AAGCTAATGC 1320
 CAAACAGAGA AAGGTCGAG CTGGAAGAGT TCAACCTGGT CATTGCTATC ATCTGTATAA 1380
 25 TGGTCTTAGA GCAAGTCTTC TAGATGACTA TCAACTGCCA GAAATTTTGA GAACTCCTTT 1440
 GGAAGAACTT TGTTTACAAA TAAAGATTTT AAGGCTAGGT GGAATTGCTT ATTTTCTGAG 1500
 TAGATTAATG GACCCACCAT CAAATGAGGC AGTGTACTC TCATAAGAC ACCTGATGGA 1560
 GCTGAACGCT TTGGATAAAC AAGAAGAATT GACACCTCTT GGAGTCCACT TGGCAGGATT 1620
 ACCCGTTGAG CCACATATTG GAAAAATGAT TCTTTTGGGA GCATGTTCT GCTGCTTAGA 1680
 30 CCCAGTACTC ACTAATGCTG CTAGTCTCAG TTTCAAAGAT CCATTTGTCA TTCCACTGGG 1740
 AAAAGAAAGT ATTGCAGATG CAAGAAGAAA GGAATTGGCA AAGGATCTA GAAGTGATCA 1800
 CTTAATAGTT GTGAATGCGT TTGAGGGCTG GGAACAGGCT AGGCGACGTG GTTTCAGATA 1860
 CGAAAAGGAC TATGCTGGG AATATTTTCT GTCTTCAAAC ACACGTCAGA TGCTGCATAA 1920
 CATGAAGAGA CAGTTTGGTG AGCATCTTCT TGGAGCTGGA TTTGTAGACA GTAGAAATCC 1980
 35 TAAAGATCCA GAATCTAATA TAAATTCAGA TAATGAGAAG ATAATPAAAG CTGTATCTG 2040
 TGCTGGTTTA TATCCCAAAG TTGCTAAAT TCGACTAAAT TTGGSTAAA AAGAAAAAT 2100
 GGTAAAGTT TACACAAAAA CCGATGGCCT GGTTCCTGTT CATCTAAAT CTGTTAATGT 2160
 GGAGCAAAAC GACTTTTCACT ACAACTGGCT TATCTATCAC CTAAAGATGA GAACAAGCAG 2220
 TATATATTTG TATGACTGCA CAGAGGTTTC CCCATCTGTT CTCTTGTGTT TTGGAGGTGA 2280
 40 CATTTCCATC CAGAAGGATA ACGATCAGGA AACTATTGCT GTAGATGAGT GGATGTATT 2340
 TCAGTCTCCA GCAAGAAITG CCCATCTTGT TAAGGAATTA AGAAGGAAC TAGATATTCT 2400
 TCTGCAAGAG AAGATTGAAA GTCTCTATCC TGTAGACTGG AATGACACTA AATCCAGAGA 2460
 CTGTGCAGTA CTGTCACTTA TTATAGACTT GATCAAAACA CAGGAAAGG CAATCCAGG 2520
 GAACTTTCCG CCACGATGCC AGGATGGATA TTACAGCTGA CAGCTTTTCA GGGGTGGTCT 2580
 45 GAAAAGCCAG TTGACAGCC ATTCTTCATC ATTTGTTTAA TTTTGGCTGG ATGCCAAACC 2640
 CTGGGACATG AACAAATTTT ATGTGTAAGG TAGAAGCCTT CAGTAGGTAG TAAAGACTTA 2700
 ATGTGCATGA CTGTATGTTA TATGTAGAGA TATATATATA TATATATATA CCATAAAGC 2760
 AATATGTTCT CTGATCATAT ACTCTGCTGT GGTCTATGCC ACTCTTTGGG AGTATATTCC 2820
 50 CTTTATATAT ATTGAGTATT GTACCACTTG AGAATTCCT TTGTCTGTT ATCAAAATTT 2880
 AATCTTTCTG CTCATAATGA TTGATGATAC CACCAGTAAA AATAGGATGT TTACCCCAAA 2940
 ACAAGTGTCA ATTAAGAATT TGAACACAAC CACATTTTCT AAAATGAAC TTCTATCGGA 3000
 AGTAAATTAA TTTGTTGTAA TAAAGTCCAG TATTTAATAA AATGTACAT GTTAGATCTC

SEQ ID NO:276 PBYS Protein sequence:

Protein Accession #: BAA96012

55 IRNRSYIDRD SEYLLQENEP DGTLDQKLE DLQKKKNDLR YIEMQHREK LPSYGMQKEL 60
 VNLIDNHQVT VISGETCGCK TTQVTQFILD NYIERGKGS CRIVCTQPRR ISASVAERV 120
 AAERAESCGS GNSTGYQRL QSRLPRKQGS ILYCTTGIL QWLQSDPYLS SVSHIVLDEI 180
 60 HERNLQSDVL MTVVKDLINF RSDLKVLMS ATLNAEFSE YFGNCPMIHI PGFTFPVVEY 240
 LLEDVIEKIR YVPEQKEHRS QFKRGFMQGH VNRQEKEKE AIYKERWPDY VRELRRRYSA 300
 STVDVIEEME DDKVDNLIV ALIRYIVLEE EDGAILVFLP GWDNISTLHD LLMSQVMFKS 360
 DKFLIPLHS LMPTVNQTV FKRTPPGVRK IVIATNIAET SITIDVYVY IDGGKIKETH 420
 FDTQNNISTM SAEWVSKANA KQRKGRAGRV QPGHCYHLYN GLRASLLDDY QLEILRTPL 480
 65 EELCLQIKIL RLGIAFYLS RIMDPPSNEA VLLSIRHLE LNALDKQEE TPLGVHLARL 540
 PVEPHIGKMI LFGALFCCLD PVLTAASLS FKDPFVPLG KEKIDARRK ELAKDTRSDH 600
 LTVVNAFEGW EEARRRGFRY EKDYCWEYFL SSNTLQMLHN MKGQFAEHL GAGFVSSRNP 660
 KDPESNINSV NEKIKAVIC AGLYPKVAKI RLNLGKKRKM VKVYTKTDGL VAVHPKSVNV 720
 EQTDFHYNWL IYHLKMRSS IYLYDCTEVS PYCLLFFGGD ISQKNDNDQE TIAVDEWIVF 780
 70 QSPARIAHLV KELRKELDIL LQEKIESPHV VDWNDTKSRD CAVLSAIDL IKTQEKATPR 840
 NFPPRQDGY YS

SEQ ID NO:277 PBYS DNA SEQUENCE

75 Nucleic Acid Accession#: AA464018
 Coding sequence: 64-1669(underlined sequence corresponds to start and stop codon)

GATTTATCC TGGAACATTA CAGTGAAGAT GGCTATTTAT ATGAAGATGA AATTGCAGAT 60
 CTTATGGATC TGAGACAAGC TTGTCGGACG CCTAGCCGGG ATGAGGCCGG GGTGGAAGT 120

CTGATGACAT ACTTCATCCA GCTGGGCTTT GTCGAGAGTC GATTCTTCCC GCCACACGG 180
 CAGATGGGAC TCCTGTTTAC CTGGTATGAC TCTCTACCG GGGTCCGGT CAGCCAGCAG 240
 AACCTGCTGC TGGAGAAGGC CAGTGTCTCTG TTCAACACTG GGGCCCTCTA CACCCAGATT 300
 GGGACCCGGT GTGATCGGCA GACGCAGGCT GGGCTGGAGA GTGCCATAGA TGCCTTTCAG 360
 5 AGAGCCCGCAG GGGTTTTAAA TTACCTGAAA GACACATTTA CCCATACTCC AAGTTACGAC 420
 ATGAGCCCTG CCATGGCTCAG CGTGCTCGTC AAAATGATGC TTGCACAAGC CCAAGAAAAGC 480
 GTGTTTGAGA AAATCAGCCT TCTGGGATC CGGAATGAAT TCTTCATGCT GGTGAAGGTG 540
 GCTCAGGAGG CTGCTAAGGT GGGAGAGGTC TACCAACAGC TACACGCAGC CATGAGCCAG 600
 10 GCGCCCGTGA AAGAGAACAT CCCCTACTCC TGGGCCAGCT TAGCCTGCGT GAAGGCCAC 660
 CACTACGCGG CCCTGGGCCA CTACTTCACT GCCATCCTCC TCATCGACCA CCAGGTGAAG 720
 CCAGGCACCG ATCTGGACCA CCAGGAGAAG TGCCGTGCC AGCTCTACGA CCACATGCCA 780
 GAGGGGCTGA CACCTTGGC CACACTGAAG AATGATCAGC AGCGCCGACA GCTGGGGAAG 840
 TCCCCTTGC GCAGAGCCAT GGCTCATCAC GAGGAGTCGG TCGGGGAGGC CAGCCTTGC 900
 AAGAAGCTGC GGAGCATTTGA GGTGCTACAG AAGGTGCTGT GTGCCGCACA GGAACGCTCC 960
 15 CGGCTCACGT ACGCCAGCA CCAGGAGGAG GATGACCTGC TGAACCTGAT CGACGCCCCC 1020
 AGTGTGTGTG CTAAACTGA GCAAGAGGTT GACATTATAT TGCCCCAGTT CTCCAAGCTG 1080
 ACAGTCACGG ACTTCTTCCA GAAGCTGGGC CCTTATCTG TGTTTTCGGC TAACAAGCG 1140
 TGGACGCTC CTCGAAGCAT CCGCTTCACT GCAGAGAAG GGGACTTGGG GTTCACTTG 1200
 20 AGAGGGAACG CCCCCTTCA GTTTCACCTC CTGGATCCTT ACTGCTGTC CTCGGTGCCA 1260
 GGAGCCCGGG AAGGAGATTA TATTGTCTCC ATTCACTTG TGGATTGTA GTGGCTGACG 1320
 CTGAGTGAGG TTATGAAGCT GCTGAAGAGC TTTGGCGAGG ACGAGATCGA GATGAAAGTC 1380
 GTGAGCCTCC TGGACTCCAC ATCATCCATG CATAATAAGA GTGCCACATA CTCGTTGGGA 1440
 ATGCAGAAAA CGTACTCCAT GATCTGCTTA GCCATTGATG ATGACGACAA AACTGATAAA 1500
 25 ACCAAGAAA TCTCCAAGAA GCTTCTCTC CTGAGTTGGG GCACCAACAA GAACAGACAG 1560
 AAGTCAGCCA GCACCTTGTG CTTCCCATCG GTCGGGGCTG CACGCCTCA GGTCAGAAG 1620
 AAGTGCCCT CCCCTTCAG CTTCTCAAC TCAGACAGTT CTGGTACTAA

30 **SEQ ID NO:278 PBV6 Protein sequence:**
 Protein Accession #: NP_149084

DFILEHYSED GYLVEDEIAD LMDLRQACRT PSRDEAGVEL LMTYFIQLGF VESRFFPPTR 60
 QMGLLEFTWYD SLTGVPVSQQ NLLLEKASVL FNTGALYTIQI GTRCDRQTQA GLESAIDAFQ 120
 35 RAAGVLNLYLK DTFHTPSYD MSPAMLSVLV KMMLAQAES VFEKISLPGI RNEFFMLVKV 180
 AQEAAKVGEV YQQLHAAMSQ APVKENIPYS WASLACVKAH HYAALAHYFT AILLIDHQVK 240
 PGIDLDHQEK CLSQLYDHMP EGLTPLATLK NDQQRRLGK SHLRRAMAHH EESVREASLC 300
 KKLRSIEVLQ KVLCAAQERS RLTYAQHQEE DDLNLIDAP SVVAKTEQEV DIILPQFSKL 360
 TVTDFQKLGL PLSVFSANKR WTPRSIRFT AEEGDLGFTL RGNAPVQVHF LDPYCSASVA 420
 40 GAREGDIYVS IQLVDCKWLT LSEVMKLLKS FGEDEIEMKV VSLDSTSSM HNKSATYSVG 480
 MQKTYSMICL AIDDDDKTDK TKKISKLLSF LSWGTNKNRQ KSASTLCLPS VGAARPQVKK 540
 KLPSPFSLN SDSSWY

45 **SEQ ID NO:279 PBV8 DNA SEQUENCE**
 Nucleic Acid Accession#: AF107493
 Coding sequence: 125-556 (underlined sequence corresponds to start and stop codon)

	1	11	21	31	41	51	
50	GAATTCGGCA	CGAGCCTTGT	TGGAGGTTCT	GGGGCGCAGA	ACCGCTACTG	CTGCTTCGGT	60
	CTCTCCCTGG	GAAAAATAAA	AATTTGAACC	TTTTGGAGCT	GTGTGCTAAA	TCTTCAGTGG	120
	GACATATGGT	TCAGACAAAA	GAGTGAGTAG	AACAGAGCGT	AGTGGAAAGT	ACGGTTCCAT	180
	CATAGACAGG	GATGACCGTG	ATGAGCGTGA	ATCCCGAAGC	AGCGGAGGGG	ACTCAGATTA	240
55	CAAAAGATCT	AGTGATGATC	GGAGGGGTGA	TAGATATGAT	GACTACCGAG	ACTATGACAG	300
	TCCAGAGAGA	GAGCGTGAAA	GAAGGAACAG	TGACCGATCC	GAAGATGGCT	ACCATTCAGA	360
	TGGTGACTAT	GGTGAGCAGC	ACTATAGGCA	TGACATCAGT	GACGAGAGGG	AGAGCAAGAC	420
	CATCATGCTG	CGCGGCCTTC	CCATCACCAT	CACAGAGAGC	GATATTCGAG	AAATGATGGA	480
	GTCCTTCGAA	GGCCCTCAGC	CTGCGGATGT	GAGGCTGATG	AAGAGGAAAA	CAGGTGAGAG	540
60	CTTGCTTAGT	TCCTGATATT	ATTGTTCTCT	TCCCCATTCC	CACCTCAGTC	CCTAAAGAAC	600
	ATCCTGATTC	CCCCAGTCTT	CAAGCACATG	AATTCAGAAT	GAAAGGTTTG	CCATGGCTAA	660
	GGAATGTGAC	TCTTTGAAAA	CCATGTTAGC	ATCTGAGGAA	CTTTTATAAA	CTTTGTTTAA	720
	GGGACTTTTT	TTTCTCTAGG	TAAGTAATGA	TTTATAAACT	CCTTTTTTTT	TTTGACTATA	780
	GTCGGTTGCA	TGGTTACTTT	AAGCGTGGAA	TCAAATGGAG	TGGCATTTAG	TTCAGGCGGC	840
65	TTGTTTCCTT	CCATGGCAAA	GTATCAAGAA	GATCCCCAAG	TCAAGTCACA	TTTGTAAGC	900
	TGCTTCCCAA	TTGGCTTTGT	CACGCAGTGT	TGAAGCAGTG	GGAGAGAGAT	TCACCTGTTA	960
	TAAAGGAAC	GACTAACACA	AGTATCCCGT	CTATATCTGA	ATGCTGTCTC	TAGGTGTAAG	1020
	CCGTGGTTTC	GCCTTCGTGG	AGTTTATCA	CTTGCAAGAT	GCTACCAGCT	GGATGGAAGC	1080
	CAATCAGGTT	GCCTCACTCA	CCAAGTCTAG	ATATTCATGA	AAATGGAACA	AGCTGTGACA	1140
70	ATTTTAAAA	AAGGTTGAAG	GAGTGGTTTG	TTCCAAAGGA	GTGACTTTTT	TTTAAAAAAA	1200
	AAGCTTTGTA	TATATATAAA	TGTATGTAC	TAGAATAAGT	ACAGTACCAA	GGACTTCATT	1260
	ATAGAATTG	TTCTGCCTTT	AAACATGGCT	ACCTACCTGG	CAGGGCTTTG	TTAACTACTG	1320
	AATACCTGTC	TGGTAATCAT	TAAAACATCT	TTATGTTTCC	CTTTTCTCTA	GTTTGTATA	1380
	TTCTATATAT	GTCCATTGAG	AGTAAGCTTA	GTATATCAAA	CTCTCCATTT	GACAGTGAAG	1440
75	AGAACAATAGT	GAAAGTCTGT	GGCGGCATTT	TTATAAGTAA	TTCTTATTTT	CTGCCTGAAG	1500
	ACCACAAAGC	CTCTCGGAGG	CGTAACCTGT	CAGACCGGTC	TTCAGGGAAT	ATTTAAGGAC	1560
	TTAGTGAAGT	TTATGAACAA	TAAGTCTGAT	GAGATTAGCC	TGGGAGTGGT	GTCTGTCAGC	1620
	TGCTATATCT	AGAGTGGCAT	TAACATTCTA	ATCTCCTTGA	GAATGCCTTT	TATAGCTCTG	1680
	TCAAAGCAAG	TCATTGATGG	TTCTTCGAGG	TAGTGTAAAC	TGAAGTGTTT	TTCAAGTTGT	1740
	CAAGATAATG	TTCAAGTCTT	GGCACTTAAA	TAACATTTTT	TGCAAGAACT	CCAAGGCACA	1800

5	TTATTGAATG CCTTAAACCA AGTGCATTCT GGAAGTTTG CTTGACTCAT TATCTTGCTT 1860
	TTCTGCAGCA TTCTGTGATT TGAGTCATCC ATGAATCCAT GAATAAAGT TACATTCTTT 1920
	GATTGGTAAT ATTGCCATTT ATAACAAGAC TCACTAATGA GGGTATCACT TTGACTGACT 1980
	GATTTGTTAA AGTTTAAAG CCTCTCATTT TCCTAACCCA GAAATCACAG CCTGATTTTA 2040
	TTAAAAGTAG AGCTTCATTC ATTTTCATACC ATAGATACCA TCCTAGTAAA TCCAGAACAT 2100
	ATACAAGGTT CATGTGAGTC TGCTTCTTG ACATGATAGC ATTGTTTGAT GCAGTGGATA 2160
	TGTCAAGATG ACTAACCTAG GAGTTTGAAG CTCTTAAGAA ACTAAACCT GTAGACATT 2220
	TAAAAGTCTC CACAATTTTA ATGTATACAA AGCTATGTTA CTGTGTAACA CATTACAGTT 2280
10	CAAATTCACCT CCAGAAATAA AAGGCCAGTA GGATTAGGGA CTCACCTGGTA GTTTGGAGTC 2340
	TCCCAGCACA CATCCCTCCT AGTGGGATGA TCTATTCACA TATCTCCCAG CTTTTTTATT 2400
	TTTGCCTCTG TATATCACAG TGAGTGGATG GCCCTTCAGC TTTTCTCTC CTGCCAGAC 2460
	ATGCAGCTCT GCCTTTAGAT ATCGCAGAGA CAAATTCAC AGCATGTCTT AAATCTTCCA 2520
	GGATTTGCAA GAACCAAAAT GCTCAACAGT ATGTATGTTT AGAGGGGTTA GACTCCTTTT 2580
15	TAAAATCTGG ATATCTAAC ACCTACTTAA ATCTGTTTGA TAGTGTGCAA CCACCCCCAC 2640
	CCTTGATCCT CCCACCCCA AAAAAAAAA AAAAA

SEQ ID NO:280 PBV8 Protein sequence:
Protein Accession #: XP_003261

20	MGSDKRVSRT ERSGRYGSII DRDRDERES RSRRRSDYK RSSDDRRGDR YDDYRDYDSP 60
	ERERERRNSD RSEDGYHSDG DYGEHDYRHD ISDERESKTI MLRGLPITIT ESDIREMMES 120
	FEQPQPADVR LMKRKTGESL LSS

25

SEQ ID NO:281 PC12 DNA SEQUENCE

Nucleic Acid Accession#: AF208291
Coding sequence: 109-3705 (underlined sequence corresponds to start and stop codon)

30	1 11 21 31 41 51
	CGGCCGCTTT TTCTCAAGA TGGCAGATTC CCACTGAGGC TGAGGGGGGCC GAGCTCGCGC 60
	GCCGCCGTTCC CTCTCTCGTT GCCATGAACC GCGGACACCC CGGCCCCGAT GGGCCCCGTG 120
35	TACGAAGGTA TGGCCTCACA TGTGCAAGTT TTCTCCCTTC ACACCCCTCA ATCAAGTGCC 180
	TTCTGTAGTG TGAAGAAACT AAAAGTAGAG CCAAGTTCCA ACTGGGACAT GACTGGGTAC 240
	GGCTCCACCA GCAAGAGTGA CAGCCAGAGC AAGAATACAT CACCTTCTCA GCCAGCCTCC 300
	ACRAACGCTA GCACCTCCTT GCCGGTCCCA AACCCTAAGCC TACCTTACGA GCAGACCATC 360
	GTCCTTCCAG GAAGCACCGG GCACATCGTG GTCACTCAGC CAAGCAGCAC TTCTGTCAAC 420
40	GGGCAAGTCC TCGGCGGACC ACACAACCTA ATGCGTCGAA GCACTGTGAG CCTCCTTGAT 480
	ACCTACCAAA AATGTGGACT CAAGCGTAAG AGCGAGGAGA TCGAGAACAC AAGCAGCGTG 540
	CAGATCATCG AGGAGCATCC ACCCATGATT CAGAATAATG CAAGCGGGGC CACTGTGCGC 600
	ACTGCCACCA GCTCTACTGC CACCTCCAAA AACAGCGGCT CCAACAGCGA GGGCGACTAT 660
	CAGCTGGTGC AGCATGAGGT GCTGTGCTCC ATGACCAACA CCTACGAGGT CTTAGAGTTC 720
45	TTGGGCGGAG GGAGCTTTGG ACAAGTGGTC AAGTGTGGA AACGGGGCAC CAATGAGATC 780
	GTAGCCATCA AGATCCTGAA GAACCGCCCA TCCTATGCCG GACAAGGTCA GATTGAAGTG 840
	AGCATCTCGG CCCGGTTGAG CACGGAGAGT GCCGATGACT ATAACCTCGT CCGGGCCTAC 900
	GAATGCTTCC AGCACAAGAA CCACACGTGC TTGGTCTTCG AGATGTTGGA GCAGAACCTC 960
	TATGACTTTC TGAAGCAAAA CAAGTTTAGC CCTTGCCGCC TCAAATACAT TCGCCAGATT 1020
50	CTCCAGCAGG TAGCCACAGC CCTGATGAAA CTCAAAGCC TAGGTCTTAT CCACGCTGAC 1080
	CTCAAACCCG AAAACATCAT GCTGGTGGAT CCATCTAGAC AACCATACAG AGTCAAGGTC 1140
	ATGCATTTTG GTTCAGCCAG CCACGTCCTC AAGGCTGTGT GCTCCACCTA CTTGCAGTCC 1200
	AGATATTACA GGGCCCCGTA GATCATCCTT GGTTTACCAT TTTGTGAGGC AATPGACATG 1260
	TGGTCCCTGG TGTGTGTTAT TGCAGAATG TTCTGGGTTT GGCCGTATATA TCCAGGAGCT 1320
	TCGGAGTATG ATCAGATTCG GTATATTTC CAAACACAGG GTTTGCTTGC TGAATATTTA 1380
55	TTAAGCGCGG GGACAAAGAC AACTAGGTTT TTCAACCGTG ACACGGACTC ACCATATCCT 1440
	TTGTGGAGAC TGAAGACACC AGATGACCAT GAAGCAGAGA CAGGGATTAA GTCAAAAGAA 1500
	GCAAGAAAGT ACATTTTCAA CTGTTTAGAT GATATGGCCC AGGTGAACAT GACGACAGAT 1560
	TTGGAAGGGA GCGACATGTT GGTAGAAAAG GCTGACCGGC GGGAGTTTCA TGACCTGTTG 1620
60	AAGAAGATGC TGACCATTGA TGCTGACAAG AGAATCACTC CAATCGAAAC CCTGAACCAT 1680
	CCCTTTGTCA CCATACACACA CTTACTCGAT TTTCCTCCCA GCACACACGT CAAATCATGT 1740
	TTCCAGAAAC TGGAGATCTG CAAGCGTCGG GTGAATATGT ATGACACGGT GAACACAGAGC 1800
	AAAACCCCTT TCATACAGCA CGTGGCCCCC AGCAGCTCCA CCAACCTGAC CATGACCTTT 1860
	AACAACCCAGC TGACCACTGT CCACAACCAG GCTCCCTCCT CTACCACTGC CACTATTTC 1920
65	TTAGCCAATC CCGAAGTCTC CATACTAAAC TACCCATCTA CACTCTACCA GCCCTCAGCG 1980
	GCATCCATGG CTGCACTGGC CCAGCGGAGC ATGCCCTGTC AGACAGGAAC AGCCACAGATT 2040
	TGTCCCGCGC CTGACCCGTT CCAGCAAGCT CTATCTGTGT GTCCCCCGG CTTCACAGGC 2100
	TTGCAAGCCT CTCCCTCTAA GCACGCTGGC TACTCGGTGC GAATGGAAAA TGCAGTTCCC 2160
	ATCGTCACTC AAGCCCGAGG AGCTCAGCCT CTTCAGATCC AACCAGGTCT GCTTGCCAG 2220
70	CAGGCTTGGC CAAGTGGGAC CCAGCAGATC CTGCTTCCC CAGCATGGCA GCAACTGACT 2280
	GGAGTGGCCA CCCACATCT AGTGCAGCAT GCCACCGTGA TTCCCGAGAC CATGGCAGGC 2340
	ACCCAGCAGC TGGCGGACTG GAGAAATACG CATGCTCACG GAAGCCATTA TAATCCCATC 2400
	ATGCAGCAGC CTGCACTATT GACCGGTCAT GTGACCTTTC CAGCAGCACA GCCCTTAAAT 2460
	GTGGGTGTGG CCCACGTGAT GCGGCAGCAG CCAACCAGCA CCACCTCCTC CCGGAAGAT 2520
75	AAGCAGCACC AGTCATCTGT GAGAAATGTC TCCACCTGTG AGGTGTCTCT CTCTCAGGCC 2580
	ATCAGCTCCC CACAGCGATC CAAGCGTGTG AAGGAGAAAC CACCTCCCCG CTGTGCCATT 2640
	GTGCACAGTA GCCCGGCTCG CAGCACCTCG GTCACTGTG GGTGGGGCGA CGTGGCCTTC 2700
	AGCACCACCC GGGAAACGCA GCGGCAGACA ATTGTCTATC CCGCACTTCC CAGCCCCACG 2760
	GTCAGCGTCA TCACCATCAG CAGTGACACG GACGAGGAGG AGGAACAGAA ACACGCCCCC 2820
80	ACCCAGCAGT CTCTCAAGCA AAGAAAAAAC GTCATCAGCT GTGTACAGT CCACGACTCC 2880
	CCCTACTCCG ACTCTTCCAG CAACACCAGC CCCTACTCCG TGCAGCAGCG TGTGGGCGAC 2940

5 AACAATGCCA ATGCTTTTGA CACCAAGGGG AGCCTGGAGA ATCACTGCAC GGGGAACCCC 3000
 CGAACCATCA TCGTGCCACC CCTGAAAACC CAGGCCAGCG AAGTATTGGT GGAGTGTGAT 3060
 AGCCTGGTGC CAGTCAACAC CAGTCAACCAC TCGTCTCTCT ACAAGTCCAA GTCTCTCCAGC 3120
 AACGTGACCT CCACAGCGCG TCACTCTTCA GGGAGCTCAT CTGGAGCCAT CACCTACCCG 3180
 CAGCAGCGCG CGGGCCCCCA CTTCCAGCAG CAGCAGCCAC TCAATCTCAG CCAGGCTCAG 3240
 CAGCACATCA CCACGGACCG CACTGGGAGC CACCGAAGGC AGCAGGCCTA CATCACTCCC 3300
 ACCATGGCCC AGGCTCCGTA CTCTTCCCG CACAACAGCC CCAGCCACGG CACTGTGCAC 3360
 CCGCATCTGG CTGACAGCGC TGCCGCTGCC CACCTCCCCA CCCAGCCCCA CCTCTACACC 3420
 TACACTGCGC CGGCGGCCCT GGGCTCCACC GGCACCGTGG CCCACCTGGT GGCCTCGCAA 3480
 GGCTCTGCGC GCCACACCGT GCAGCACACT GCCTACCCAG CCAGCATCGT CCACCAGGTC 3540
 CCCGTGAGCA TGGGCCCCCG GGTCTGCCC TCGCCACCA TCCACCCGAG TCAGTATCCA 3600
 GCCCAATTG CCCACAGAC CTACATCAGC GCCTCGCCAG CCTCCACCGT CTACACTGGA 3660
 TACCCACTGA GCCCGGCCAA GGTCAACCAG TACCCTTACA TATAAACACT GGAGGGGAGG 3720
 GAGGGAGGGA GGGAGGGAGA GAATGGCCCG AGGGAGGAGG GAGAGAAGGA GGGAGGCGCT 3780
 15 CCTGGGACCG TGGGCGCTGG CTTTATTATC TGAAGATGCC GCACACAAAC AATGCAAAAC 3840
 GGGCAGGGGC GGGGGGGGGG GGGGCAGAGG GCAGGGGGAC GGGTGGGGAC ACCAGTGAAA 3900
 CTTGAACCGG GAAATGGGAG GACGTAGAGC AGAGAAGAGA ACATTTTAA AAGGAAGGGA 3960
 TTAAGAGGG TGGGAAATCT ATGGTTTTAA TTTTAAAAA

20

SEQ ID NO:282 PCI2 Protein sequence:
 Protein Accession #: NP_073577

25 MAPVYEGMAS HVQVFSPTL QSSAFCSVKK LKVEPSSNWD MTGYGSHSKV YSQSKNIPPS 60
 QPASTTVSTS LPVPNPSPLY EQTIVFPST GHIVVTSASS TSVTGQVLGG PHNLMRRSTV 120
 SLLDTYQKCG LKRRKEIEEN TSSVQIEEH PPMIQNNASG ATVATAITST ATSKNSGSNS 180
 EGDYQLVQHE VLCSMTNTYE VLEFLGRGTF GQVVKCWKRQ TNEIVAIIKL KNRPSYARQG 240
 QIEVSLARL STESADYFN VRAYECFQHK NHTCLVFEMLEQNLDFLKQ NKFSPLPLKY 300
 IRPVLQGVAT ALMKLKLGL IHADLKPENI MLVDPSRQPY RVKVIDFGSA SHVSKAVCST 360
 30 YLQSRYYRAP EHLGLPFCE AIDMWSLGCY IAEFLGWPL YPGAISEYDQI RYISQTQGLP 420
 AEYLLSAGTK TTRFFNRDID SPYPLWRLKT PDDHEAETGI KSKBEARKYIF NCLDDMAQVN 480
 MTDLBGSMD LVEKADRRF IDLLKMLTI DADKRITPIE TLNHPFVTMT HLLDFPHSTH 540
 VKSCFQNM EI KRRVNMVYDT VNQSKTPFIT HVAPOSTNL TMTFNQLT VHNQAPSSTS 600
 ATISLANPEV SILNYPSTLY QPSAASMAAV AQRSMPLQTG TAQICARPDF FQALIVCPP 660
 35 GFQGLQASPS KHAGYSVRME NAVPIVTQAP GAQLQIQPG LLAQQAWSFG TQQLLPPAW 720
 QQLTGVAITH SVQHATVIPE TMAQTQQLAD WRNTHAGSH YNPIMQPAL LTGHVTLPA 780
 QPLNVGVAHV MRQQTSTTS SRKSKQHSS VRNVSTCEVS SSQAISSPQR SKRVKENTPP 840
 RCAMVHSSPA CSTSVTCGWG DVASSTTRER QRQITVPIPT PSPTVSVITI SSDTDEEEQ 900
 40 KHAPTSTVSK QRKNVISCVT VHDSPYSDSS SNTSPYSVQQ RAGHNNANAF DTKGLENHC 960
 TGNPRTHVP PLKTQASEVL VECDSLVPVN TSHHSSYSKS KSSSNVSTS GHSSGSSSGA 1020
 ITRYRQRPFG HFQQQQLPLNL SQAQQHITTD RTGSHRRQA YITPTMAQAP YSFPHNSPSH 1080
 GTVHPHLAAA AAAAHLPTQP HLYTYTAPAA LGSTGTVAHL VASQGSARHT VQHTAYPASI 1140
 VHQPVSMPG RVLPSPTIHP SQYPAQFAHQ TYISASPAST VYTGYPPLSA KVNQYPI

45

SEQ ID NO:283 PBY1 DNA SEQUENCE

Nucleic Acid Accession#: NM_017700
 Coding sequence: 147-806 (underlined sequence corresponds to start and stop codon)

50 1 11 21 31 41 51
 AGTCACAGCC AGGTAACCTT GGAGTGAAGC GGTTTAGTTA GAAGGGAGCA GATAAACTCG 60
 TCACCTCTAGT AGCTTTAACC CTCACCCTGA GGCACCTTAG CAATCAGCCA TTGCCTGCAA 120
 GCCTCCAAAG CTGTGCTTTG CCTAATATGG AGCCCAAAGA AGCCACTGGG AAAGAAACAA 180
 TGGTCACCAA GAAAAAGAAAT CTGGCCTTCT TGAGGTCTAG ACTCTATATG CTGAGAGAAA 240
 55 GGAAGACTGA CACTGTGGTT GAGAGCAGTG TTTCTGGGGA CCACTCTGGC ACCTTGAGGA 300
 GGAGCCAATC TGACAGGACC GAATACAACC AGAAATTACA AGAAAAGATC ACTCCACAGG 360
 GTGAGTGTTC TGTAGCTGAG ACCTTAACCC CAGAGGAAGA GCATCATATG AAGAGGATGA 420
 TGGCAAAGCG GGAAGAAGATC ATTAAGGAGC TGATACAGAC AGAAAAGGAT TATCTCAATG 480
 60 ATCTAGAGCT GTGTGTTAGG GAAGTGGTTC AGCCCCGAG AAATAAAAG ACTGATAGGC 540
 TGGATGTGGA TAGCTTGTGT AGCAACATTC AGTCCGTGCA TCAGATATCA GCCAAGCTGC 600
 TGTCAATGTT GGAAGAGGCC ACAACAGACG TGGAAACGGC CATGCAAGTA ATTTGGAGAAG 660
 TATTCTTGCA GATTAAAGGG CCACTGGAAG ATATTATATA AATCTACTGC TATCACCATG 720
 ATGAAGCACA TAGTATACTG GAGTCTATG AAAAGGAAGA AGAGCTGAAG GAACATTTGA 780
 65 GCCACTGTAT CCAGTCCCTA AAGTAAGGCC TTTCACAAATG ATGATTCCTCA TCTCTCTCA 840
 GTTGCTTAGC AGGGAACATT TTAATATGGT GTAGATGAAA GGTCTCATAT AAATCCTATG 900
 TTTTATGAGA CTGTCTGGGA GCTCTGCTTT GCRTTCCCTT TATAAAAAGC TGACATGCCA 960
 GAAGCCCTGA TTGACTTTTT TTCCCCCTGC GAGAATGACT AAAAATAACA TGGAGAAGA 1020
 TTTAGAGCTC TGCAGCGATT GAAAATGCA ATATCAAAAT ATAAAATGTG GAAGAAAAGC 1080
 70 CTCFTCTTAA AGCTATTGTA ACTTGCCTGG CCCACGCTAG TTCAAGGATT ATGTGAGATA 1140
 ACACGTGGCC CCATGACCAC TGGAGCACAT GGGTTAATGG AGTTAGGGGA ATGGCCTTACA 1200
 ACTCTGAGG GCGCTCTTCT TTCCCCAAAC TCACTGTGGG GAGATGGGTG AAGACAAGTC 1260
 AGGCCTTGTT AAAGTTAGTT TCAGACAAT TACTCATGCC TTCTCTTCTC ATCCCTAAAA 1320
 CATTTGGTGG GGAGCTACAC AATGTACTTT TTCTTTTCTA GAGGAAGTAT CTATTCACTG 1380
 75 TGAATATCTG AAAAATATAA CAAAGTATGT GTAAGATAAA AACCCCTTGC TATTTCAAAA 1440
 AAAAAAAAAA AAAAAAAAAA AAAA

SEQ ID NO:284 PBY1 Protein sequence:
 Protein Accession #: NP_060170

80 1 11 21 31 41 51

5

MEPKKATGKE	NMVTKKKNLA	FLRSRLYMLE	RRKTDTVVVS	SVSGDHSGLT	RRSQSDRTEY	60
NQKLQEKMTF	QGECSVAETL	TPEEHHMKR	MMAKREKIIK	ELIQTEKDYI	NDLELCVREV	120
VQPLRNKKT	RLDVDLSLFSN	IESVHQISAK	LLSLLEEAT	DVEBAMQVIG	EVFLQIKGFL	180
EDYIKYCYH	HDEAHSILES	YEKEEELKEH	LSHCQISLK			

SEQ ID NO:285 PBQ9 DNA SEQUENCE

10

Nucleic Acid Accession#: X66534
Coding sequence: 523-2676 (underlined sequence corresponds to start and stop codon)

1	11	21	31	41	51	
CCCTTATGGC	GATTGGGCGG	CTGCAGAGAC	CAGGACTCAG	TTCCCTTGCC	CTAGTCTGAG	60
CCTAGTGGGT	GGGACTCAGC	TCAGAGTCAG	TTTTCAGAA	CAGGTTTCAG	TTGCAGAGTT	120
TTCTCTACACT	TTTCTCTGCG	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	GGCGGAGGAC	180
ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGGCG	TGATCTCACC	240
ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	CAGCCCCGAG	300
GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	GCCACCGCGG	360
TCGCCGCGCT	GTCTGCACCC	TGTCGCTGA	GCTGCTGAC	AGTGACAATG	ACATCCCACT	420
TACCACTGTC	CTTGAATGTA	TAGTGGCTTC	TGTTTGTCTG	TCTCATATAA	GAATACAGC	480
TCATCAGGAG	GAGATCGCAG	CAGGTAAGA	GACACCAACA	CCATGTTCTG	CACGAAGCTC	540
AAGGATCTCA	AGATCACAGG	AGAGTGTCTT	TTCTCCTTAC	TGGCACCAGG	TCAAGTTCCT	600
AACGAGTCTT	CAGAGGAGGC	AGCAGGAAGC	TCAGAGAGCT	GCAAAGCAAC	CGTGCCCATC	660
TGTCAGAGCA	TTCTCTGAGAA	GAACATACAA	GAAAGTCTTC	CTCAAAGAAA	AACCACTCGG	720
AGCCGAGTCT	ATCTTCACAC	TTTGGCAGAG	AGTATTTGCA	AACTGATTTT	CCCAGAGTTT	780
GAACGCTCGA	ATGTTGCACT	TCAGAGAACA	TTGGCAAAGC	ACAAAATAAA	AGAAAGCAGG	840
AAATCTTTTG	AAAGAGAAGA	CTTTGAAAAA	ACAATTGCAG	AGCAAGCAGT	CGACGAGAGT	900
CCAGTGGAGT	TATCAAAGAA	TCTCTTGGTG	AAGAGGTTT	TAAATATATG	TACGAGGAAG	960
ATGAAAACAT	CCTTGGGGTG	GTTGGAGGCA	CCCTTAAAGA	TTTTTAAACA	GCTTCAGTAC	1020
CCCTCTGAAA	CAGAGCAGCC	ATTGCCAAGA	AGCAGGAAAA	AGGGGCAGCT	TGAGGACGCC	1080
TCCATCTCAT	GCCTGGATAA	GGAGGATGAT	TTTCTACATG	TTTACTACTT	CTTCCCTAAG	1140
AGAACCACCT	CCCTGATTCT	TCCCGGCATC	ATAAAGGCAG	CTGCTCACGT	ATTATATGAA	1200
ACGGAAGTGG	AAGTGTCTGT	AATGCCCTCC	TGCTTCCATA	ATGATTGCAG	CGAGTTTGTG	1260
AATCAGCCCT	ACTTGTGTGA	CTCCGTTCAC	ATGAAAAGCA	CCAAGCCATC	CCTGTCCCCC	1320
AGCAAACCCC	AGTCTCTGCT	GGTGATTCCC	ACATCGCTAT	TCTGCAAGAC	ATTTCCATTC	1380
CATTTCATGT	TTGACAAAGA	TATGACAATT	CTGCAATTTG	GCAATGGCAT	CAGAAGGCTG	1440
ATGAACAGGA	GAGACTTTCA	AGGAAAGCCT	AATTTTGAAT	ACTTTGAAAT	TCTGACTCCA	1500
AAAATCAACC	AGACCTTTAG	CGGGATCATG	ACTATGTTGA	ATATGCAGTT	TGTTGTACGA	1560
GTGAGGAGAT	GGGACAACCT	TGTGAAGAAA	TCTTCAAGGG	TTATGACCTT	CAAAGGCCAA	1620
ATGATCTACA	TTGTGTGAAT	CAGTGCAATC	TTGTTTGTGG	GGTCACCCCTG	TGTGGACAGA	1680
TTAGAGAGAT	TTACAGGAGC	AGGGCTCTAC	CTCTCAGACA	TCCCAATTCA	CAATGCACTG	1740
AGGGATGTGG	TCTTAATAGG	GGAAACAAGC	CGAGCTCAAG	ATGGCCCTGAA	GAAGAGGCTG	1800
GGGAAGCTGA	AGGCTTACCCT	TGAGCAAGCC	CACCAAGCCC	TGGAGGAGGA	GAAGAAAAAG	1860
ACAGTAGAGC	TTCTGTGCTC	CATATTTCCC	TGTGAGGTGT	CTCAGCAGCT	GTGGCAAGGG	1920
CAAGTTGTGC	AGGCCAAGAA	GTTCAAGTAA	GTCACCATGC	TCTTCTCAGA	CATCGTTGGG	1980
TTCACTGCCA	TCTGCTCCCA	GFGCTCACCG	CTGCAGGTCA	TCACCATGCT	CAATGCACTG	2040
TACACTCGCT	TGCAGCAGCA	GFTGGAGAG	CTGGATGTCT	ACAAGGTGGA	GACCATTCGG	2100
ATGCCATTATG	TGTGGCTTTG	GGGATTACAC	AAAGAGAGTG	ATACTCATGC	TGTTTCAGATA	2160
GCCTCATATG	CCCTGAAGAT	GATGGAGCTC	TCTGATGAAG	TTATGTCTCC	CCATGGAGAA	2220
CCATATCAAG	TGCCAATTGG	ACTGCACTCT	GGATCAGTTT	TTGCTGGCGT	CGTTGGAGTT	2280
AAAATGCCCC	GTTACTGTCT	TTTTGGAAAC	AATGTCACCT	TGGCTAACAA	ATTTGAGTCC	2340
TGCAGGTATC	CACGAAAAAT	CAATGTGAGC	CCAACAACCT	ACAGATTACT	CAAAGACTGT	2400
CCTGGTTTCG	TGTTTACCCC	TGATCAAGG	GAGGAACCTC	CACCAACACT	CCCTAGTGAA	2460
ATCCCCGAA	TCTGCCATTT	TCTGGATGCT	TACCAACAAG	GAACAACTC	AAAACCATGC	2520
TTCCAAAAGA	AAGATGTGGA	AGATGCAAGC	CAATTTTTTA	GGCAAAGCAT	CAGGAATAGA	2580
TTAGCAACCT	ATATACCTAT	TTATAAGTCT	TTGGGGTTTG	ACTCATTGAA	GATGTGTAGA	2640
GCCTCTGAAA	GCATCTTAGG	GATTGTAGAT	GGCTAACRA	CAGTATTAAA	ATTTCAAGAG	2700
CCAAGTCACA	ATCTTTCTCT	TGTTTAACAT	GACAAAATGT	ACTCACTTCA	GTACTTCAGC	2760
TCTTCAAGAA	AAAAAAAATA	ACCTTAAAAA	GCTACTTTTG	TGGGAGTATT	TCTATTATAT	2820
AACCAGCACT	TACTACCTGT	ACTCAAAATT	CAGCACCTTG	TACATATATC	AGATAATTGT	2880
AGTCAATTGT	ACAAACTGAT	GGAGTCACCT	GCAATCTCAT	ATCCTGGTGG	AATGCCATGG	2940
TTATTAAAGT	GTGTTTGTA	TAGTTGTCTG	CAAAAAATA	AAAAAAAATA	AAAAAAAATA	3000
AAAA						

SEQ ID NO:286 PBQ9 Protein sequence:

Protein Accession #: Q02108

70

1	11	21	31	41	51	
MFCTKLKDLK	ITGECPFSL	APGQVPNESS	EEAAGSSSEC	KATVPICQDI	PEKNIQESLP	60
QRKTSRSRVY	LHTLAESICK	LIFPEFERLN	VALQRTLAKH	KIKESRKSLE	REDFEKTIAE	120
QAVAAGVPVE	VIKESLGEEV	FKICYEBDEN	ILGVVGGTLK	DFLNSFSTLL	KQSSHCQEAG	180
KRGRLEDAI	LCLDKEDDFL	HVYFFPKRT	TSLLILEFTIK	AAAHVLYETE	VEVSLMPPCF	240
HNDCEFEVNV	PYLLYSVHMK	STKPSLSPSK	PQSSSLVPTS	LFCKTFPFHF	MPDKDMTILQ	300
FGNGIRRLMN	RRDFQGGPNF	BEYFELTPK	INQTFSGIMT	MLNMQFVVVR	RRWDNSVKKS	360
SRVMDLKGQH	IYIVESSAIL	FLGSPCVDR	EDFTGRGLYL	SDIPIHNALR	DVVLIGEQR	420
AQDGLKKRLG	KLKATLEQAH	QALEEEKKKT	VDLLCSIFPC	EVAQQLWQGG	VVQAKKFSNV	480
TMLFSDIVGF	TAICSQCSPL	QVITMLNALY	TRFDQCCGEL	DVYKVTETGD	AYCVAGGLHK	540

80

ESDTHAVQIA LMAKMMELS DEVMSPHGEP IKMRIGLHSG SVFAGVGVK MPRYCLFGNN 600
 VTLANKFESC SVPRKINVSF TTYRLKDCP GFVFTPRSRE ELPPNFPSEI PGICHLDAY. 660
 QQGTNSKPCF QKRDVEDGNA NFLGKASGID

5

SEQ ID NO:287 PFD2 DNA SEQUENCE

Nucleic Acid Accession#: NM_000720

Coding sequence: 119-6664 (underlined sequence corresponds to start and stop codon)

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

```

1      11      21      31      41      51
|      |      |      |      |      |
AGAAATAAGGG CAGGGACCGG GGCTCCTATC TCTTGGTGAT CCCCTTCCCC ATTCCGCCCC 60
CGCCTCAACG CCCAGCACAG TGCCCTGCAC ACAGTAGTCG CTCAATAAAT GTTCGTGGAT 120
GATGATGATG ATGATGATGA AAAAAATGCA GCATCAACGG CAGCAGCAAG CGGACCACGC 180
GAACGAGGCA AACTATGCAA GAGGCACCAG ACTTCCCTCT TCTGGTGAAG GACCAACTTC 240
TCAGCCGAAT AGCTCCAAGC AAACGTGCTT GTCTTGGCAA GCTGCAATCG ATGCTGCTAG 300
ACAGGCCAAG GCTGCCCAAA CTATGAGCAC CTCTGCACCC CCACCTGTAG GATCTCTCTC 360
CCAAAGAAAA CGTCAGCAAT ACGCCAAGAG CAAAAACAG GGTAACTCGT CCAACAGCCG 420
ACCTGCCCGC GCCTTTTCTT GTTTATCACT CAATAACCCC ATCCGAAGAG CCTGCAATTG 480
TATAGTGGAA TGGAAACCAT TTGACATATT TATATTATTG GCTATTTTTC CCAATTGTGT 540
GGCCTTAGCT ATTTACATCC CATTCCTTGA AGATGATTCT AATTCAACAA ATCATAACTT 600
GGAAAAAGTA GAATATGCCT TCCTGATTAT TTTTACAGTC GAGACATTTT TGAAGATTAT 660
AGCGTATGGA TTATTTGCTAC ATCCTAATGC TTATGTTAGG AATGGATGGA ATTTACTGGA 720
TTTTGTATA GTAATAGTAG GATTGTTTAG TGTAAATTTG GAACAATTA CCAAGAAAC 780
AGAAGCGGGG AACCACATCA GCGGCAAAAT TGGAGGCTTT GATGTCAAAG CCCTCCGTGC 840
CTTTCGAGTG TTGCGACCAC TTCGACTAGT GTCAGGGGTG CCCAGTTTAC AAGTTGTCTC 900
GAACTCGATT ATAAAGGCCA TGGTTCCTCT CTTTACATA GGCCTTTTGG TATTATTTGT 960
AATCATAATC TATGCTATTA TAGGATTGGA ACTTTTATT GGAAAAATGC ACAAAACATG 1020
TTTTTTTGTCT GACTCAGATA TCGTAGCTGA AGAGGACCCA GCTCCATGTG CGTTCCTCAG 1080
GAATGGACGC CAGTGTACTG CCAATGTCAC GGAATGTAGG AGTGGCTGGG TTGGCCCGAA 1140
CGGAGGCATC ACCAACTTTG ATAACTTTGC CTTTGCCATG CTTACTGTGT TTCAGTGCAT 1200
CACCATGGAG GGTGAGACAG ACGTGCTCTA CTGGTAAAT GATGCGATAG GATGGGAATG 1260
GCCATGGGTG TATTTTGTTA GTCTGATCAT CTTTGGCTCA TTTTTCGTCC TTAACCTGGT 1320
TCTTGGTGTC CTATGAGGAG AATTCTCAAA GGAAGAGAG AAGGCAAAAG CACGGGGAGA 1380
TTTCCAGAAG CTCGGGGAGA AGCAGCAGCT GGAGGAGGAT CTAAAGGGCT ACTTGGATTG 1440
GATCACCCAA GCTGAGGACA TCGATCCGGA GAATGAGGAA GAAGGAGGAG AGGAAGGCAA 1500
ACGAATAACT AGCATGCCCA CCAGCGAGAC TGAATCTGTG AACACAGAGA ACGTCAGCGG 1560
TGAAGCCGAG AACCGAGGCT GCTGTGGAAG TCTCTGGTGC TGGTGGAGAG GGAGAGGCGC 1620
GGCCAAGGCG GGGCCCTCTG GGTGTCGGCG GTGGGTCAA GCCATCTCAA AATCCAAACT 1680
CAGCCGAGCG TGGCGTCTGT GGAACCGATT CAATCGCAGA AGATGTAGGG CCGCCGTGAA 1740
GTCTGTACAG TTTTACTTGC TGGTTATCGT CTTGGTGTTC CTGAACACCT TAACCATTTT 1800
CTCTGAGCAC TACAATCAGC CAGATTGGTT GACACAGATT CAAGATATTG CCAACAAAGT 1860
CCCTCTGGCT CTGTTACCTG GCGAGATGCT GGTAAAAATG TACAGCTTGG GCCTCCAAAG 1920
ATATTTCTGT TCCTTTTCA ACCGGTTTGA TTGCTTCTGT GTGTGTGGTG GAATCACTGA 1980
GACGATCTGT GTGGAAGTGG AAATCATGTC TCCCTGTGGG ATCTCTGTGT TTCGGTGTGT 2040
GCGCCTCTTA AGAATCTTCA AAGTGACCAG GCACTGGACT TCCCTGAGCA ACTTAGTGGC 2100
ATCCTTATTA AACTCCATGA AGTCCATCGC TTCGCTGTG CTCTGCTTTT TTCTCTTCAT 2160
TATCATCTTT TCCTTGTCTG GGATGCAGCT GTTTGGCGGC AAGTTTAATT TTGATGAAAC 2220
GCAAACCAAG CGGAGACACCT TTGACAATT CCCTCAAGCA CTCTCAGAG TGTTCAGAT 2280
CTGACAGGCG GAAGATCTGA ATGCTGTGAT GTACGATGGC ATCATGGCTT ACGGGGGCCC 2340
ATCCTCTTCA GGAATATGCG TCTGCATCTA CTTTATCATC CTCTTCATTT GTGGTAACTA 2400
TATTTCTACTG AATGTCTTCT TGGCCATCGC TGTAGACAAT TTGGCTGATG CTGAAAGTCT 2460
GAACACTGCT CAGAAAGAGG AAGCGGAAGA AAAGGAGAGG AAAAAGATTG CCGAAAAAGA 2520
GAGCCTAGAA AATAAAAGA ACAACAAACC AGAAGTCAAC CAGATAGCCA ACAGTGACAA 2580
CAAGGTTACA ATTGATGACT ATAGAGAAGA GGATGAAGAC AAGGACCCCT ATCCGCTTTG 2640
CGATGTGCCA GTAGGGGAAG AGGAAGAGGA AGAGGAGGAG GATGAACCTG AGGTTCCTGC 2700
CGGACCCCGT CCTCGAAGGA TCTCGGAGTT GAACATGAAG GAAAAAATTG CCCCCATCCC 2760
TGAAGGGAGC GCTTTCTTCA TTCTTAGCAA GACCAACCCG ATCCGCGTAG GCTGCCACAA 2820
GCTCATCAAC CACCACATCT TCACCAACCT CATCCTTGTC TTTCATCATG TGAGCAGCGC 2880
TGCCCTGGCC GCAGAGGACC CCATCCGCAG CCACTCCTTC CGGAACAGA TACTGGGTTA 2940
CTTTGACTAT GCCTTCACAG CCATCTTTAC TGTGTAGATC CTGTTGAAGA TGACAACCTT 3000
TGGAGCTTTC CTCCACAAGG GGGCCTTCTG CAGGAACATC TTCAATTGTC TGGATATGCT 3060
GGTGGTTGGG GTGCTCTCTG TGTCAATTGG GATTCAATCC AGTGCATCTC CCGTTGTGAA 3120
GATTCTGAGG GTCTTAAGGG TCTTGCCTCC CCTCAGGGCC ATCAACAGAG CAAAAGGACT 3180
TAAGCACGTG GTCCAGTCCG TCTTCTGGGC CATCCGACC ATCGGCAACA TCATGATCGT 3240
CACTACCCCT CTCAGTTTCA TGTTTGCCCTG TATCGGGGTC CAGTTGTTC AAGGGAAAGT 3300
CTATCGCTGT ACGGATGAAG CCAAAAGTAA CCTGAAGAA TGCAGGGGAC TTTTCTATCT 3360
CTACAAAGAT GGGGATGTTG ACAGTCTCTGT GGTCCGTGAA CGGATCTGGC AAAACAGTGA 3420
TTTCAACTTC GACAAAGTCC TCTCTGCTAT GATGGCGCTC TTCAAGTCT CCACGTTTGA 3480
GGGCTGGCCT GCGTTGCTGT ATAAAGCCAT CGACTCGAAT GGAGAGAACA TCGGCCCAAT 3540
CTACAAACAC CGCGTGGAGA TCTCCATCTT CTTCATCATC TACATCATCA TTGTAGCTTT 3600
CTTCATGATG AACATCTTTG TGGGCTTTGT CATCGTTACA TTTCAAGGAA AAGGAGAAAA 3660
AGAGTATAAG AACTGTGAGC TGGACAAAA TCAGCGTCAG TGTGTGAAT ACGCCTTGAA 3720
AGCAGTCCC TTGCGGAGAT ACATCCCAA AAACCCCTAC CAGTACAAGT TCTGGTACGT 3780
GTTGAACCTT TCGCCTTTTC AATACATGAT GTTTGTCTCT ATCATGCTCA ACACACTCTG 3840
CTTGGCCATG CAGCCTACG AGCAGTCCAA GATGTTCAAT GATGCCATCG ACATTCGAA 3900
CATGGTCTTC ACGGGGTGT TCACCGTCGA GATGGTTTTC AAAGTCATCG CATTTAAGCC 3960
TAAGGGGTAT TTTAGTGACG CCTGGAACAC GTTTGACTCC CTTCATCTAA TCGGCAGCAT 4020
TATAGACGTG GCCCTCAGCG AAGCGGACCC AACTGAAAGT GAAAAATGCC CTGTCCCAAC 4080

```

5 TGCTACACCT GGGAACTCTG AAGAGAGCAA TAGAATCTCC ATCACCTTTT TCCGTCITTT 4140
 CCGAGTGATG CGATTGGTGA AGCTTCTCAG CAGGGGGGAA GGCATCCGGA CATTGCTGTG 4200
 GACTTTTATT AAGTCCATTTC AGGCGCTCCC GTATGTGGCC CTCTCATAG CCATGCTGTT 4260
 CTTTCATCTAT GCGGTCAATTG GCATGCAGAT GTTTGGGAAA GTTGCCATGA GAGATAACAA 4320
 CCAGATCAAT AGGAACAATA ACTTCCAGAC GTTTCGCCAG GCGGTGCTGC TGCTCTTCAG 4380
 GTGTGCAACA GGTGAGGCCCT GGCAGGAGAT CATGCTGGCC TGCTCTCCAG GGAAGCTCTG 4440
 TGACCCGTAG TCAGATTACA ACCCCGGGGA GGAGTATACA TGTGGGAGCA ACTTTGCCAT 4500
 TGTCTATTTC ATCAGTTTTC ACATGCTCTG TGCAATTCTG ATCATCAATC TGTTTGTGGC 4560
 10 TGTCTATCATG GATAATTTCG ACTATCTGAC CCGGGACTGG TCTATTTTGG GGCCTCACCA 4620
 TTTTAGATGAA TTCAAAAGAA TATGGTCAGA ATATGACCCT GAGGCAAGG GAAGGATAAA 4680
 ACACCTTGAT GTGGTCACTC TGCTTCGACG CATCCAGCCT CCCCTGGGGT TTGGGAAGTT 4740
 ATGTCCACAC AGGGTAGCGT GCAAGAGATT AGTTGCCATG AACATGCCTC TCAACAGTGA 4800
 CGGGACAGTC ATGTTTAATG CAACCTCTGT TGCTTTGGTT CGAACGGCTC TTAAGATCAA 4860
 15 GACCGAAGGG AACCTGGAGC AAGCTAATGA AGAAGTTCGG GCTGTGATAA AGAAAAATTG 4920
 GAAGAAAACC AGCATGAAAT TACTTGACCA AGTTGTCCCT CCAGCTGGTG ATGATGAGGT 4980
 AACCGTGGGG AAGTTCCTATG CCACCTTCCT GATACAGGAC TACTTTAGGA AATTCAAGAA 5040
 ACGGAAGAA CAAGGACTGG TGGGAAAAGTA CCTTGCAGAG AACACCACAA TTGCCCTACA 5100
 GCGGGGATTA AGGACATCGC ATGACATTGG GCCAGAAATC CGGCGTGCTA TATCGTGTGA 5160
 20 TTTGCAAGAT GACGAGCCTG AGGAAACAAA ACGAGAAGAA GAAGATGATG TGTTCAAAAG 5220
 AAATGTTGCC CTGCTTGAAA ACCATGTCAA TCATGTTAAT AGTGATAGGA GAGATTCCCT 5280
 TCAGCAGACC AATACCACCC ACCGTCCCCT GCATGTCCAA AGGCCTTCAA TTCCACTCTC 5340
 AAGTGATACT GAGAAACCCG TGTTCCTCC AGCAGGAAAT TCGGTGTGTC ATAACCATCA 5400
 TAACCATAT TCCATAGGAA AGCAAGTTCC CACCTCAACA AATGCCAATC TCAATAATGC 5460
 25 CAATATGTCC AAAGCTGCC ATGGAAGCG GCCCAGCATT GGAACCTTG AGCATGTGTC 5520
 TGAAAATGGG CATCATTTCT CCCACAAGCA TGACCGGGAG CCTCAGAGAA GGTCCAGTGT 5580
 GAAAAGAACC CGCTATTATG AAACCTTACAT TAGGTCCGAC TCAGGAGATG AACAGCTCCC 5640
 AACTATTTGC CCGGAAGACC CAGAGATACA TGGCTATTTT AGGACCCCC ACTGCTTGGG 5700
 GGAGCAGGAG TATTTCAGTA GTGAGGAATG CTACGAGGAT GACAGCTCGC CCACCTGGAG 5760
 30 CAGGCAAAAC TATGGCTACT ACAGCAGATA CCCAGGCAGA AACATCGACT CTGAGAGGCC 5820
 CCGAGGCTAC CATCATCCCC AAGGATTCCT GGAGGACGAT GACTCGCCCG TTTGCTATGA 5880
 TTCAACGAGA TCTCAAGGA GACGCTTACT ACCTCCCRCC CCAGCATCCC ACCGAGATC 5940
 CTCCTTCAAC TTTGAGTGCC TGCGCCGGCA GAGCAGCCAG GAAGAGGTCC CGTCTGCTCC 6000
 CATCTTCCCC CATCGCAGG CCTGCTCTCT GCATCTAATG CAGCAACAGA TCATGGCAGT 6060
 35 TGCCGCGCTA GATTTCAAGTA AAGCCAGAA GTACTCACCG AGTCACTCGA CCGGTCCTG 6120
 GGCCACCCCT CCAGCAACCC CTCCCTACCG GGAAGTGGCA CCGTGTGACA CCCCCCTGAT 6180
 CCAAGTGGAG CAGTCAGAGG CCCTGGACCA GGTGAACGGC AGCCTGCCGT CCCTGCAACC 6240
 CAGCTCCTGG TACACAGACG AGCCCGACAT CTCCTACCGG ACTTTCACAC CAGCCAGCCT 6300
 GACTGTCCCC AGCAGCTTCC GGAACAAAA CAGCGACRAG CAGAGGAGTG CGGACAGCTT 6360
 40 GGTGGAGGAT GTCTGATAT CCGAAGGCTT GGGACGCTAT GCAAGGGACC CAAAATTGTG 6420
 GTCAGCAACA AAACACGAAA TCGCTGATGC CTGTGACCTC ACCATCGACG AGATGGAGAG 6480
 TGCAGCCAGC ACCCTGCTTA ATGGGAACGT GCGTCCCGCA GCCAACGGGG ATGTGGGCC 6540
 CCTCTCACAC CGGCAGGACT ATGAGCTACA GGACTTTGCT CCTGGCTACA GCGACGAAGA 6600
 GCCAGACCTT GGGAGGGATG AGGAGGACCT GCGGGATGAA ATGATATGCA TCACCACTCT 6660
 45 GTAGCCCCA CGAGGGGGCA GACTGGCTCT GGCTCAGGT GGGGCGCAGG AGAGCCAGGG 6720
 GAAAAGTGCC TCATAGTTAG GAAAGTTTAG GCACTAGTTG GGAGTAATAT TCAATTAAAT 6780
 AGACTTTTGT ATAAGAGATG TCATGCCTCA AGAAAGCCAT AAACCTGGTA GGAACAGGTC 6840
 CCAAGCGGTT GAGCTTGGCA GAGTACCATG CGCTCGGCC CAGCTGCAGG AAACAGCAGG 6900
 CCCCGCCCTC TCACAGAGGA TGGGTGAGGA GGCCAGACCT GCCTGCCCTC ATTGTCCAGA 6960
 50 TGGGCACTGC TGTGGAGTCT GCTTCTCCCA TGTACCAGG CACCAGCCCC ACCCACTGA 7020
 AGGCATGGGG GCGGGGTGCA GGGGAAAGTT AAAGGTGATG ACGATCATCA CACCTCGTGT 7080
 CGTTACCTCA GCCATCGGTC TAGCATATCA GTCACTGGGC CCAACATATC CATTTTAA 7140
 CCCTTTCCCC CAAATACACT GCGTCTGGT TCCTGTTTAG CTGTTCTGAA ATA

SEQ ID NO:288 PFD2 Protein sequence:

Protein Accession #: A38198

55
 60
 65
 70
 75
 80

1	11	21	31	41	51	
MMMMMMKKM	QHQRQQQADH	ANEANYARGT	RLPLSGEGPT	SQPNSSKQTV	LSWQAAIDAA	60
RQAKAAQTMS	TSAPPPVGS	SQRKRQYAK	SKKQGNSSNS	RPARALFCLS	LNNPIRRACI	120
SIVEWKPFDI	FILLAI FANC	VALAIYIPFP	EDDSNSTNHN	LEKVEYAFLI	IFTVETFLKI	180
IAYGLLLHPN	AYVRNWNLL	DFVIVIVGLF	SVILEQLTKE	TEGGNHSSGK	SGGPDVKALR	240
AFRVLRLRL	VSGVPSLQV	LNSIIKAMVP	LLHIALLVLF	VIIIIYAIIGL	ELFIGKMHKT	300
CFFADSDIVA	BEDPAPCAPS	GNGRQCTANG	TECRSGWVGP	NGGITNFDNF	AFAMLTVPQC	360
ITMEGWTDVL	YWVNDAGWE	WPWVYFVSLI	ILGSPFVLNL	VLGVLSGEFS	KEREKAKARG	420
DFQKLEKQQ	LEEDLKGYLD	WITQAEIDIP	ENEEEGGEEG	KRNTSMPTSE	TESVNTENVS	480
GEGENRGCCG	SLWCWRRRR	AAKAGFSGR	RWQAISSKSK	LSRRWRWRNR	FNRRCRAAV	540
KSVTFYWLVI	VLVFLNLTIT	SSEHYNQPDW	LTQIQDIANK	VLLALFTCEM	LVKMYSLGLQ	600
AYFVSLFNRF	DCFVVCGGIT	ETILVELEIM	SLPGISVFR	VRLRLRFKVT	RHWTSLSNLV	660
ASLNSMKSI	ASLLELLFLF	IIIFSLGMO	LFGGKFNDE	TQTKRSTFDN	FPQALLTVFQ	720
ILTGEDMNAV	MYGIMAYGG	PSSSGMIVCI	YFILEICGN	YILLNVFLAI	AVDNLDAES	780
LNTAQKEEAE	EKEKKEIARK	ESLENKKNNK	PEVNQIANS	NKVITIDYRE	EDEDKDPYPP	840
CDVFGVEEEE	EEEDDEPEVP	AGPRPRRISE	LNMKEKIAP	PEGSAFFILS	KTNPIRVGCH	900
KLINHHIFPN	LILVILMSS	AALAAEDPIR	SHSFRNTILG	YFDYAFATIF	TVEILLKMTT	960
FGAFLHKGAF	CRNFVNLDM	LVGVSVLSVF	GIQSSAISVV	KILRVLRLVR	PLRAINRAKG	1020
LKHVVQCVFV	AIRPTGNIIM	VPTLLQFMFA	CIGVQLFKGK	PYRCTDEAKS	NPEECRGLFI	1080
LYKGDVDVSP	VVRERIWNQS	DFNFDNVLSA	MMALFTVSTF	EGWFPALLYKA	IDSNGENIGP	1140
IYNRVEIISI	FFIYIYIIVA	FFMMNIFVGF	VIVTFQEQGE	KEYKNCELDK	NQRQCVEYAL	1200
KARPLRYIIP	KNPYQYKFYV	VUNSSPFEYM	MFVLIMLNTL	CLAMQHYEQS	KMFNDAMDIL	1260
80 NMVFTGVFTV	EMVLKVIAFK	PKGYFSDAWN	TFDSLIVIGS	IIDVALSEAD	PTESENVFVP	1320

	TATPGNSEES	NRISITFFRL	FRVMRLVKLL	SRGEGIRTL	WTFIKSFOAL	PYVALLIAML	1380
	FFIYAVTGMQ	MFGKIVAMRDN	NQINRNNNFQ	TFFQAVLLLF	RCATGEANQE	IMLACLPGKL	1440
	CDPESDYNFG	EYVTCGSNFA	IVYFISFYML	CAFLIINLFV	AVIMDNFDYL	TRDWSILGPH	1500
5	HLDEFKRIWS	EYDPEAKGRI	KHLDVVTLRL	RIQPPPLGFGK	LCPHRVACKR	LVAMNMPLNS	1560
	DGTVMFNATL	FALVRTALKI	KTEGNLEQAN	EBLRAVIRKI	WKRTSMKLLD	QVVPAGDDE	1620
	VTVGKIFYATF	LIQDYFRKFK	KRKEQGLVGK	YPAKNTTIAL	QAGLRLTHDI	GPEIRRAISC	1680
	DLQDDEPEET	KREEDDVFK	RNGALLGNHV	NHVNSDRRDS	LQQTNTTHRP	LHVQRPSIPP	1740
	ASDTEKPLFF	PAGNSVCHNH	HNHNSIGKQV	PTSTNANLNN	AMMSKAAHGK	RPSIGNLEHV	1800
10	SENGHSSHK	HDREPORRSS	VKRTRYETV	IRSDSGDEQL	PTICREDPEI	HGYFRDPHCL	1860
	GEQYFSSSE	CYEDDSPTW	SRQNYGYYSR	YFGRNIDSER	FRGYHHPQGF	LEDDDSFVCY	1920
	DSRRSPRRRL	LFPTPASHRR	SSFNPECLRR	QSSQEEVPSS	PFPHRTALP	LHLMQQQIMA	1980
	VAGLDSKAAQ	KYSPSHSTRS	WATPPATPPY	RDWTPCYTFL	IQVEQSEALD	QVNGSLPSLH	2040
	RSSWYTDDEP	ISYRTFTPAS	LTVPSSFRNK	NSDKQRSADS	LVEAVLISEG	LGRYARDPKF	2100
15	VSATKHEIAD	ACDLTIDEME	SAASTLLNGN	VRPRANGDVG	PLSHRQDYEL	QDFGPGYSDE	2160
	EPDFGRDEED	LADEMICITT	L				

SEQ ID NO:289 OB16 DNA SEQUENCE

Nucleic Acid Accession#: NM_002812

Coding sequence: 150-3362 (underlined sequence corresponds to start and stop codon)

20

	1	11	21	31	41	51	
25	AAC	TCCGGGACGCC	TCGGGGTTCGG	GCTCGGCTG	CGGCTGCTGC	TGCGGCGCCC	60
	GCGCTCCGGT	GCGTCCGCCT	CCTGTGCCCG	CCGCGGAGCA	GTCTGCGGCC	CGCGTGCGGC	120
	CCTCAGCTCC	TTTTCCTGAG	CCCGCCGCGA	TGGGAGCTGC	GCGGGGATCC	CCGGCCAGAG	180
	CCCGCCGGTT	GCCTCTGCTC	AGCGTCTCTG	TGCTGCCGCT	GCTGGGCGGT	ACCCAGACAG	240
	CCATTGCTCT	CATCAAGCAG	CCGTCTCTCC	AGGATGCATC	GCAGGGGCGC	CGGGCGCTGC	300
30	TTCTGCTGTG	GATTGAGGCT	CCGGGCGCGG	TACATGTGTA	CTGGCTGCTC	GATGGGCGCC	360
	CTGTCCAGGA	CAGGAGCGGG	CGTTTCGCCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
	ACCGGCTGCA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480
	AAGCCCGCAG	TGCCCAACGCC	TCCTTCAACA	TCAAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
	TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTCACA	CTTCTGTGCC	600
35	ACATTGATGG	GCACCCCTCG	CCCACCTACC	AATGGTPTCC	AGATGGGACC	CCCCTTCTCT	660
	ATGGTCAGAG	CAACCCACACA	GTCAAGCAGCA	AGGAGCGGAA	CCTGACGCTC	CGGCGAGCTG	720
	GTCTCTAGCA	TAGTGGGCTG	TATTCCTGCT	GCGCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
	GCAGCCAGAA	CTTCACTTGT	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
	CCCAGGACGT	GGTAGTAGCG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TTCTCTAGCCC	900
40	AGCCACCCCT	GAGCCTCGAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
	GCCCCCGACA	CCTCCGCGAG	GCCACAGTGT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
	TCCGCGCAGC	CAATGACAGG	ATCTACCGCT	GCAATTGGCA	GGGGCAGAGG	GGCCCAACCA	1080
	TCATCTCTGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
	GGGTGTTTAC	AGCTGGCAGC	GAGGAGCGTG	TGACCTGCCT	TCCCCCAAG	GGTCTGCCAG	1200
45	AGCCACCGCT	GTGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGTCTACC	1260
	AGAAGGGCCA	CGAGCTGGTG	TTGGCCATA	TTGCTGAAG	TGATGCTGGT	GTCTACACCT	1320
	GCCACCGCGC	CAACCTGGCT	GGTCAGCGGA	GACAGGATGT	CACACATCACT	GTGGCCACTG	1380
	TGCCCTCTCT	GCTGAAGAAG	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCCGGCTACT	1440
	TGGATTGCTG	GACCCAGGCC	ACACAAAAAC	CTACAGTTGT	CTGGTACAGA	AACCCAGATGC	1500
50	TCATCTCAGA	GGACTCAGCG	TTGAGGTTCT	TCAAGAAATG	GACCTTGGCG	ATCAACAGCG	1560
	TGGAGGTGTA	TGATGGGACA	TGGTACCGTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
	AGGCGCAAGC	CCGTGTCCAA	GTGCTGGAAA	AGCTCAAGTT	CACACCACCA	CCCCAGCCAC	1680
	AGCAGTGCAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCGCTG	TTCAGCCACA	GGCCGAGAGA	1740
	AGCCCATAT	TAAGTGGGAA	CGGGCAGATG	GGAGCAGCCT	CCCAGAGTGT	GTGACAGACA	1800
55	ACGCTGGGAC	CCTGCATTTT	GCCCCGGTGA	CTCAGATGTA	CGCTGGCAAC	TACACTTGCA	1860
	TTGCTTCCAA	CGGGCCGACG	GGCCAGATTG	GTGCCCATGT	CCAGCTCACT	GTGGCAGTPT	1920
	TTATCACCTT	CAAAGTGGAA	CCAGAGCGTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
	TGCAGTGCGA	GGCCCAAGGG	GACCCCAAGC	CGCTGATTTA	GTGGAAGAGC	AAGGACCGCA	2040
	TCCTGGACCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAATGGC	TCCCTGGTGA	2100
60	TCCATGACGT	GGCCCTTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAAGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCCCTCTAT	TCTGGGACAA	GCCTGTGCGG	GAGGAGTCGG	2220
	AGGGCCCTGG	CAGCCCTCCC	CCCTACAGCA	TGATCCAGAC	CATTGGGTTG	TCCGTGGGTTG	2280
	CCGCTGTGGC	CTACATCAAT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAAGCG	GCTGCAGAAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCCTCAACG	2400
65	GAGGGCCTTT	GCAGAACCGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCCGGC	GCCACCAACA	AAGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCCAAGGTC	TAGCTTGACG	CCCATCAACA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTTGGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGAGTTTG	GAGATGTTTG	2700
70	GGAAAGCTGA	CCACGCCAAC	GTGGTGGCGC	TCCTGGGGCT	GTGCGGGGAG	GCTGAGCCCC	2760
	ACTACATGCT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCCT	AGGATTTCCA	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACCTGCTG	GTCAGTGCCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
75	TCAGCAAGGA	TGTGTACAA	AGTGAGTACT	ACCACCTCCG	CCAGGCTGGG	GTGCCCTGTC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGCTGGGG	3120
	CCCTCGGTGT	GCTGATGTGG	GAAAGTGTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
	CAGATGATGA	AGTACTGGCA	GATTTCAGAG	CTGGGAAGGC	TAGACTTCTT	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
80	GGCCCTCCTT	CAGTGAATTT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCCTCAGG	ATGGCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420

5
10
15

CAGCATGATG GGCAAGATCC CTGTCTCTCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA 3480
 TTGCTGAGGT CTGAGCAGGG CCTGGCCCTTT CCTCTCTTTC CTCACCTCTCA TCCTTTGGGA 3540
 GGTGACTTGG GACCCAAACT GGGCGACTAG GGTCTTGAGC TGGGCAGTTT CCCCTGCCAC 3600
 CTCTTCTCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAAC CCCAATTCTT GGCCTTCAAC 3660
 TTCTCCCTCT GACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGGCTT GGGGAGGGCT 3720
 AGGCTTGGGA TGAGCTGGGT TTGTGGGGAG TTCCTTAATA TTCTCAAGTT CTGGGCACAC 3780
 AGGGTTAAATG AGTCTCTTGC CCACCTGGTCC ACTTGGGGGT CTAGACCAGG ATTTATAGAGG 3840
 ACACAGCAAG TGATCTCTCC CCACCTCTGGG CTGTGTGACA CTGACCCAGA CCCACGTCTT 3900
 CCCACCCCTT CTCTCTCTTC CTCATCTTAA GTGCCTGGCA GATGAAGGAG TTTTCAGGAG 3960
 CTTTTGACAC TATATAAACG GCGCTTTTTC TATGCACCAC GGGCGGGCTT TATATGTAAT 4020
 TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CTTGAGATG AGGAGGGTGG 4080
 GCCATCTCTA CCCACACTT TTATTGTGTG CGTTTTTGTG TTGTTTTGTG TTTTGTGTTT 4140
 TGTTTTTGTG TTTACACTCG CTGCTCTCAA TAAATAAGCC TTTTTTA

SEQ ID NO:290 ORF6 Protein sequence:

Protein Accession #: NP_002812

20
25
30
35
40

1 11 21 31 41 51
 | | | | |
 MGAARGSPAR PRRLLPLLSVL LLPLLGTTQT AIVFIKQPSQ QDALQGRRAL LRCEVEAPGP 60
 VHVYWLDDGA FVQDTERFPA QSSLSFAAV DRLQDSCTFQ CVARDDVTGE EARSANASFN 120
 IKWIEAGFPV LKHPASEAEI QPQTQVTLRC HLDGHPRTY QWFRDGTPLS DGQSNHTVSS 180
 KERNLTLRPA GPEHSGLYSC CAHSAGGQAC SSQNFSLTSLA DESFARVULA FQDVVVARYE 240
 EAMFHCFQSA QPPPSLQWLF EDETPTNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR 300
 CIGQGQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCPLPKGLF EPSVWWEHAG 360
 VRLPHTGRVY QKHGELVLAN LAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKPKPD 420
 SLEEGCKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFV FKNGLRINS VEVYDGTWYR 480
 CMSSTFAGSI BAQARVQVLE KLFKTPPPQP QCCMEFDKEA TVPCSATGRE KPTIKWERAD 540
 GSSLPEWTFD NAGTLHFARV TRDDAGNYTC IASNGFPQQI RAHVQLTVAV FITEKVEPER 600
 TTVYQGHIAL LQCEAQSDPK PLIQWKGKDR ILDPKLGPR MHIFQNGSLV IHDVAPEDSG 660
 RYTCIAGNSC NIKHTEAPLY VVDKFPVEES EGFGSPPPYK MIQTIGLSVG AAVAYIIAIVL 720
 GLMFYCKKRC KAKRLQKQPE GEPEMECLN GGFLONGQPS AEIQEEVALT SLGSGPAATN 780
 KRHSTDGMH FPRSSLQPTT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840
 LDPRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSK 900
 PLSTKQKVAL CTQVALGMEH LSNRNFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
 YHFRQAWVPL RWSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLADLQ 1020
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP

SEQ ID NO:291 AAB1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002205

Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

45
50
55
60
65
70
75
80

1 11 21 31 41 51
 | | | | |
 ATGGGGAGCC GGAGCCGAGA GTCCCTCTCT CACGCCGTGC AGCTGCGCTG GGGCCCCCGG 60
 CGCCGACCCC GCGTSSSTGC GCTGCTGTGG CTGCTSSSTGC CGCCGCCACC CAGGGTCGGG 120
 GGCTTCAACT TAGACGCGGA GGCCCCAGCA GTACTCTCGG GGGCCCCGGG CTCTTCTTTC 180
 GGATTCTCAG TGGAGTTTAA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCCAAGGCTA ATACAGGACA GCCAGGAGTG CTGACGGGTG GTGCTGTCTA CCTCTGTCTC 300
 TGGGGTGCCA GCGCCACACA GTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCTCGGCTC 360
 CTGAGTGTCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCTTGTGAG 420
 TGGTTCGGGG CAACAGTTTC AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCTGCGCGCT CAGATTTAG CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGCAGTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAAGAT CTATTATACC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840
 TTCACTGTGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCTCTAA TGGCTCAGAC ATTCTGATCC TCTACAATT CTGAGGGGAA 960
 CAGATGGCCT CCTACTTTGG CTATGCACTG GCGGCCACAG ACCTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGTCTC ATGGATCGGA CCCCTGACGG CGGCGCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CAGCCCCACC 1140
 CTTACCTTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTTTGT ATTTCTCTGG GCGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
 CAGGTTCTGC AGCCCTCTGG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACCTTGA TGGCAATGGA TATCTCTGATC TGATTGTGGG GTCTTCTGGT 1440
 GTGGACAAGG CTGTGTGTATA CAGGGGCCGC CCCATCTGTG CCGCTAGTGC CTCCCTCACC 1500
 ATCTTCCCCG CCATGTCTCA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
 GCCTGCATCA ACCTTAGCTT CTGCTCAAT GCTTCTGGAA AACACGTTCG TGAATCCATT 1620
 GGTTCACAG TGGTACTTCA GCTGGACTGG CAGAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCCTGG CCTCCAGGCA GGCAACCTTG ACCCAGACCC TGGTCAATCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
 CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
 CACGCGCTCA GGCACGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCCTG ACCTGCAGCT GGAAGTGTTC 1980

5
10
15
20

```

GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAAATGCCC TGAACCTCAC TTTCATGOC 2040
CAGAAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGSTACCGC CCTCCAGAG 2100
GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
TTTGCCGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340
TCCTTTCGGC TCTCCGTGGA GGCTCAGGCC CAGGTCACCC TGAACGGTGT CTCCAAGCCT 2400
GAGGCAGTGC TATTTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCC CAGCTCCATT 2520
AGCCAGGGTG TGCTGGAAC TCACTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT 2580
GTGACCAGAG TTACGGGACT CAATGCAACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640
GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGAAGCTCC AAGCCGAGC 2700
TCTGCTTCCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTC CAGGCTGCGC 2760
TGTGAGCTCG GGCCCTTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC 2820
TGGGCCAAGA CTTTCCTGCA CGGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCAGGC AGCTGCCCCA AAAAGAGCGT 2940
CAGGTGGCCA CAGCTGTGCA ATGGAACCAAG GCAGAAAGCA GCTATGGCGT CCCACTGTGG 3000
ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CGCCATGGA AAAGCTCAG 3120
CTCAAGCCTC CAGCCACCTC TGATGCCTGA

```

SEQ ID NO:292 AAB1 Protein sequence:

Protein Accession #: NP_002196

25
30
35
40
45

```

1 11 21 31 41 51
MGSRTPEPL HAVQLRWGFR RRPPLLPPLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCE WGAAPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEFVEYKSLQ WFGATVRAHG SSLACAPLY SWRTEKEPLS DPVGTCTYLS 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFKTKGRV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQQLQT RQASSIYDDS YLGYSVAUGE FSGDDTDFV AGVPKGNLTY 300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPELL MDRTPDGRFP 360
EVGRVYYVLQ HPAGVBPTPT LTLTGHDFFG RFGSSLTPLG DLDQDGVNDV AIGAPFGGET 420
QQGVVVFYFP GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGG YPDLVGSFG 480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCIN ASGKHVADSI 540
GFTVELQLDW QKQGGVRRRA LFLASRQATL TQTLTIQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNF SLDPAQVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLDG KNALNLTFHA QNVGEGGAYE AELRVTAPE AEYSGLVRHP GNFSLSLSDY 720
FAVNQSSLLV CDLGNPMKAG ASLWGGRLFT VPHLRDTKRT IQDFQLLSK NLNNSQSDVV 780
SFRLSVEAQA QVTNLGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPESGLHH QKREAPSR 900
SASSGPILK CPEABCFRLR CELGPLHQBE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

```

SEQ ID NO:293 LBH4 DNA SEQUENCE

Nucleic Acid Accession #: BC001291

Coding sequence: 44-541 (start and stop codons are underlined)

50
55
60
65
70
75

```

1 11 21 31 41 51
GGGGGCGCCG CGCGCTGACC CTCCCTGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT 60
GCTGCTGGTC GTGGCCCTAC CGCGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
AGATCCAGAG AACTCCAGC GAACGGACGA GGTGACAACT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTCG AGTGCCAGAA CCAAGGAGG TGCAAATGGA CAGAGCCATA 240
CTGCGTTATA GCGGCCGTGA AAATATTTC ACCTTTTTC ATGGTTGCGA AGCAGTGCTC 300
CGCTGTTTGT GCGCCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCATGCCC TTCTTTTACC TCAAGTGTG TAAAATTGCG TACTGCAATT TAGAGGGGCC 420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCCTCC TGCTGCTGGC CTCCATTGCA GCCGGCCTCA GCCTGTCTTG 540
AGCCACGGGA CTGCCACGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
ACCTGTGCA TTAACCTGT TTTCTGTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660
GGGATGGGAG AGTGGGGATC AGGTGCAGT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
ACATTCAAG AGAGTCCAGA TCTCCTGAGT AGTGATTITG GTGACAAGTT TTTCTCTTGT 780
AAATCAAACC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CCCCCTCTG 840
CCTCTGAGGG CTTCAGTATT GATGGGGAGG GAGGCCTAAG TACCACATCAT GGAGAGTATG 900
TGCTGAGATG CTTCGGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGAGTGG GGCACACGTT 1020
AGGGCTGCCC CCAATCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTC TCAACCTTTC 1080
CTACAGATT CCAGGAGGCA GAAGATAACT AATTGTGTG AAGAACTTA GACTTCAACC 1140
ACCAGCTGGC ACAGGTGCAC AGATTCTATA ATCCACACAC GTGTGTGTTT AACATCTGAA 1200
ACTTAGGCCA AGTAGAGAGC ATCAGGTGTA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAAAATA ACAAGGGGAC 1320
TTCAAAAGTT CACGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

```

SEQ ID NO:294 LBH4 Protein sequence:
 Protein Accession #: AAH01291

5 1 11 21 31 41 51
 | | | | | |
 10 MALLALLLVV ALPRVWTDAN LTARQRDPED SQRIDEGDNR VWCHVCEREN TFECQNPRRC 60
 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEPMPPF FYLKCKCKIRY 120
 CNLEGPPIINS SVFKEYAGSM GESCGGLWLA ILLLASIAA GLSLS

15 It is understood that the examples described above in no way serve to limit the
 true scope of this invention, but rather are presented for illustrative purposes. All
 publications, sequences of accession numbers, and patent applications cited in this
 specification are herein incorporated by reference as if each individual publication or patent
 20 application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a prostate cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat prostate cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having
2 prostate cancer.

1 13. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a prostate cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated transcript to a level of the prostate cancer-
3 associated transcript in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a prostate cancer-associated antibody in the
6 biological sample by contacting the biological sample with a polypeptide encoded by a
7 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
8 as shown in Tables 1-16, wherein the polypeptide specifically binds to the prostate cancer-
9 associated antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated antibody to a level of the prostate cancer-
3 associated antibody in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.

1 18. The method of claim 16, wherein the patient is a human.

- 1 19. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring
9 the efficacy of the therapy.
- 1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated polypeptide to a level of the prostate cancer-
3 associated polypeptide in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 21. The method of claim 19, wherein the patient is a human.
- 1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-16.
- 1 23. The nucleic acid molecule of claim 22, which is labeled.
- 1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label
- 1 25. An expression vector comprising the nucleic acid of claim 22.
- 1 26. A host cell comprising the expression vector of claim 25.
- 1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-16.
- 1 28. An antibody that specifically binds a polypeptide of claim 27.
- 1 29. The antibody of claim 28, further conjugated to an effector component.

- 1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.
- 1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 32. The antibody of claim 29, which is an antibody fragment.
- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a prostate cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to prostate cancer in a
2 patient, the method comprising contacting a biological sample from the patient with a
3 polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-16.
- 1 38. A method for identifying a compound that modulates a prostate cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a prostate cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.

- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.
- 1 44. A method of inhibiting proliferation of a prostate cancer-associated
2 cell to treat prostate cancer in a patient, the method comprising the step of administering to
3 the subject a therapeutically effective amount of a compound identified using the method of
4 claim 38.
- 1 45. The method of claim 44, wherein the compound is an antibody.
- 1 46. The method of claim 45, wherein the patient is a human.
- 1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having prostate cancer or a
3 cell isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of prostate cancer.
- 1 48. The assay of claim 47, wherein the control is a mammal with prostate
2 cancer or a cell therefrom that has not been treated with the test compound.
- 1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having prostate cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having prostate
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

1 52. The method according to claim 1, wherein said biological sample is
2 contacted with a plurality of polynucleotides comprising a first polynucleotide that
3 selectively hybridizes to a sequence at least 80% identical to a first sequence as shown in
4 Tables 1-16; and a second polynucleotide that selectively hybridizes to a second sequence at
5 least 80% identical to a second sequence as shown in Tables 1-16.

1 53. A method according to claim 52, wherein the plurality of
2 polynucleotides comprises a third polynucleotide that selectively hybridizes to a sequence at
3 least 80% identical to a third sequence as shown in Tables 1-16..

1 54. A method of detecting a prostate cancer associated transcript, the
2 method comprising contacting a biological sample from the patient with a plurality of
3 polynucleotides wherein at least two of said polynucleotides selectively hybridize to a
4 difference sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 55. A method of detecting a prostate cancer, the method comprising the
2 steps of:

3 (i) providing a biological sample from a patient;

4 (ii) contacting the biological sample with a first polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a first sequence as shown in Tables 1-16 to
6 determine the level of a prostate cancer-associated transcript in the biological sample; and
7 with a second polynucleotide that selectively hybridizes to a second sequence at least 80%
8 identical to a sequence not shown in Tables 1-16; wherein the expression of said second
9 sequence is not substantially changed in prostate cancer, to determine the level of expression
10 of a control transcript in the biological sample;

11 (iii) comparing the level of the prostate cancer-associated transcript to a level
12 of the normal tissue associated transcript in the biological sample.

1 56. A method of quantitating a prostate cancer-associated transcript in a
2 cell from a patient, the method comprising contacting a biological sample from the patient
3 with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a
4 sequence as shown in Tables 1-16.

1 57. The method of claim 56, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.

1 58. The method of claim 56, wherein the biological sample is a tissue
2 sample.

1 59. The method of claim 56, wherein the biological sample comprises
2 isolated nucleic acids.

1 60. The method of claim 56, wherein the nucleic acids are mRNA.

1 61. The method of claim 59, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.

1 62. The method of claim 56, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.

1 63. The method of claim 56, wherein the polynucleotide is labeled.

1 64. The method of claim 63, wherein the label is a fluorescent label.

1 65. The method of claim 56, wherein the polynucleotide is immobilized on
2 a solid surface.

1 66. The method of claim 56, wherein the patient is undergoing a
2 therapeutic regimen to treat metastatic prostate cancer.

1 67. The method of claim 56, wherein the patient is suspected of having
2 metastatic prostate cancer.

1 68. A biochip comprising a plurality of polynucleotides that selectively
2 hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 69. A method of screening drug candidates comprising:
2 i) providing a cell that expresses an expression profile gene selected from the
3 group consisting of an expression profile gene set forth in Tables 1-16 or fragment thereof;
4 ii) adding a drug candidate to said cell; and
5 iii) determining the effect of said drug candidate on the expression of said
6 expression profile gene.

1 70. A method according to claim 59 wherein said determining comprises
2 comparing the level of expression in the absence of said drug candidate to the level of
3 expression in the presence of said drug candidate.

1 SF 1277890 v1